

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:25 ; Search time 3588.29 Seconds
(without alignments)
19096.316 Million cell updates/sec

Title: US-09-647-140A-1
Perfect score: 4231
Sequence: 1 gacagcggtgcgcgcga.....ttcatttgaattttctccc 4231

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
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 - 2: em_esthm.*
 - 3: em_esthu.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
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 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: gb_gss.*
 - 18: em_gss_hum.*
 - 19: em_gss_inv.*
 - 20: em_gss_pin.*
 - 21: em_gss_vit.*
 - 22: em_gss_fun.*
 - 23: em_gss_mam.*
 - 24: em_gss_mus.*
 - 25: em_gss_Other.*
 - 26: em_gss_pro.*
 - 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734	17.3	1084	13	BM462073
2	706.6	16.7	1139	14	BQ069612
3	664.8	15.7	896	14	BQ889997
4	636.4	15.0	682	12	BE879353
5	612.4	14.5	727	12	BE879718
6	582.8	13.8	689	13	BI771442

7	546	12.9	926	12	BE885514
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10	454.8	10.7	639	10	BE225682
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14	429.2	10.1	628	10	BB623281
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26	362	8.6	635	9	AU130197
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35	308.6	7.3	486	12	BF889744
36	294.8	7.0	510	11	U66686
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ALIGNMENTS

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KEYWORDS	human.				
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1084)				
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Clone Sequencing by: Agencourt Bioscience Corporation found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12111 row: c column: 19 High quality sequence stop: 657. Location/Qualifiers 1..1084				
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AJ453358	AJ453358
AI893173	md07d11.y
AJ453340	AJ453340
AA305627	EST176623
BM048029	603620348
BM553694	AGENCOURT
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1139)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2061 row: n column: 21
High quality sequence start: 10
High quality sequence stop: 618.
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Best Local Similarity 98.4%; Pred. No. 1.8e-188;
Matches 745; Conservative 0; Mismatches 9; Indels 3; Gaps 3;
QY 12 GCGCGCGAGCCCCAGCATCCCTGCTTGAGGTCCAGGAGCGGAGCCCGCGCCACCGCG 71
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QY 72 CCTGATCAGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 131
Db 83 CCTGATCAGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
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QY 312 AAGAAGTTTTTAAGAGCTGAGAAATGACGACACAGACCCCTTCTTTTAAACAGAGCAATATAA 371
Db 323 AAGAAGTTTTTAAGAGCTGAGAAATGACGACACAGACCCCTTCTTTTAAACAGAGCAATATAA 382

Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Prepared by: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9685 row: i column: 03
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Location/Qualifiers
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Average insert size 1.1 kb. Library constructed by Life Technologies."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 727)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Prepared by: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9682 row: b column: 06
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Average insert size 1.1 kb. Library constructed by Life Technologies."
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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RESULT 8
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DEFINITION DKF2p686F08149 5', mRNA sequence.
ACCESSION AL701816
VERSION AL701816.1 GI:19685172
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: Wambutt R
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKF2p686F08149) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1. .497
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p686F08149"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
BASE COUNT 159 a 84 c 126 g 128 t
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Best Local Similarity 99.6%; Pred. No. 2.5e-125;
Matches 495; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1581 TGAGGAGTAATATTTTATTTGGGAAGAAATATGAAAGGACGATATCAAAAGCTCATAA 1640
Db 1 TGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAGGACGATATCAAAAGCTCATAA 60
QY 1641 AGGCTTGCTCTCAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTGTGATAG 1700
Db 61 AGGCTTGCTCTCAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTGTGATAG 120
QY 1701 GAGATCGGGGAACACCTCAGTGGAGGCGAAGAACCGGTTAAACCTTGCAGAGACAG 1760
Db 121 GAGATCGGGGAACACCTCAGTGGAGGCGAAGAACCGGTTAAACCTTGCAGAGACAG 180
QY 1761 TGTATCAAGATGCTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGTAGTCGGAAG 1820
Db 181 TGTATCAAGATGCTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGTAGTCGGAAG 240
QY 1821 TTAGCAGACACTTGTTCGAACTGTGATTTTGCATGAGAAGATCAACAATTT 1880
Db 241 TTAGCAGACACTTGTTCGAACTGTGATTTTGCATGAGAAGATCAACAATTT 300
QY 1881 TAGTGACTCATCATGTTGTCAGTACCTCAAGCTGCAAGTTCAGATTTCTGATTTAAAGATG 1940

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Db 301 TAGTACTCATGTTGCGAGTACCTCAAGCTGCAAGTCAGATTCAGATTCGATTTGAAGATG 360
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QY 1941 GTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGATATAGATTTGGCT 2000
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Db 361 GTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGATATAGATTTGGCT 420
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QY 2001 CCCTTTAAAGAGGATATAGAGGAAGTGAACAACCTCCAGTTCAGGAA-CTCCACA 2059
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Db 421 CCCTTTAAAGAGGATATAGAGGAAGTGAACAACCTCCAGTTCAGGAACTCCACA 480
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QY 2060 CTAAGGAATCGTACCTT 2076
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Db 481 CTAAGGAATCGTACCTT 497

RESULT 9
BE674208/c
LOCUS BE674208 478 bp mRNA linear EST 08-SEP-2000
DEFINITION 7d76907.x1 NCI-CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278940 3'
similar to TR:075555 075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA
sequence.
ACCESSION BE674208
VERSION BE674208.1 GI:10034749
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: rcapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 446.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3278940"
/clone_lib="NCI-CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI-CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 122 a 107 c 80 g 168 t 1 others
ORIGIN

Query Match 11.0%; Score 467.4; DB 10; Length 478;
Best Local Similarity 98.5%; Pred. No. 8.5e-121;
Matches 471; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3287 CTGAGCATCTGACGAGCACTCATTAATCAACAAGAAAGTTGGCATTTGGGAAGAAC 3346
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Db 478 CTGAGCATTTGACGAGCACTCATTAATCAACAAGAAAGTTGGCATTTGGGAAGAACT 419
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QY 3347 GGAGCTGGAAGAAAGTTCCTCATCTCAGCCCTTTTAGATTGTCAGAACCGAGGTAAA 3406
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Db 418 GGAGNTGGAAGAAAGTTCCTCATCTCAGCCCTTTTAGATTGTCAGAACCTGAAGGTAAA 359
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QY 3407 ATTGGATTGATAGATCTTTGACAACCTGAAATTTGGACTTCACGATTTTAAAGGAAGAAATG 3466
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Db 358 ATTGGATTGATAGATCTTTGACAACCTGAAATTTGGACTTCACGATTTTAAAGGAAGAAATG 299
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QY 3467 TCAATCATACCTCAGGAACCTGTTTGTCTCAGTGAACAATGAGGAAAAAACCCTGGATCCC 3526
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Db 298 TCAATCATACCTCAGGAACCTGTTTGTCTCAGTGAACAATGAGGAAAAAACCCTGGATCCC 239
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QY 3527 TTTAAGGAGCACACGCGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAA 3586
|||||
Db 238 TTTAATGAGCACACGCGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAA 179
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QY 3587 ACCATTGAAGATCTTCTGTGTAATAATGGATACCTGAATTAGCAGAATCAGGATCCAAATTTT 3646
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Db 178 ACCATTGAAGATCTTCTGTGTAATAATGGATACCTGAATTAGCAGAATCAGGATCCAAATTTT 119
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QY 3647 AGTGTGGACAACAAGAACCTGTTGCTGCTCCAGGCAATTCACGAAAAAATCAGATA 3706
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Db 118 AGTGTGGACAACAAGAACCTGTTGCTGCTCCAGGCAATTCACGAAAAAATCAGATA 59
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QY 3707 TTGATTATTGATGAAGCGAGCGCAAAATGTGGATCCAGAACTGATGATTAATACAAA 3764
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Db 58 TTGATTATTGATGAAGCGAGCGCAAAATGTGGATCCAGAACTGATGATTAATACAAA 1

RESULT 10
LOCUS BB225682
DEFINITION BB225682 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530093I19 3' similar to U83660 Human multidrug
resistance-associated protein homolog (MRP4) mRNA, mRNA sequence.
ACCESSION BB225682
VERSION BB225682.2 GI:16353983
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 639)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
On Jul 3, 2000 this sequence version replaced gi:8896327.
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
waghi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format

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[illegible]

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RESULT 12
LOCUS      AUI26646
DEFINITION AUI26646 NT2RP1 Homo sapiens cDNA clone NT2RP1001350 5', mRNA
sequence.
ACCESSION  AUI26646
VERSION     AUI26646.1 GI:10951362
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota.T., Nishikawa.T., Suzuki.Y., Kawai.Y., Ishii.S., Saito.K.,
Nakamura.Y., Nagai.T., Sugano.S. and Isogai.T. Suzuki.Y., Kawai.Y.,
HRI human cDNA project (Ota.T., Nishikawa.T., Suzuki.Y., Kawai.Y.,
Ishii.S., Saito.K., Nakamura.Y., Nagai.T., Sugano.S., Isogai.T.)
Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
            Location/Qualifiers
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                /clone_lib="NT2RP1"
                /cell_type="teratocarcinoma"
                /cell_line="NT2"
FEATURES
Source

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/note="Vector: pUC19FLU3; mRNA from NT2 neuronal precursor
cells after 48-hours retinoic acid (RA) induction"
BASE COUNT      161 a      80 c      106 g      115 t      3 others
ORIGIN
Query Match      10.2%; Score 433; DB 9; Length 465;
Best Local Similarity 98.6%; Pred. No. 4.8e-111;
Matches 436; Conservative 0; Mismatches 6; Indels 0; Gaps 0
QY 3480 AGSAACCTCTTTTGTTCACCTGCAACAACTCAGAAAAACCTGGATCCCTTTAAGGAGCACA 3539
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Db 14 AGGAACCTCTTTTGTTCACCTGGAACAAATGAGAAAAACCTGGATCCCTTTAATGAGCACA 73
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QY 3540 CGGATGAGGAACCTGTGGAATGCTTACAGAGGTCAACCTTAAAGAAACCATTTGAAGATC 3599
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Db 74 CGGATGAGGAACCTGTGGAATGCTTACAGAGGTCAACCTTAAAGAAACCATTTGAAGATC 133
      |||||
QY 3600 TTCTCGTAAAAATGGATACTGAATTAGCAGAACTCAGGATCCAAATTTTACTGTGTGGACAAA 3659
      |||||
Db 134 TTCTCGTAAAAATGGATACTGAATTAGCAGAACTCAGGATCCAAATTTTACTGTGTGGACAAA 193
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QY 3660 GACAACCTGGTGTGCCCTTGCCAGGGCAATTCCTCAGGAAAAATCAGATATTTGATTATTGATG 3719
      |||||
Db 194 GACAACCTGGTGTGCCCTTGCCAGGGCAATTCCTCAGGAAAAATCAGATATTTGATTATTGATG 253
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QY 3720 AAGCGACGCGCAAACTGTGATCCAAAGACTGATGAGTTATACAAAAAATCCGGGAGA 3779
      |||||
Db 254 AAGCGACGCGCAAACTGTGATCCAAAGACTGATGAGTTATACAAAAAATCCGGGAGA 313
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QY 3780 AATTTGCCCACTGCACCGTGCTTAACCATTTGCACAGATTTGAACACCATTTATGACAGCG 3839
      |||||
Db 314 AATTTGCCCACTGCACCGTGCTTAACCATTTGCACAGATTTGAACACCATTTATGACAGCG 373
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QY 3840 ACAAGATAATGGTTTTAGATTACGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTTTCG 3899
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Db 374 ACAAGATAATGGTTTTAGATTACGGAAGACTGAAAGAAATATGATGATGATGTTTTGCG 433
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QY 3900 TGCAAAAATAAGAGAGCGCTATT 3921
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Db 434 GGC AAAATAAGAGAGCGCCTTTT 455
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RESULT 13	
BB643073	
LOCUS	734 bp mRNA linear EST 26-OCT-2001
DEFINITION	BB643073 RIKEN full-length enriched, 9.5 days embryo parthenogenotome
ACCESSION	Mus musculus cDNA clone B130008G09 5', mRNA sequence.
VERSION	BB643073.1 GI:16477826
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 734)
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki, D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL: http://genome.qsc.riken.go.jp/

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:00:25 ; Search time 529.063 Seconds
(without alignments)
18009.573 Million cell updates/sec

Title: US-09-647-140A-1

Perfect score: 4231

Sequence: 1 gacaggcgctggcgccgga.....ttcattgaattttcc 4231

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23:	/SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4231	100.0	4231	22	AAH81778
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4	4211	99.5	6082	22	AAH93828
5	4211	99.5	6082	22	AAH85142
6	4211	99.5	6082	22	AAH85142
7	4196.6	99.2	4515	23	ABV24580
8	4196.6	99.2	4515	23	ABV24580
9	4196.6	99.2	4515	23	ABV24580

10	4196.6	99.2	4515	23	ABV24580
11	4196.6	99.2	4515	23	ABV24580
12	4196.6	99.2	4515	23	ABV24580
13	3973.2	93.9	3978	24	AAK92135
14	3910.2	92.4	6140	22	AAS63922
15	3910.2	92.4	6140	22	AAH93829
16	3910.2	92.4	6140	22	AAH85143
17	3910.2	92.4	6140	22	ABV24580
18	1218	28.8	1427	21	AAH16178
19	1045.4	24.7	1074	22	AAS64134
20	1045.4	24.7	1074	22	AAH93898
21	1045.4	24.7	1074	24	ABV24580
22	796	18.8	888	23	ABV24580
23	707.4	16.7	768	23	ABV12837
24	655.4	15.5	3391	23	ABV12837
25	655	15.5	2275	21	AAH81778
26	621	14.7	684	23	ABV33965
27	611.8	14.5	5504	23	ABV33965
28	589.8	13.9	633	23	ABV33965
29	569.4	13.5	4507	23	ABV33965
30	563.6	13.3	12059	23	ABV33965
31	551.6	13.0	7743	23	ABV33965
32	546.6	12.9	4351	23	ABV33965
33	541.6	12.8	643	23	ABV33965
34	528.8	12.5	4047	23	ABV33965
35	512.6	12.1	3720	23	ABV33965
36	491.8	11.6	4035	23	ABV33965
37	489.4	11.1	8496	23	ABV33965
38	460.2	10.9	486	18	AAH81778
39	450.4	10.6	4918	24	ABV33965
40	448.8	10.6	4918	18	AAH81778
41	439.6	10.4	4041	23	ABV33965
42	437.4	10.3	4781	22	AAH81778
43	437.4	10.3	4847	19	AAH81778
44	437.4	10.3	4847	21	AAH81778
45	437.4	10.3	5838	20	AAH81778

ALIGNMENTS

RESULT 1

AAZ30078

ID AAZ30078 standard; cDNA; 4231 BP.

XX AAZ30078;

XX AAZ30078;

DT 26-JAN-2000 (first entry)

XX cDNA encoding a human MPR-related ABC transporter designated MOAT-B.

XX Human; MPR-related ABC transporter; MOAT protein; MOAT-B;

KW MOAT mediated transport; anticancer drug sensitivity;

KW transporter mediated cellular efflux; anticancer; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

Location/Qualifiers
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/transl_except= (pos: 1715..1717, aa: Pro)
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/note= "MPR-related ABC transporter"

XX WO9949735-A1.

XX WO9949735-A1.

XX WO9949735-A1.

XX WO9949735-A1.

XX WO9949735-A1.

XX (FOXC-) FOX CHASE CANCER CENT.
 XX Kruh G, Lee K, Belinsky M, Bain L;
 XX WPI: 1999-610812/52.
 XX P-PSDB; AAY43541.
 XX New transporter gene useful for screening for anti-cancer drugs
 XX Claim 1; Page 130-131; 153pp; English.
 XX The present sequence encodes a human MPR-related ABC transporter (MOAT)
 CC protein, designated MOAT-B. The protein comprises a multi-domain
 CC structure including a tandem repeat of nucleotide binding folds
 CC appended C-terminal to a hydrophobic domain, having Walker A and B ATP
 CC binding sites and several potential membrane spanning domains. The MOAT
 CC nucleic acids are useful for screening a test compound for inhibition of
 CC MOAT mediated transport, indicated by restoration of anticancer drug
 CC sensitivity, which in turn causes a reduction of transporter mediated
 CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
 CC probes to detect the presence or expression of genes encoding MOAT
 CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
 CC MOAT proteins.
 XX Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 other;
 SQ
 Query Match 100.0%; Score 4231; DB 20; Length 4231;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGACAGCGTGGCGCGGAGCCGAGCCAGATCCCTGCTGAGTCCAGGAGCGGAGCCCG 60
 DB 1 GGACAGCGTGGCGCGGAGCCGAGCCAGATCCCTGCTGAGTCCAGGAGCGGAGCCCG 60
 QY 61 GGCCACCGCGCTGATCAGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 61 GGCCACCGCGCTGATCAGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 QY 121 GCCCGGTACACAGGAGTGAAGCCCAACCGCTGAGGAGCGGAGCAATCTGCTCAGCGCT 180
 DB 121 GCCCGGTACACAGGAGTGAAGCCCAACCGCTGAGGAGCGGAGCAATCTGCTCAGCGCT 180
 QY 181 GTTCTTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAACGGAGATTTAGAGGA 240
 DB 181 GTTCTTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAACGGAGATTTAGAGGA 240
 QY 241 TGATATGATTCAGTGTCTGCCAGAGACCGCTCAGACACCTTGGAGAGGAGTTGCAAG 300
 DB 241 TGATATGATTCAGTGTCTGCCAGAGACCGCTCAGACACCTTGGAGAGGAGTTGCAAG 300
 QY 301 GTTCTGGGATAAAGATTTTAAAGCTGAGAAATGACGACAGAGCCCTTTTAAACAAG 360
 DB 301 GTTCTGGGATAAAGATTTTAAAGCTGAGAAATGACGACAGAGCCCTTTTAAACAAG 360
 QY 361 AGCAATCAAAAGTGTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTTAAATGA 420
 DB 361 AGCAATCAAAAGTGTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTTAAATGA 420
 QY 421 GGAAGTGCCTAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTTTGAAGA 480
 DB 421 GGAAGTGCCTAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTTTGAAGA 480
 QY 481 TTATGATCCATGGATTTCTGGCTTTGAACACAGCTACGCTTATGCCAGCGTGTGAC 540
 DB 481 TTATGATCCATGGATTTCTGGCTTTGAACACAGCTACGCTTATGCCAGCGTGTGAC 540
 QY 541 TTTTGGCAGCTCATTTTGGCTTATCTGATCAGTATATTTTATCATGTTTACGTTGTC 600
 DB 541 TTTTGGCAGCTCATTTTGGCTTATCTGATCAGTATATTTTATCATGTTTACGTTGTC 600
 QY 601 TGGGATGAGTTACGAGTAGGATGCGCATGATGATTTATCGGAAGGCACTTCGCTTAG 660
 DB 601 TGGGATGAGTTACGAGTAGGATGCGCATGATGATTTATCGGAAGGCACTTCGCTTAG 660
 QY 661 TAACATGGCCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCTCAATGATGT 720
 DB 661 TAACATGGCCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCTCAATGATGT 720
 QY 721 GAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGGGAGGAGCACTGCAAGC 780
 DB 721 GAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGGGAGGAGCACTGCAAGC 780
 QY 781 GATCGCAGTCACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCCTGCTGGATGGC 840
 DB 781 GATCGCAGTCACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCCTGCTGGATGGC 840
 QY 841 AGTTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTGTCTCATCAGTGG 900
 DB 841 AGTTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTGTCTCATCAGTGG 900
 QY 901 GAGTAAACTGCAACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTTAACTGG 960
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 QY 1081 TTCGTTTTTTCAGTGCAGCAAGCAAAATCATCTGTTTGTGACCTTCACCACCTACGTCCT 1140
 DB 1081 TTCGTTTTTTCAGTGCAGCAAGCAAAATCATCTGTTTGTGACCTTCACCACCTACGTCCT 1140
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 DB 1141 CGGAGTGTGATCAGACCGCAGCGCGGTGTTGTTGGAGTGCAGCTGTATGGGGTGTGCG 1200
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 QY 1381 ATCAGAGACCCCAACTCTCAAGCGCTTTTCTTACTGTGACACCTGGCGAATTTGTAGC 1440
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 DB 1441 TGTGTCGCGCCCGTGGGAGGAGGAAATCATCATTGTTAAAGTGCCTGCTCGGGGAAT 1500
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 DB 1501 GGGCCCAAGTCAAGGCTGTCAGCGTGCATGGAAGAAATTTGCTCTCAGCAGCC 1560
 QY 1561 CTGGGTGTTCTCGGGAATCTGTAGGAGTAAATTTTATTTGGGAAGAAATATCAAAAGGA 1620
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 DB 1621 AGGATATGAAAGTCAAAAGCTTTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGA 1680
 QY 1681 TGGTATCTGACTGTGATAGGAGATCGGGAAACCGCTGAGTGGAGGCGAGAAACAG 1740
 DB 1681 TGGTATCTGACTGTGATAGGAGATCGGGAAACCGCTGAGTGGAGGCGAGAAACAG 1740

Db 601 TGGGATGAGTTACGAGTAGCCATGTGCCATATGATTATTCGGAAGCACTTCCTCTTAG 660
 QY 661 TAACATGGCCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCTCAATGATGT 720
 Db 661 TAACATGGCCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCTCAATGATGT 720
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 Db 721 GAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGGGAGGAGCACTGCAAGC 780
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 Db 841 AGTTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTGTCTCATCAGTGG 900
 QY 901 GAGTAAACTGCAACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTTAACTGG 960
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 Db 1321 GCCGTGAGATGTTAAAGATGTCATGTCAGAGGATTTTACTGCTTTTGGGATAGGC 1380
 QY 1381 ATCAGAGACCCCAACTCTCAAGCGCTTTTCTTACTGTGACACCTGGCGAATTTGTAGC 1440
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 Db 1441 TGTGTCGCGCCCGTGGGAGGAGGAAATCATCATTGTTAAAGTGCCTGCTCGGGGAAT 1500
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 Db 1621 AGGATATGAAAGTCAAAAGCTTTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGA 1680
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 Db 1681 TGGTATCTGACTGTGATAGGAGATCGGGAAACCGCTGAGTGGAGGCGAGAAACAG 1740

1741 GGTAAACCTTGAAGAGAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCT 1800
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1861 GCATGAGAAGATCACAATTTTGTAGTACTCATCAGTTGCGAGTACCTCAAGCTGCAAGTCA 1920
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1921 GATTCTGATATTGAAGATGGTAAATGTGTCAGAGGGGACTTACACTGAGTTCTCTAAA 1980
1981 ATCTGATATAGATTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAACCTCC 2040
1981 ATCTGATATAGATTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAACCTCC 2040
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2521 TGAGTCAATCTGAAGCTCCGCTATTTCTTTGATAGAATCCAATAGGAAGATTTT 2580
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2641 TTTTCATCCAGACATTTGCTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2700
2701 TTGATCGCAATACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2760
2701 TTGATCGCAATACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2760
2761 TTTTGAACAGCTCAAGAGATGTGAAGCGCTGGAATCTACAACTCGGAGTCCAGTGCTTTTC 2820
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2821 CCACTTGTCTATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAG 2880
2821 CCACTTGTCTATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAG 2880
2881 GTGTGAGGAATGTTGATGCACACAGGATTTACATTCAGAGGCTTGGTTCCTTTT 2940
2881 GTGTGAGGAATGTTGATGCACACAGGATTTACATTCAGAGGCTTGGTTCCTTTT 2940
2941 GACAACGCTCCGCTGGTTCGCTGATGCTGGATGCCATCTGTGCCATGTTGTCATCAT 3000
2941 GACAACGCTCCGCTGGTTCGCTGATGCTGGATGCCATCTGTGCCATGTTGTCATCAT 3000
3001 CGTTGCCCTTGGTTCGCTGATGCTGGATGCCATCTGTGCCATGTTGTTGGC 3060
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3061 ACTGTCTATGCCCTCAGCTCATGCTGGATGTTTCACTGGTGTGTTCCACAAAGTCTGA 3120
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3301 AGCACCTTAAATCACAAGAAAGTTGGCATTTGGGAAGAACCGGAGCTGGAAGAAG 3360
3301 AGCACCTTAAATCACAAGAAAGTTGGCATTTGGGAAGAACCGGAGCTGGAAGAAG 3360
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3421 GATCTTGAACACTGAAATTTGGATTTTCAAGATTTAAGGAAGAAATGTCAATCATCTCA 3480
3481 GGAACCTGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3481 GGAACCTGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3541 GGATGAGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
3541 GGATGAGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
3601 TCCTGGTAAATGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3601 TCCTGGTAAATGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3661 ACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3661 ACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3721 AGCGACGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
3721 AGCGACGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
3781 ATTTGCCACCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
3781 ATTTGCCACCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
3841 CAAGATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3900
3841 CAAGATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3900
3901 GCAAAATAAGAGAGACCTTATTTTACAAAGATGCTGCAACAACCTGGGCAAGCCGAGCCGCC 3960

|||||
Db 3901 GCAAAATAAGAGAGCCTATTTTACAAAGATGGTCAACAACTGGGCAAGGCAGAAAGCCGC 3960
QY 3961 TGCCTCTACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATATATCCACATATTTGGTCA 4020
Db 3961 TGCCTCTACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATATATCCACATATTTGGTCA 4020
QY 4021 CACTGACCACATGGTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACATATTTTCGA 4080
Db 4021 CACTGACCACATGGTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACATATTTTCGA 4080
QY 4081 GACAGCACTGTGAATCCCAACCAAAATGTCAAGTCCGTTCCGAGGAGCATTTTCCACTAGTT 4140
Db 4081 GACAGCACTGTGAATCCCAACCAAAATGTCAAGTCCGTTCCGAGGAGCATTTTCCACTAGTT 4140
QY 4141 TTTGGACTATGTAACACCATTTGACTTTTTTTTACTTTGGCAACAAATATTTATACATA 4200
Db 4141 TTTGGACTATGTAACACCATTTGACTTTTTTTTACTTTGGCAACAAATATTTATACATA 4200
QY 4201 CAAGATGCTAGTTCATTTGAATATTTCTCCC 4231
Db 4201 CAAGATGCTAGTTCATTTGAATATTTCTCCC 4231

RESULT 2

AAH81778
ID AAH81778 standard; DNA; 4231 BP.
XX AC
XX AAH81778;
XX
DT 21-SEP-2001 (first entry)
XX
DE Human differential transcription-associated cDNA SEQ ID 287.
XX
KW Differential transcription; human; rat; tumour cell; cytostatic;
KW Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX
XX Homo sapiens.
OS
PN WO200157058-A2.
XX
XX 09-AUG-2001.
PD
XX 31-JAN-2001; 2001WO-EP01003.
PF
XX 31-JAN-2000; 2000DE-1004102.
PR
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
PA
XX Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;
PI Grips M, Hellriegel M, Schmitz A, Sers C;
XX
XX WPI; 2001-483415/52.
XX

Nucleic acids differentially expressed between tumor and normal cells,
useful for diagnosis or therapy of tumors and for screening active
agents

Disclosure; Page 442-443; 579pp; German.

This invention describes a nucleic acid (I) with differential expression
between tumour and normal cells and which has cytostatic activity. (I)
work as modulators of Ras activity by inducing expression of tumour
suppressor genes. (I), and polypeptides encoded by them, are useful as
targets for diagnosis or therapy and in screening to determine the
effects of an active compound (potential pharmaceutical) on a cell line,
particularly for diagnosis and treatment of tumors, especially by
modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
methods) or by modulating the amount and/or location of (I)-encoded
polypeptides (by administration of the polypeptide or its activator,
antibody (optionally as a conjugate) or inhibitor). The method allows
identification of many Class II tumour suppressor genes (i.e. genes that
are not primary targets for tumour-initiating mutations).

CC AAH81492-AAH82376 represent the human and rat derived nucleic acid
CC fragments described in the method of the invention.
XX
SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 other;
Query Match 100.0%; Score 4231; DB 22; Length 4231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACAGCGTGGCGCGGAGCCCGCCAGCATCCCTGCTTGGTCCAGAGCGGAGCCGC 60
Db 1 GGACAGCGTGGCGCGGAGCCCGCCAGCATCCCTGCTTGGTCCAGAGCGGAGCCGC 60
QY 61 GGCACCGCCGCTGATCAGCGGACCCCGCCGCGCCGCCCGCCGCGCAAGATGCT 120
Db 61 GGCACCGCCGCTGATCAGCGGACCCCGCCGCGCGCCGCCCGCCGCGCAAGATGCT 120
QY 121 GCCCGTGTACAGAGGTGAAGCCCAACCCGCTGCGAGGCGCAACATCTGCTCACGGGT 180
Db 121 GCCCGTGTACAGAGGTGAAGCCCAACCCGCTGCGAGGCGCAACATCTGCTCACGGGT 180
QY 181 GTTCTTCTGCTGCTCAATCCCTTGTAAATTTGGCCATAAAGCGAGATTAGAGGA 240
Db 181 GTTCTTCTGCTGCTCAATCCCTTGTAAATTTGGCCATAAAGCGAGATTAGAGGA 240
QY 241 TGATATGTTATTCAGTGTGCGCAGAAGACCGCTCACAGCACCTTTGGAGAGGAGTTGCAAG 300
Db 241 TGATATGTTATTCAGTGTGCGCAGAAGACCGCTCACAGCACCTTTGGAGAGGAGTTGCAAG 300
QY 301 GTTCTGGGATAAAGAGTGTAAAGAGCTGAGATGAGCGCACAGAGCCCTTCTTTAAACAAG 360
Db 301 GTTCTGGGATAAAGAGTGTAAAGAGCTGAGATGAGCGCACAGAGCCCTTCTTTAAACAAG 360
QY 361 AGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAAATGA 420
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QY 421 GGAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTGAAAA 480
Db 421 GGAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTGAAAA 480
QY 481 TTATGATCCCATGGATCTGTGGCTTGAACACAGCGTACGCCCTATGCCAGGTGCTGAC 540
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Db 541 TTTTTCACGCTCATTTTGGCTATCTGCTATCTATATTTTATCAGCTTCACTGTC 600
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Db 601 TGGGATGAGGTTACGAGTAGCCCATGTGCCATATGATTTATCGGAAGCACTTCCTCTTAG 660
QY 661 TACATGCGCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGT 720
Db 661 TACATGCGCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGT 720
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Db 721 GAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGCGGAGGACCACTGCAGGC 780
QY 781 GATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTCCCTGCTGGATGGC 840
Db 781 GATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTCCCTGCTGGATGGC 840
QY 841 AGTTCTAATCATTTCTCTGCGCTTGCAGGAGTGTGTTGGGAAGTGTGTTCTCATCAGT 900
Db 841 AGTTCTAATCATTTCTCTGCGCTTGCAGGAGTGTGTTGGGAAGTGTGTTCTCATCAGT 900
QY 901 GAGTAAACTGCAACTTTCACGATGCCAGGATCAGGACCATGAATGAAGTTAACTGG 960
Db 901 GAGTAAACTGCAACTTTCACGATGCCAGGATCAGGACCATGAATGAAGTTAACTGG 960

QY	961	TATAAGGATAATAAAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTT	1020
Db	961	TATAAGGATAATAAAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTT	1020
QY	1021	GAGAAAGAGGAGATTTCAGAGATTCTGAGAAGTTCTGCTCAGGGGAGTGAATTTGGC	1080
Db	1021	GAGAAAGAGGAGATTTCAGAGATTCTGAGAAGTTCTGCTCAGGGGAGTGAATTTGGC	1080
QY	1081	TTTCGTTTTTCAGTGCAGCAAGCAAAATCATCTGTTGTGTGACCTTCACCACTACGTGCTCCT	1140
Db	1081	TTTCGTTTTTCAGTGCAGCAAGCAAAATCATCTGTTGTGACCTTCACCACTACGTGCTCCT	1140
QY	1141	CGCGAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGATGGGCTGTGGG	1200
Db	1141	CGCGAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGATGGGCTGTGGG	1200
QY	1201	GCTGACGGTTACCCCTTCCTTCCCCTCAGCCATTGAGAGGGTGTACAGAGCAATCGTCAG	1260
Db	1201	GCTGACGGTTACCCCTTCCTTCCCCTCAGCCATTGAGAGGGTGTACAGAGCAATCGTCAG	1260
QY	1261	CATCCGAAGAATCCAGACCTTTTTCCTACTTCGATGAGATATCACAGCGCAACCGTCAGCT	1320
Db	1261	CATCCGAAGAATCCAGACCTTTTTCCTACTTCGATGAGATATCACAGCGCAACCGTCAGCT	1320
QY	1321	GCCGTGAGATGATAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTTGGGATAAGGC	1380
Db	1321	GCCGTGAGATGATAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTTGGGATAAGGC	1380
QY	1381	ATCAGAGACCCCACTCTACAGGGCTTTCCTTTACTGTCAGCTGGGGAATGTTAGC	1440
Db	1381	ATCAGAGACCCCACTCTACAGGGCTTTCCTTTACTGTCAGCTGGGGAATGTTAGC	1440
QY	1441	TGTGTCGGCCCCGTGGGAGCAGGGAAGTCATCTGTTTAAGTCGGCTGCTCGGGGAATTT	1500
Db	1441	TGTGTCGGCCCCGTGGGAGCAGGGAAGTCATCTGTTTAAGTCGGCTGCTCGGGGAATTT	1500
QY	1501	GGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAAGATTGCCTATGTCTCAGCAGCC	1560
Db	1501	GGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAAGATTGCCTATGTCTCAGCAGCC	1560
QY	1561	CTGGGTGTTCTCGGGAACCTCTGAGAGTAATTTTTATTGGGAAGAATATGAAAAGGA	1620
Db	1561	CTGGGTGTTCTCGGGAACCTCTGAGAGTAATTTTTATTGGGAAGAATATGAAAAGGA	1620
QY	1621	ACGATATGAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTCTGTGGAGGA	1680
Db	1621	ACGATATGAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTCTGTGGAGGA	1680
QY	1681	TGGTGATCTGACTGTGATPAGGAGATCGGGGAACACCGTGTAGTGGAGGCGAGAAACAGC	1740
Db	1681	TGGTGATCTGACTGTGATPAGGAGATCGGGGAACACCGTGTAGTGGAGGCGAGAAACAGC	1740
QY	1741	GGTAAACCTTCAGAGCAGGTATCAAGATGCTGACACATCTATCTCCTGGAGATCCCTCT	1800
Db	1741	GGTAAACCTTCAGAGCAGGTATCAAGATGCTGACACATCTATCTCCTGGAGATCCCTCT	1800
QY	1801	CAGTGCAGTAGATCGGAAGTTAGCAGACACTTGTTCGAACCTGTCTATTGTGCAAAATTTT	1860
Db	1801	CAGTGCAGTAGATCGGAAGTTAGCAGACACTTGTTCGAACCTGTCTATTGTGCAAAATTTT	1860
QY	1861	GCATGAGAAGATCAAAATTTTGTGACTCATCAGTGTGACCTCAAGCTGCAAGTCA	1920
Db	1861	GCATGAGAAGATCAAAATTTTGTGACTCATCAGTGTGACCTCAAGCTGCAAGTCA	1920
QY	1921	GATTCGTATATGAAAGATGATAAAATGGTGCAGNAGGGGACTTACACTGAGTTCCCTAAA	1980
Db	1921	GATTCGTATATGAAAGATGATAAAATGGTGCAGNAGGGGACTTACACTGAGTTCCCTAAA	1980
QY	1981	ATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATATGAGGAAAGTGAACACCTCC	2040
Db	1981	ATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATATGAGGAAAGTGAACACCTCC	2040
QY	2041	AGTTCAGGAACCTCCACACTAAGGAATCGTACCTCTCAGAGTCTTCGGTTTTGTGCTCA	2100

[illegible]

2281 TGCGAGTCAGGTTGCCTATGTCCTCAAGATTGGTGGCTTTCATCTACTGCGCAACAACA 2340
 2351 TGCGAGTCAGGTTGCCTATGTCCTCAAGATTGGTGGCTTTCATCTACTGCGCAACAACA 2410
 2341 AAGTATGCTAAATGTCACCTGTAATAGGAGGAGAAATGTAACCGAGAGAGTAGATCTTAA 2400
 2411 AAGTATGCTAAATGTCACCTGTAATAGGAGGAGAAATGTAACCGAGAGAGTAGATCTTAA 2470
 2401 CTGGTACTTAGGAATTAATTCAGGTTTAACCTGAGTACCGTTCTTTTGGCATAGCAAG 2460
 2471 CTGGTACTTAGGAATTAATTCAGGTTTAACCTGAGTACCGTTCTTTTGGCATAGCAAG 2530
 2461 ATCTCTATTGGTATTCTACGTCCTTGTGTTAACTTTCACAACTTTGCACACAAATGTT 2520
 2531 ATCTCTATTGGTATTCTACGTCCTTGTGTTAACTTTCACAACTTTGCACACAAATGTT 2590
 2521 TGAGTCAATTCGAAAGCTCCGGTATTAATCTTTGTATAGAAATCCAAATAGGAAGATTTT 2580
 2591 TGAGTCAATTCGAAAGCTCCGGTATTAATCTTTGTATAGAAATCCAAATAGGAAGATTTT 2650
 2581 AATCGTTTCTCCAAAGACATTTGACATTTGATGATGATTTGCTGCCGCTGACGTTTTTGA 2640
 2651 AATCGTTTCTCCAAAGACATTTGACATTTGATGATGATTTGCTGCCGCTGACGTTTTTGA 2710
 2641 TTTCATCCAGACATTTCTACAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTGATTC 2700
 2711 TTTCATCCAGACATTTCTACAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTGATTC 2770
 2701 TTGGATCGCAATACCCCTGGTTCCTCCCTTGGAAATCATTTTCATTTTCTCGGGGATATT 2760
 2771 TTGGATCGCAATACCCCTGGTTCCTCCCTTGGAAATCATTTTCATTTTCTCGGGGATATT 2830
 2761 TTGGAAACGTCGAAGAGATGTGAAGCGCTCGAATCTACAACTCGGAGTCCAGTGTTC 2820
 2831 TTGGAAACGTCGAAGAGATGTGAAGCGCTCGAATCTACAACTCGGAGTCCAGTGTTC 2890
 2821 CCACCTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGATACAAAGCAGAGAGAG 2880
 2891 CCACCTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGATACAAAGCAGAGAGAG 2950
 2881 GTGTCAGGAACGTTTGTATGCACACAGGATTTACATTCAGAGGCTGTGTTCTGTTTTT 2940
 2951 GTGTCAGGAACGTTTGTATGCACACAGGATTTACATTCAGAGGCTGTGTTCTGTTTTT 3010
 2941 GACAAGTCCCGTGGTTCGCGCTCGTGTGATGCCATCTGTGCCATGTTTGTCTCATAT 3000
 3011 GACAAGTCCCGTGGTTCGCGCTCGTGTGATGCCATCTGTGCCATGTTTGTCTCATAT 3070
 3001 CGTTGGCTTTGGGTCCTCTGATTTGCAAAAACCTCTGGATGCCGGGAGGTTGGTTTGGC 3060
 3071 CGTTGGCTTTGGGTCCTCTGATTTGCAAAAACCTCTGGATGCCGGGAGGTTGGTTTGGC 3130
 3061 ACTGTCTATGCCCCTCACGCTCATGGGATGTTTTCAGTGGTGTGTTGCAAAAGTCTGA 3120
 3131 ACTGTCTATGCCCCTCACGCTCATGGGATGTTTTCAGTGGTGTGTTGCAAAAGTCTGA 3190
 3121 AGTTGAGATATGATGATCTAGTAGAAGGTCATTTGAATACAGACCTTGAAGAAAGA 3180
 3191 AGTTGAGATATGATGATCTAGTAGAAGGTCATTTGAATACAGACCTTGAAGAAAGA 3250
 3181 AGCAGCTGGGAATATCAGAAAGCCACACCGCTGGCCCTGAGAGGATGATAT 3240
 3251 AGCAGCTGGGAATATCAGAAAGCCACACCGCTGGCCCTGAGAGGATGATAT 3310
 3241 CTTTGACATGTGAACCTCATGTACAGTCCAGGTGGGCTCTGTGACTGAAGCATCTGAC 3300
 3311 CTTTGACATGTGAACCTCATGTACAGTCCAGGTGGGCTCTGTGACTGAAGCATCTGAC 3370
 3301 AGCACTCAATTAATCACAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAG 3360
 3371 AGCACTCAATTAATCACAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAG 3430
 3361 TTCCTCATCTCAGCCCTTTTATGATTGTACAGAACCCGAGGATAAATTTGGATTGATAA 3420

3431 TTCCCTCATCTCAGCCCTTTTAGATTGTCCAGAACCCGAGGTAAAAATTTGGATTGATA 3490
 3421 GATCTTGACAACTGAAATTTGACCTTACAGTTTAAGGAAGAAATGTCAATCATACCTCA 3480
 3491 GATCTTGACAACTGAAATTTGACCTTACAGTTTAAGGAAGAAATGTCAATCATACCTCA 3550
 3481 GGAACCTGTTTGTCTACTGGAACAATGAGGAAACCTCGATCCCTTTAAGGAGCACAC 3540
 3551 GGAACCTGTTTGTCTACTGGAACAATGAGGAAACCTCGATCCCTTTAAGGAGCACAC 3610
 3541 GGATGAGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAAGATCT 3600
 3611 GGATGAGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAAGATCT 3670
 3601 TCCTGGTAAATGATGATCTGAATTTAGCAGATCAGGATCCAAATTTAGTGTGGACAAAG 3660
 3671 TCCTGGTAAATGATGATCTGAATTTAGCAGATCAGGATCCAAATTTAGTGTGGACAAAG 3730
 3661 ACAACTGTTGCTTCCAGGCAATTTCTCAGGAAACATCAGATATTGATTATTGATGA 3720
 3731 ACAACTGTTGCTTCCAGGCAATTTCTCAGGAAACATCAGATATTGATTATTGATGA 3790
 3721 AGCAGCGCAATTTGATGATCCAGAACTGATGATTAATACAAAAAAATCCGGGAGAA 3780
 3791 AGCAGCGCAATTTGATGATCCAGAACTGATGATTAATACAAAAAAATCCGGGAGAA 3849
 3781 ATTTGCCCACTGACCGCTGAACCATTTGCACAGATTTGAACACCATTTATGACACGGA 3840
 3850 ATTTGCCCACTGACCGCTGAACCATTTGCACAGATTTGAACACCATTTATGACACGGA 3909
 3841 CAAGATAATGTTTATGATTCAGGAGACTGAAAGAAATATGATGAGCGGTATGTTTGCT 3900
 3910 CAAGATAATGTTTATGATTCAGGAGACTGAAAGAAATATGATGAGCGGTATGTTTGCT 3969
 3901 GCAAAATAAGAGAGCGCTTTTACAGATGTTGCAACAACCTGGGCAAGGAGAGCGCG 3960
 3970 GCAAAATAAGAGAGCGCTTTTACAGATGTTGCAACAACCTGGGCAAGGAGAGCGCG 4029
 3961 TGCCCTCACTGAAACAGCAAAACAGGTATATCTCAAAAGAAATTTATCCACATATTGTGA 4020
 4030 TGCCCTCACTGAAACAGCAAAACAGGTATATCTCAAAAGAAATTTATCCACATATTGTGA 4089
 4021 CACTGACCAATGTTTACAAACACTTCCAAATGAGACGCGCTCGACCTTAATATTTTCGA 4080
 4090 CACTGACCAATGTTTACAAACACTTCCAAATGAGACGCGCTCGACCTTAATATTTTCGA 4149
 4081 GACAGCACTGTGAATCCAAACAAATGTCAAGTCCGTTCCGAAGGCAATTTTCCACTAGTT 4140
 4150 GACAGCACTGTGAATCCAAACAAATGTCAAGTCCGTTCCGAAGGCAATTTTCCACTAGTT 4209
 4141 TTTGGACTATGTAACACACATTTGATCTTTTACTTTTCTGCGCAACAAATATTTATACATA 4200
 4210 TTTGGACTATGTAACACACATTTGATCTTTTACTTTTCTGCGCAACAAATATTTATACATA 4269
 4201 CAAGATGCTAGTTCAATTTGAATTTTCTCCC 4231
 4270 CAAGATGCTAGTTCAATTTGAATTTTCTCCC 4300

RESULT 4

AAH93828

ID AAH93828 standard; cdna; 6082 BP.

XX AAH93828;

XX 04-OCT-2001 (first entry)

XX Human prostate-specific 1st full length cdna sequence for P510S.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

XX cytostatic; gene therapy; metastasis; ss.

|||||
Db 1571 GCGCCCAAGTCACGGCTGGTCAGCGTGCATGGGAAGAAATGCTATGCTGCTCAGCAGCC 1630
Qy 1561 CTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTATTTGGAAGAAATATGAAGA 1620
Db 1631 CTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTATTTGGAAGAAATACGAAGA 1690
Qy 1621 ACGATATGAAAAATCATAAAGGCTTGCTGCTGAAAAAGGATTTACAGCTGTTGGAGA 1680
Db 1691 ACGATATGAAAAAGTCATAAAGGCTTGCTGCTGAAAAAGGATTTACAGCTGTTGGAGA 1750
Qy 1681 TGGTGATCTGACTGTGATAGGATCGGGGAACACGCTGAGTGGAGGCGCAAGACGAG 1740
Db 1751 TGGTGATCTGACTGTGATAGGATCGGGGAACACGCTGAGTGGAGGCGCAAGACGAG 1810
Qy 1741 GGTAAACCTTCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGAGATCCCTCT 1800
Db 1811 GGTAAACCTTCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGAGATCCCTCT 1870
Qy 1801 CAGTGCAGTATAGCGGAAGTTAGCAGACACTGTTGCAACTGTGTATTTGCAAAATTTT 1860
Db 1871 CAGTGCAGTATAGCGGAAGTTAGCAGACACTGTTGCAACTGTGTATTTGCAAAATTTT 1930
Qy 1861 GCATGAGAAGATCAAAATTTAGTGACATCATCAGTTGACGTACCTCAAAGCTGCAAGTCA 1920
Db 1931 GCATGAGAAGATCAAAATTTAGTGACATCATCAGTTGACGTACCTCAAAGCTGCAAGTCA 1990
Qy 1921 GATTCTGATATTGAAAGATGTTAAATGTTGAGAGGAGGACTTACACTGAGTTCCTAAA 1980
Db 1991 GATTCTGATATTGAAAGATGTTAAATGTTGAGAGGAGGACTTACACTGAGTTCCTAAA 2050
Qy 1981 ATCTGGTATAGATTGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACACCTCC 2040
Db 2051 ATCTGGTATAGATTGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACACCTCC 2110
Qy 2041 AGTTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2100
Db 2111 AGTTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2170
Qy 2101 ACAATCTTCTAGACCCCTCTTGAAGATGGTGCTCTGGAGAGCCAAAGATACAGAAATGT 2160
Db 2171 ACAATCTTCTAGACCCCTCTTGAAGATGGTGCTCTGGAGAGCCAAAGATACAGAAATGT 2230
Qy 2161 CCCAGTTACATATCAGAGGAGAACCTGTTGAGGAAGAGTTGTTTTCAGGCCATATA 2220
Db 2231 CCCAGTTACATATCAGAGGAGAACCTGTTGAGGAAGAGTTGTTTTCAGGCCATATA 2290
Qy 2221 GAATTAATCTCAGAGCTGGTGCTCACTGGATGTTCTTCAATTTTCTTCTTCTTAAACAC 2280
Db 2291 GAATTAATCTCAGAGCTGGTGCTCACTGGATGTTCTTCAATTTTCTTCTTCTTAAACAC 2350
Qy 2281 TGCAGCTCAGTTGCCATGCTTCAAGATGGTGCTTCACTAGTGGCTTTTCACTAGCGGCAACAA 2340
Db 2351 TGCAGCTCAGTTGCCATGCTTCAAGATGGTGCTTCACTAGTGGCTTTTCACTAGCGGCAACAA 2410
Qy 2341 AAGTATGCTAATCTCACTGTAATGGAGGAGAAATGTAACCGAGAGCTAGATCTTAA 2400
Db 2411 AAGTATGCTAATCTCACTGTAATGGAGGAGAAATGTAACCGAGAGCTAGATCTTAA 2470
Qy 2401 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCCTGTTCTTTTGGCATAGCAAG 2460
Db 2471 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCCTGTTCTTTTGGCATAGCAAG 2530
Qy 2461 ATCTCTATTTGATTTCTACGCTCCCTGTTGTTAACTCTTCAAACTTTGCAACAAATGTT 2520
Db 2531 ATCTCTATTTGATTTCTACGCTCCCTGTTGTTAACTCTTCAAACTTTGCAACAAATGTT 2590
Qy 2521 TGAGTCAATTTGAAAGCTCCGCTATTTATTTCTTATAGAAATCCAATAGGAAGATTTT 2580
Db 2591 TGAGTCAATTTGAAAGCTCCGCTATTTATTTCTTATAGAAATCCAATAGGAAGATTTT 2650
Qy 2581 AAATCGTTTCTCCAAAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTTTTGA 2640
|||||

Db 2651 AAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTGA 2710
Qy 2641 TTTCATCCAGACATTTGCTACAAGTGGTTGGTGGTCTCTGTTGGCTGTGCGCGTGATTC 2700
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Qy 2701 TTGGATCGCAATACCCTTGGTTCCTTGGAAATCATTTTCAATTTTCTTCGGGATATTT 2760
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Qy 2761 TTGGAAACGTCGAAGATGCTGAAGCGCTGGAAATCTACAACCTCGGAGTCCAGTGTTC 2820
Db 2831 TTGGAAACGTCGAAGATGCTGAAGCGCTGGAAATCTACAACCTCGGAGTCCAGTGTTC 2890
Qy 2821 CCACCTTGTCTATCTTCTCTCAGGGCTCTGGACCATCCGGGCATACAAACGACAAGAGAG 2880
Db 2891 CCACCTTGTCTATCTTCTCTCAGGGCTCTGGACCATCCGGGCATACAAACGACAAGAGAG 2950
Qy 2881 GTGTCAAGAACTGTTTGTATGCACACAGGATTTACATTCAGAGCTTGGTTCCTTTT 2940
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Qy 2941 GACAACGTCCTGCTGCTGCGCTGCTGGATGCCATCTGTGCCATGTTTGTCTCAT 3000
Db 3011 GACAACGTCCTGCTGCTGCGCTGCTGGATGCCATCTGTGCCATGTTTGTCTCAT 3070
Qy 3001 CGTTGCTTGGTTCCTGATTTCTGGCAAAACTCTGGATGCCGGCAGGTTGGTTTGGC 3060
Db 3071 CGTTGCTTGGTTCCTGATTTCTGGCAAAACTCTGGATGCCGGCAGGTTGGTTTGGC 3130
Qy 3061 ACTGTCTATGCCCTCACGCTCANTGGGATGTTTCAAGTGGTGTTCGACAAAGTGTGA 3120
Db 3131 ACTGTCTATGCCCTCACGCTCANTGGGATGTTTCAAGTGGTGTTCGACAAAGTGTGA 3190
Qy 3121 AGTTGAGAATATGATCATCTCAGTGAAGGCTCATTTGAATACACAGACCTTCAAAAGA 3180
Db 3191 AGTTGAGAATATGATCATCTCAGTGAAGGCTCATTTGAATACACAGACCTTCAAAAGA 3250
Qy 3181 AGCACCTTGGGAATATCAGAAACGCCACACAGCCTGCCCATGAGGAGTGTAAAT 3240
Db 3251 AGCACCTTGGGAATATCAGAAACGCCACACAGCCTGCCCATGAGGAGTGTAAAT 3310
Qy 3241 CTTTGACATGTGAATTTGATGTACAGTCCAGTGGGCTCTGGTACTGAAGCATCTGAC 3300
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Qy 3301 AGCACTCATTAATACAAAGAAAGTTGSCATTTGGGAAGAACCGAGCTGGAAGAG 3360
Db 3371 AGCACTCATTAATACAAAGAAAGTTGSCATTTGGGAAGAACCGAGCTGGAAGAG 3430
Qy 3361 TTCCCTCATCTCAGCCCTTTTAGATTTGTCAAGAACCGAGCTGGAATTTGGATTGATA 3420
Db 3431 TTCCCTCATCTCAGCCCTTTTAGATTTGTCAAGAACCGAGCTGGAATTTGGATTGATA 3490
Qy 3421 GATCTTGACAACTGAAATTTGGACTTCACAGTTTGAAGAGAAATGTCATCTACCTCA 3480
Db 3491 GATCTTGACAACTGAAATTTGGACTTCACAGTTTGAAGAGAAATGTCATCTACCTCA 3550
Qy 3481 GGAACCTGTTTGTTCACCTGGAACATGAGAAACCTTGGATCCCTTTAAGGAGCAGAC 3540
Db 3551 GGAACCTGTTTGTTCACCTGGAACATGAGAAACCTTGGATCCCTTTAAGGAGCAGAC 3610
Qy 3541 GGATGAGAACTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCATTTGAAGATCT 3600
Db 3611 GGATGAGAACTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCATTTGAAGATCT 3670
Qy 3601 TCCTGGTAAATGGATACCTGAAATTTAGCAAGATCAGGATCCAATTTAGTGTGGAGAAAG 3660
Db 3671 TCCTGGTAAATGGATACCTGAAATTTAGCAAGATCAGGATCCAATTTAGTGTGGAGAAAG 3730
Qy 3661 ACAACTGGTGTCCCTTGGCAGGCAATTTCTCAGGAAGAAATCAGATATTGATTTTATGA 3720
Db 3731 ACAACTGGTGTCCCTTGGCAGGCAATTTCTCAGGAAGAAATCAGATATTGATTTTATGA 3790
|||||

QY 781 GATCGAGTCACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCCTGCTGGATGGC 840
 Db 851 GATCGAGTCACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCCTGCTGGATGGC 910
 QY 841 AGTTCTAATCATCTCTGCGCCCTGCAAGAGCTGTTTGGGAAGCTGTTCTCATCACTGAG 900
 Db 911 AGTTCTAATCATCTCTGCGCCCTGCAAGAGCTGTTTGGGAAGCTGTTTCTCATCACTGAG 970
 QY 901 GAGTAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATCAAGTTATACTGG 960
 Db 971 GAGTAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATCAAGTTATACTGG 1030
 QY 961 TATAAGGATAATAAATGTACGCCCTGGGAAGAGTCAATTTCAAACTCTATTAACCAATTT 1020
 Db 1031 TATAAGGATAATAAATGTACGCCCTGGGAAGAGTCAATTTCAAACTCTATTAACCAATTT 1090
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 Db 1091 GAGAAAGAGGAGATTTCCAAAGATCTGAGAAGTTCCTGCTCAGGGGATGAATTTGGC 1150
 QY 1081 TTGCTTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCACCACTACGTCCTCT 1140
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 QY 1141 CGGCAGTGTATCAGACCCAGCGCGGTGTTGTCGAGAGTGCAGCTGTATGGGCTGTGG 1200
 Db 1211 CGGCAGTGTATCAGACCCAGCGCGGTGTTGTCGAGAGTGCAGCTGTATGGGCTGTGG 1270
 QY 1201 GCTGACGGTTACCTCTCTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATCGTCAG 1260
 Db 1271 GCTGACGGTTACCTCTCTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATCGTCAG 1330
 QY 1261 CATCCGAAGAATCCAGACCTTTTGTACTTGATGAGATATCACAGCGCAACCGTCAGCT 1320
 Db 1331 CATCCGAAGAATCCAGACCTTTTGTACTTGATGAGATATCACAGCGCAACCGTCAGCT 1390
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 Db 1391 GCCGTGAGATGTAAGAAAGATGGTGCAGAGTATTTACTGCTTTTGGATGAAGC 1450
 QY 1381 ATCAGAGACCCCAACTCTACAAGGCTTTCTCTTACTGTGACAGCTGGCGAATTTAGC 1440
 Db 1451 ATCAGAGACCCCAACTCTACAAGGCTTTCTCTTACTGTGACAGCTGGCGAATTTAGC 1510
 QY 1441 TGTGCTGCGCCCGTGGGAGCAGGAAGTCATCACTGTTTAAGTGCCTGCTCGGGGAAT 1500
 Db 1511 TGTGCTGCGCCCGTGGGAGCAGGAAGTCATCACTGTTTAAGTGCCTGCTCGGGGAAT 1570
 QY 1501 GSCCCCAAGTCAGGGCTGGTGCAGGTGCATGGAGAATTTGCTATGCTCAGCAGCC 1560
 Db 1571 GSCCCCAAGTCAGGGCTGGTGCAGGTGCATGGAGAATTTGCTATGCTCAGCAGCC 1630
 QY 1561 CTGGGTGTTCTCGGAACCTCTCAGGAGTAATATTTTATTTGGGAAGAAATATGAAGA 1620
 Db 1631 CTGGGTGTTCTCGGAACCTCTCAGGAGTAATATTTTATTTGGGAAGAAATATGAAGA 1690
 QY 1621 ACGATATGAAAGTCATAAAGGCTTGTGCTCTGAAAGAGTATTTACAGCTGTGGAGGA 1680
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 Db 1751 TGGTATCTGACTGTATAGGAGATCGGGGAACACAGCTGAGTGGAGGCGAAGACAGC 1810
 QY 1741 GGTAAACCTTGAAGAGAGTGTATCAGAGTCTCAGATCTATCTCCTGGAGATCTCT 1800
 Db 1811 GGTAAACCTTGAAGAGAGTGTATCAGAGTCTCAGATCTATCTCCTGGAGATCTCT 1870
 QY 1801 CAGTGCAGTAGATCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTT 1860
 Db 1871 CAGTGCAGTAGATCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTT 1930

QY 1861 GCATGAGAAGATCAAAATTTTAGTGACTCATATGTTGCAGTACCTCAAGCTGCAAGTCA 1920
 Db 1931 GCATGAGAAGATCAAAATTTTAGTGACTCATATGTTGCAGTACCTCAAGCTGCAAGTCA 1990
 QY 1921 GATTCTGATATTGAAGATGGTAAATGGTGCACAAGGGGACTTACACTGAGTTCCTTAA 1980
 Db 1991 GATTCTGATATTGAAGATGGTAAATGGTGCACAAGGGGACTTACACTGAGTTCCTTAA 2050
 QY 1981 ATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGATAATGAGGAAAGTGAACAACCTCC 2040
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 QY 2041 AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2100
 Db 2111 AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2170
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 QY 2341 AAGTATGCTAAATGTCTACTCTAAATGGAGGAGAAATGTAAACGAGAGAGCTAGATCTTAA 2400
 Db 2411 AAGTATGCTAAATGTCTACTCTAAATGGAGGAGAAATGTAAACGAGAGAGCTAGATCTTAA 2470
 QY 2401 CTGGTACTTAGGAATTTATTCAGTGTAACTGTAAGTACCTGTTCTTTTGGCATAGCAAG 2460
 Db 2471 CTGGTACTTAGGAATTTATTCAGTGTAACTGTAAGTACCTGTTCTTTTGGCATAGCAAG 2530
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 Db 2531 ATCTCTATTTGGTATTTCTACGCTCTCTTAACTCTTCAACAACCTTGCACAACAATTTGT 2590
 QY 2521 TGAGTCAATTTCTGAAAGCTCCGGTATTTATTTGTATGAGAAATCCAAATAGGAAGATTTT 2580
 Db 2591 TGAGTCAATTTCTGAAAGCTCCGGTATTTATTTGTATGAGAAATCCAAATAGGAAGATTTT 2650
 QY 2581 AAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCCGCTGACGTTTTAGA 2640
 Db 2651 AAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCCGCTGACGTTTTAGA 2710
 QY 2641 TTTTCATCCAGACATTTCTACAGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 2700
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 QY 2701 TTGGATCGCAATACCTTGGTTCCTTGGAACTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2760
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 QY 2821 CCACCTGTCTCTCTCCAGGGGCTCGGACCATCGGGCATACAAAGCAGAGAGAG 2880
 Db 2891 CCACCTGTCTCTCTCCAGGGGCTCGGACCATCGGGCATACAAAGCAGAGAGAG 2950
 QY 2881 GTCTCAGGAACCTGTTTGTATGTCACACAGGATTTTACATTCAGAGGCTTGGTCTGTTTTT 2940
 Db 2951 GTCTCAGGAACCTGTTTGTATGTCACACAGGATTTTACATTCAGAGGCTTGGTCTGTTTTT 3010
 QY 2941 GACAACCTCCCGCTGGTGTGGCCCTGCTGCGCTGCTGAGATGCTGTCATCTGTCATCAT 3000

Db	3011	 GACAACTGGCGTGGTTCCGCCTCGCTGGATGCCATCTGTSCCATGTTTGTCATCAT	3070
QY	3001	CCTTGCTCTTTGGTCCTCCTGATTCTGGCAAAAACCTCTGGATCCGGCGACAGTTCGTTGGC	3060
Db	3071	CCTTGCTTTGGGTCCCTGATTCTGCAAAAAACCTCTGGATCCGGCGACAGTTCGTTGGC	3130
QY	3061	ACTGTCTATGCCCCCTCACGCTCATGGGGATGTTTTCAGTGTGTGTCGACAAAGTCTGA	3120
Db	3131	ACTGTCTATGCCCCCTCACGCTCATGGGGATGTTTTCAGTGTGTGTCGACAAAGTCTGA	3190
QY	3121	AGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAAAAAGA	3180
Db	3191	AGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAAAAAGA	3250
QY	3181	AGCACTCTGGGAATATCAGAAAGCCCACCACAGCCTCGCCCCCATGAAGGAGTGATAAT	3240
Db	3251	AGCACTCTGGGAATATCAGAAAGCCCACCACAGCCTCGCCCCCATGAAGGAGTGATAAT	3310
QY	3241	CTTTGACAATGTGAATCTCATGTACAGTCAGGTGGCCTCTGGTACTCAAGCATCTGAC	3300
Db	3311	CTTTGACAATGTGAATCTCATGTACAGTCAGGTGGCCTCTGGTACTCAAGCATCTGAC	3370
QY	3301	AGCACTCATTAATCACAAGAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGAAAAAG	3360
Db	3371	AGCACTCATTAATCACAAGAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGAAAAAG	3430
QY	3361	TTCCTCTCATCTCAGCCCTTTTTAGATGTGCAGAACCCGAAGGTAAAAATTGGATTGATAA	3420
Db	3431	TTCCTCTCATCTCAGCCCTTTTTAGATGTGCAGAACCCGAAGGTAAAAATTGGATTGATAA	3490
QY	3421	GATCTTGACAACTGAAATTTGGACTTTCAGATTTAAGGAAGAAAAATGTCAATCATCTCA	3480
Db	3491	GATCTTGACAACTGAAATTTGGACTTTCAGATTTAAGGAAGAAAAATGTCAATCATCTCA	3550
QY	3481	GGAACCTGTTTGTCTACTGGACAAATCAGGAAAAACCTGGATCCCTTTAAGGACACAC	3540
Db	3551	GGAACCTGTTTGTCTACTGGACAAATCAGGAAAAACCTGGATCCCTTTAAGGACACAC	3610
QY	3541	GGATGAGGAACCTGTGGAAATGCCCTTACAAGAGGTACAACCTTAAGAAAAACCATTTGAAGATCT	3600
Db	3611	GGATGAGGAACCTGTGGAAATGCCCTTACAAGAGGTACAACCTTAAGAAAAACCATTTGAAGATCT	3670
QY	3601	TCCTGGTAAAAATGGATACTGAATTAGCAGAACTCAGGATCCAATTTTAGTGTGGACAAAG	3660
Db	3671	TCCTGGTAAAAATGGATACTGAATTAGCAGAACTCAGGATCCAATTTTAGTGTGGACAAAG	3730
QY	3661	ACAACTGGTGTGCCCTTGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTTATGATGA	3720
Db	3731	ACAACTGGTGTGCCCTTGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTTATGATGA	3790
QY	3721	AGCGAGCGCAAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAA	3780
Db	3791	AGCGAGCGCAAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAA	3849
QY	3781	ATTTGCCCATGCAACCGTGCTAACCAATTGCACAGATTTGAACCACTATTATGGACAGGA	3840
Db	3850	ATTTGCCCATGCAACCGTGCTAACCAATTGCACAGATTTGAACCACTATTATGGACAGGA	3909
QY	3841	CAAGATATGGTTTTAGATTTCAGAGAACTCAAGAATATGATGAGCCGATGTTTTGCT	3900
Db	3910	CAAGATATGGTTTTAGATTTCAGAGAACTCAAGAATATGATGAGCCGATGTTTTGCT	3969
QY	3901	GCAAAATAAGAGAGCCCTATTTTACAAGATGGTGCACAACTGGGCAAGGCAGAACCGC	3960
Db	3970	GCAAAATAAGAGAGCCCTATTTTACAAGATGGTGCACAACTGGGCAAGGCAGAACCGC	4029
QY	3961	TGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATTTGGTCA	4020
Db	4030	TGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATTTGGTCA	4089
QY	4021	CACHTGACCACATGGTTTACAACACCTTCCAATGGACGCCCTCGACCTTAATCTATTTTCGA	4080

Db	4090	CACTGACCCACATGGTTTACAAACACTTCCCAATGGACAGCCCTCGACCTTAACTATTTCGA	4140
Qy	4081	GACAGCACTGTGAATCCAAACCAAAATGTCAAGTCCGTTCCGGAAGGCATTTTCCACTAGTT	4140
Db	4150	GACAGCACTGTGAATCCAAACCAAAATGTCAAGTCCGTTCCGGAAGGCATTTGCCCACAGTT	4209
Qy	4141	TTTGACATATGTAACCAACCATGTACTTTTTTTTACTTTGGCAACAATATTATACATA	4200
Db	4210	TTTGCACTATGTAACCAACCATGTACTTTTTTTTACTTTGGCAACAATATTATACATA	4269
Qy	4201	CAAGATGCTAGTTTCATTTGAAATATTTCTCCC	4231
Db	4270	CAAGATGCTAGTTTCATTTGAAATATTTCTCCC	4300
RESULT 6			
ABL95292			
ID	ABL95292 standard; cDNA; 6082 BP.		
XX	ABL95292;		
XX	19-JUL-2002 (first entry)		
DT	Human P510S cDNA sequence SEQ ID NO 535.		
XX	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;		
KW	gene therapy; gene; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	US2002022248-A1.		
PN	21-FEB-2002.		
XX	12-JAN-2001; 2001US-0759143.		
XX	25-FEB-1997; 97US-0806099.		
PR	01-AUG-1997; 97US-0904804.		
PR	09-FEB-1998; 98US-0020956.		
PR	25-FEB-1998; 98US-0030607.		
PR	14-JUL-1998; 98US-0115453.		
PR	23-SEP-1998; 98US-0159812.		
PR	15-JAN-1999; 99US-0232149.		
PR	09-APR-1999; 99US-0288946.		
PR	13-JUL-1999; 99US-0352616.		
PR	12-NOV-1999; 99US-0439313.		
PR	18-NOV-1999; 99US-0443686.		
PR	14-JAN-2000; 2000US-0483672.		
PR	27-MAR-2000; 2000US-0536857.		
PR	09-MAY-2000; 2000US-0568100.		
PR	12-MAY-2000; 2000US-0570737.		
PR	13-JUN-2000; 2000US-0593793.		
PR	27-JUN-2000; 2000US-0605783.		
PR	10-AUG-2000; 2000US-0636215.		
PR	29-AUG-2000; 2000US-0651236.		
PR	08-SEP-2000; 2000US-0657279.		
PR	02-OCT-2000; 2000US-0679426.		
PR	10-OCT-2000; 2000US-0685166.		

AA	(XUJJ/)	XU J.
PA	(MITL/)	DILLON D C.
PA	(DITC/)	MITCHAM J L.
PA	(HARL/)	HARLOCKER S L.
PA	(JIAN/)	JIANG Y.
PA	(KALO/)	KALOS M D.
PA	(FANG/)	FANGER G R.
PA	(RETT/)	RETTET M W.
PA	(STOL/)	STOLK J A.
PA	(DAYC/)	DAY C H.
PA	(VEDV/)	VEDVICK T S.
PA	(CART/)	CARTER D.
PA	(LISX/)	LI S X.
PA	(WANG/)	WANG A.

QY 1801 CAGTCAGTAGATGCGGAAGTTAGCAGACACTGTTGTCGAACCTGTGATTTGTCAAATTTT 1860
DB 1871 CAGTCAGTAGATGCGGAAGTTAGCAGACACTGTTGTCGAACCTGTGATTTGTCAAATTTT 1930
QY 1861 GCATGAGAAGATCACAAATTTTGTAGTCACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCA 1920
DB 1931 GCATGAGAAGATCACAAATTTTGTAGTCACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCA 1990
QY 1921 GATTCGTATATTGAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTCCTATAA 1980
DB 1991 GATTCGTATATTGAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTCCTATAA 2050
QY 1981 ATCTGGTATAGATTTTGGTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAACTCC 2040
DB 2051 ATCTGGTATAGATTTTGGTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAACTCC 2110
QY 2041 AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2100
DB 2111 AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2170
QY 2101 ACAATCTTCTAGACCTCTCTGAAAGATGGTGCTCTGGAGAGCCAAAGATACAGAGAATCT 2160
DB 2171 ACATCTTCTAGACCTCTCTGAAAGATGGTGCTCTGGAGAGCCAAAGATACAGAGAATCT 2230
QY 2161 CCCAGTTACACTATCAGAGGAGAACCGTTCTGGAAGAAAGTTGGTTTTTCAGGCCCTATAA 2220
DB 2231 CCCAGTTACACTATCAGAGGAGAACCGTTCTGGAAGAAAGTTGGTTTTTCAGGCCCTATAA 2290
QY 2221 GAATTAATCTCAGAGCTGGTCACTGGATGCTCTTCAATTTTCCATTTCTCTTAAACAC 2280
DB 2291 GAATTAATCTCAGAGCTGGTCACTGGATGCTCTTCAATTTTCCATTTCTCTTAAACAC 2350
QY 2281 TGCAGCTCAGTTGGCTATGCTTCAAGATTTGGTGGCTTTCATCTAGTGGGCAACAAACA 2340
DB 2351 TGCAGCTCAGTTGGCTATGCTTCAAGATTTGGTGGCTTTCATCTAGTGGGCAACAAACA 2410
QY 2341 AAGTATGCTAAATGTCATCTAATGAGGAGGAGAAATGTAACCGAGAGCTAGATCTTAA 2400
DB 2411 AAGTATGCTAAATGTCATCTAATGAGGAGGAGAAATGTAACCGAGAGCTAGATCTTAA 2470
QY 2401 CTGGTACTTAGGAATTTATCAGTTTAACTCTAGCTACCGTTCCTTTTGGCATAGCAAG 2460
DB 2471 CTGGTACTTAGGAATTTATCAGTTTAACTCTAGCTACCGTTCCTTTTGGCATAGCAAG 2530
QY 2461 ATCTCTATTGGTATTCTACGCTCTTGTAACTCTTCAACAACTTTGCAACAAATAATGTT 2520
DB 2531 ATCTCTATTGGTATTCTACGCTCTTGTAACTCTTCAACAACTTTGCAACAAATAATGTT 2590
QY 2521 TGAGTCAATCTGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAATAGGAAGATTTT 2580
DB 2591 TGAGTCAATCTGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAATAGGAAGATTTT 2650
QY 2581 AAATCGTTTCTCCAAAGACATTGACACTTGGATGATTGCTGCCGCTGACGTTTTTGA 2640
DB 2651 AAATCGTTTCTCCAAAGACATTGACACTTGGATGATTGCTGCCGCTGACGTTTTTGA 2710
QY 2641 TTTTCATCCAGACATTGCTTACAAGTGGTTGGTGCTCTGTGGCTGTGGCGCTGATTC 2700
DB 2711 TTTTCATCCAGACATTGCTTACAAGTGGTTGGTGCTCTGTGGCTGTGGCGCTGATTC 2770
QY 2701 TTGATGCAATACCTTTGGTTCCCTTTGGAATCAATTTTCAATTTTCTTCGCGCATATTT 2760
DB 2771 TTGATGCAATACCTTTGGTTCCCTTTGGAATCAATTTTCAATTTTCTTCGCGCATATTT 2830
QY 2761 TTTTGAACGCTCAAGATGTTGAAGCGCTGGAATCTCACTCGGAGTCCAGTGTTC 2820
DB 2831 TTTTGAACGCTCAAGATGTTGAAGCGCTGGAATCTCACTCGGAGTCCAGTGTTC 2890
QY 2821 CCACCTGTCACTTCTCTCCAGGGGCTCTGGACCATCCGGCATACAAGCAGAGAGAG 2880
DB 2891 CCACCTGTCACTTCTCTCCAGGGGCTCTGGACCATCCGGCATACAAGCAGAGAGAG 2950

QY 2881 GTGTGAGAACTGTTGATGCACACAGGATTTACATTCAGAGGCTTGGTTCTTGTGTTTTT 2940
DB 2951 GTGTGAGAACTGTTGATGCACACAGGATTTACATTCAGAGGCTTGGTTCTTGTGTTTTT 3010
QY 2941 GACAACCTCCCGTGGTTGCGCCGCTCTGCGTCTGAGTGCATCTGTGCCATCTGTTGTCATCAT 3000
DB 3011 GACAACCTCCCGTGGTTGCGCCGCTCTGCGTCTGAGTGCATCTGTGCCATCTGTTGTCATCAT 3070
QY 3001 CGTTGCTTTTGGTCCCTGATTCTGGCAAAACTCTGATGCGCGGAGGTTGGTTGGC 3060
DB 3071 CGTTGCTTTTGGTCCCTGATTCTGGCAAAACTCTGATGCGCGGAGGTTGGTTGGC 3130
QY 3061 ACTGTCTATGCTCCCTCACGCTCATGGGATGTTTTCAGTGGTGCTTTCGACAAAGTGTGA 3120
DB 3131 ACTGTCTATGCTCCCTCACGCTCATGGGATGTTTTCAGTGGTGCTTTCGACAAAGTGTGA 3190
QY 3121 AGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATGAAATACACAGACCTTGAAGAAGA 3180
DB 3191 AGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATGAAATACACAGACCTTGAAGAAGA 3250
QY 3181 AGCACCTTGGGAATATCAGAAACGCCACCACAGGCTTGGCCCATGAAGAGTGAAT 3240
DB 3251 AGCACCTTGGGAATATCAGAAACGCCACCACAGGCTTGGCCCATGAAGAGTGAAT 3310
QY 3241 CTTTGCATCTGCAACTTTCATGTACAGTCCAGGTGGGCCCTCTGTACTGAAGCATCTGAC 3300
DB 3311 CTTTGCATCTGCAACTTTCATGTACAGTCCAGGTGGGCCCTCTGTACTGAAGCATCTGAC 3370
QY 3301 AGCATCTAATAATCAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAG 3360
DB 3371 AGCATCTAATAATCAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAG 3430
QY 3361 TTCCTCTACTCAGCCCTTTTAGATGTTGTCAGAACCCGAGGTAAATTTGGATTGATAA 3420
DB 3431 TTCCTCTACTCAGCCCTTTTAGATGTTGTCAGAACCCGAGGTAAATTTGGATTGATAA 3490
QY 3421 GATCTTGACAACCTGAAATTTGGACTTTCAGATTTTAAAGAAAGAAATGTCAATCATACCTCA 3480
DB 3491 GATCTTGACAACCTGAAATTTGGACTTTCAGATTTTAAAGAAAGAAATGTCAATCATACCTCA 3550
QY 3481 GGNACCTGTTTGTTCACGTGGAACATGAGGAAACCTGGATCCCTTTTAAAGGAGCACAC 3540
DB 3551 GGNACCTGTTTGTTCACGTGGAACATGAGGAAACCTGGATCCCTTTTAAAGGAGCACAC 3610
QY 3541 GGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTGAAGATCT 3600
DB 3611 GGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTGAAGATCT 3670
QY 3601 TCCTGTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660
DB 3671 TCCTGTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3730
QY 3661 ACAACTGGTGTGCTTCCAGGCAATTTCTCAGGAAATTCAGATATTCAGATATTCAGATGATGAT 3720
DB 3731 ACAACTGGTGTGCTTCCAGGCAATTTCTCAGGAAATTCAGATATTCAGATATTCAGATGATGAT 3790
QY 3721 AGCAGCGCAATGTCGATCCAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
DB 3791 AGCAGCGCAATGTCGATCCAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3849
QY 3781 ATTTGCCCACTGCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACT 3840
DB 3850 ATTTGCCCACTGCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACT 3909
QY 3841 CAAGATATGTTTGTAGATTCAGGAAAGTGAAGAAATATGATGAGCCGCTATGTTTGTCT 3900
DB 3910 CAAGATATGTTTGTAGATTCAGGAAAGTGAAGAAATATGATGAGCCGCTATGTTTGTCT 3969
QY 3901 GCAAAATGAAGAGGCTTATTTTACAAGATGTTGCAACAACTGGGCAAGGAGGAGGAGGAGGAGGAG 3960
DB 3970 GCAAAATGAAGAGGCTTATTTTACAAGATGTTGCAACAACTGGGCAAGGAGGAGGAGGAGGAGGAG 4029
QY 3961 TGCCCTCTACTGAAACAGCAAAACAGGATATATCTTCAAAAGAAATTTATCCATATTTGTTCA 4020

Db 3121 ATCTAGTAAAGGTCATTGAATACACAGACCTTGAAAAAGAACGACACCTTGGGAATAT 3180
 QY 3197 CAGAAAGCCACCACAGCCTGGCCCATGAAGAGTGTATAATCTTTGACAAATGTGAAC 3256
 Db 3181 CAGAAAGCCACCACAGCCTGGCCCATGAAGAGTGTATAATCTTTGACAAATGTGAAC 3240
 QY 3257 TTCTATGACAGTCCAGGTGGCCCTCTGGTACTGAAGCATCTGACAGCACTCATTAATCA 3316
 Db 3241 TTCTATGACAGTCCAGGTGGCCCTCTGGTACTGAAGCATCTGACAGCACTCATTAATCA 3300
 QY 3317 CAAGAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC 3376
 Db 3301 CAGAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC 3360
 QY 3377 CTTTTAGATTGTGCAACCCGGAAGTAAATTTGGATTGATTAAGATCTTTGACAACCTGAA 3436
 Db 3361 CTTTTAGATTGTGCAACCCGGAAGTAAATTTGGATTGATTAAGATCTTTGACAACCTGAA 3420
 QY 3437 ATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTTC 3496
 Db 3421 ATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTTC 3480
 QY 3497 ACTGGAACATGAGGAAAAACCTGGATCCTTTAAGGAGCACACGATGAGGAACCTGTGG 3556
 Db 3481 ACTGGAACATGAGGAAAAACCTGGATCCTTTAAGGAGCACACGATGAGGAACCTGTGG 3540
 QY 3557 AATGCTTTACAAGAGTACAACTTTAAGAAAAACCATTTGAAGATCTTCTGGTAAATGGAT 3616
 Db 3541 AATGCTTTACAAGAGTACAACTTTAAGAAAAACCATTTGAAGATCTTCTGGTAAATGGAT 3600
 QY 3617 ACTGAATTAGCAGATCAGATCCCAATTTAGTTGGCAAGAACAACTGGTGTGCTT 3676
 Db 3601 ACTGAATTAGCAGATCAGATCCCAATTTAGTTGGCAAGAACAACTGGTGTGCTT 3660
 QY 3677 GCCAGGCAATTTCTAGGAAAAATCAGATTATGATTATGATGAGCGACGCAAAATGTG 3736
 Db 3661 GCCAGGCAATTTCTAGGAAAAATCAGATTATGATTATGATGAGCGACGCAAAATGTG 3720
 QY 3737 GATCCAAAGAACTGATGAGTTAATACAAAAAAATTCGGGAGAAATTTGCCCACTGCACC 3796
 Db 3721 GATCCAAAGAACTGATGAGTTAATACAAAAAAATTCGGGAGAAATTTGCCCACTGCACC 3780
 QY 3797 GTGCTAACCATTTGCACAGATTTGACACCAATTTATGACAGGACAAAGATAATGTTTA 3856
 Db 3781 GTGCTAACCATTTGCACAGATTTGACACCAATTTATGACAGGACAAAGATAATGTTTA 3840
 QY 3857 GATTCAGGAAGTGAAGAAATATGATGAGCGGTATGTTTGTGCAAAATAAAGAGAGC 3916
 Db 3841 GATTCAGGAAGTGAAGAAATATGATGAGCGGTATGTTTGTGCAAAATAAAGAGAGC 3900
 QY 3917 CTATTTTACAAGATGTCACAACTGGCAAGGCAAGCGCGCTGCCCTCACTGAAACA 3976
 Db 3901 CTATTTTACAAGATGTCACAACTGGCAAGGCAAGCGCGCTGCCCTCACTGAAACA 3960
 QY 3977 GCAAAACAGGTACTTCAAAAGAAATTTCCACATATTTGGTTCACACTGACACATGGTT 4036
 Db 3961 GCAAAACAGGTACTTCAAAAGAAATTTCCACATATTTGGTTCACACTGACACATGGTT 4020
 QY 4037 ACAAACTTCCAAATGGAGAGCCCTCGACCTTTAACTATTTTCGAGACAGCACTGTAATC 4096
 Db 4021 ACAAACTTCCAAATGGAGAGCCCTCGACCTTTAACTATTTTCGAGACAGCACTGTAATC 4080
 QY 4097 CAACCAAAATGTCAGTCCGTTCCGAAGCAATTTTCCACTAGTATTTTGGACTATGTAAC 4156
 Db 4081 CAACCAAAATGTCAGTCCGTTCCGAAGCAATTTTCCACTAGTATTTTGGACTATGTAAC 4140
 QY 4157 CACATGTACTTTTTTTTACTTTTGGCAACAATATTTATACATACAAAGATGCTAGTTAT 4216
 Db 4141 CACATGTACTTTTTTTTACTTTTGGCAACAATATTTATACATACAAAGATGCTAGTTAT 4200
 QY 4217 TTGAATATTTCTCCC 4231
 Db 4201 TTGAATATTTCTCCC 4215

RESULT 8
 ABV22410
 ID ABV22410 standard; cDNA; 4515 BP.
 XX AC ABV22410;
 XX DT 13-SEP-2002 (first entry)
 XX DE Human prostate expression marker cDNA 22401.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX OS Homo sapiens.
 XX PN WO200160860-A2.
 XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P.
 XX PR 16-MAR-2000; 2000US-189862P.
 XX PR 25-MAY-2000; 2000US-207454P.
 XX PR 09-JUN-2000; 2000US-211314P.
 XX PR 18-JUL-2000; 2000US-219007P.
 XX PR 13-DEC-2000; 2000US-255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX PS Claim 1; Page 3893-3894; 11750pp; English.
 XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;

Query Match 99.2%; Score 4196.6; DB 23; Length 4515;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 18 GGAGCCCCAGCATCCCTGCTTGTAGGTCCAGGAGCGGCGGCGCCGCTGTAT 77
 Db 1 GGAGCCCCAGCATCCCTGCTTGTAGGTCCAGGAGCGGCGGCGCCGCTGTAT 60
 QY 78 CAGCGGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 137
 Db 61 CAGCGGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 138 TGAAGCCCCAACCCGCTGTCAGGAGCGGAACATCTGCTCACGCGGTCTTCTTGTGGCTCA 197

Db	121	 TGAGCCCAACCGCTGCAGGACGGAACTCCTGCTCACCGTGTTCCTTCTGTGTGGCTCA	180
Qy	198	ATPCCCTTGTTTAAAAATTGGCCATAAACCAGAGATTAGAGGAAGATGATATGTATTTCAGTGC	257
Db	181	ATCCCTTGTTTAAAAATTGGCCATAAACCGAGATTAGAGGAAGAATGATATGTATTTCAGTGC	240
Qy	258	TGCCAAGAAGACCGCTCACAGACCTTGGAGAGGAGTTGCAAGGGTTCTGGGATAAAGAAG	317
Db	241	TGCCAAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGATAAAGAAG	300
Qy	318	TTTTTAAGAGCTGAAGATGACGCACAGNAGCCTTCTTTAACAGAGACAATCATAAAGTGTT	377
Db	301	TTTTTAAGAGCTGAAGATGACGCACAGAGCCCTTCTTTAACAGAGACAATCATAAAGTGTT	360
Qy	378	ACTGGAAATCTTATTTTAGTTTGGGAATTTTACGTTTAAATTGAGGAAAGTGCCAAGTAA	437
Db	361	ACTGGAAATCTTATTTTAGTTTGGGAATTTTACGTTTAAATTGAGGAAAGTGCCAAGTAA	420
Qy	438	TCCAGCCCCATATTTTGGGAAAATATTAATTTATTTTGAATAATATGATCCCATGGATT	497
Db	421	TCCAGCCCCATATTTTGGGAAAATATTAATTTATTTTGAATAATATGATCCCATGGATT	480
Qy	498	CTGTGGCTTTGAACACAGCGTAGCCCTATGCCACGGTGTCTGACTTTTTCGACGCTCATTT	557
Db	481	CTGTGGCTTTGAACACAGCGTAGCCCTATGCCACGGTGTCTGACTTTTTCGACGCTCATTT	540
Qy	558	TGGCTATACTGCATFCATATATTTTATCCAGCTTCAGTGTGCTGGATGAGSTTACCAG	617
Db	541	TGGCTATACTGCATFCATATATTTTATCCAGCTTCAGTGTGCTGGATGAGSTTACCAG	600
Qy	618	TAGCCATGTGCCATATGATTTATCGGAAGGCACCTCGCTTAGTAACATGGCCATGGGGA	677
Db	601	TAGCCATGTGCCATATGATTTATCGGAAGGCACCTCGCTTAGTAACATGGCCATGGGGA	660
Qy	678	AGACAACACAGGCGCAGATAGTCAATCTCGTGFCCAATGATGTGAACAAGTTTGATCAGG	737
Db	661	AGACAACACAGGCGCAGATAGTCAATCTCGTGFCCAATGATGTGAACAAGTTTGATCAGG	720
Qy	738	TGACAGTGTTCCTTACACTTCCTGTGGCAGGACCACTGCAGCGGATCCGAGTGACTGCC	797
Db	721	TGACAGTGTTCCTTACACTTCCTGTGGCAGGACCACTGCAGCGGATCCGAGTGACTGCC	780
Qy	798	TACTCTGGATGGAGATAGGAATATCGTCCCTGCTGGGATGGCAGTTCTTAATCATCTCCC	857
Db	781	TACTCTGGATGGAGATAGGAATATCGTCCCTGCTGGGATGGCAGTTCTTAATCATCTCCC	840
Qy	858	TGCCCTTGCAAAGCTGTTTGGGAAGTTGTTCTCATCTCAGGAGTAAACTGCAACTT	917
Db	841	TGCCCTTGCAAAGCTGTTTGGGAAGTTGTTCTCATCTCAGGAGTAAACTGCAACTT	900
Qy	918	TCACGATGCCAGGATCAGACCATGAATGAAGTTTAACTGGTAAAGGATAATAAANA	977
Db	901	TCACGATGCCAGGATCAGACCATGAATGAAGTTTAACTGGTAAAGGATAATAAANA	960
Qy	978	TGTACGCCCTGGGAAAAGTCAATTTTCAAATCTTATTACCAATTTGAGAAGAAGGAGATTT	1037
Db	961	TGTACGCCCTGGGAAAAGTCAATTTTCAAATCTTATTACCAATTTGAGAAGAAGGAGATTT	1020
Qy	1038	CCAAGATCTCGAGAAGTTCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTCAGTGCAA	1097
Db	1021	CCAAGATCTCGAGAAGTTCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTCAGTGCAA	1080
Qy	1098	GCAAAATCATCGTGTGTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTGATCACAG	1157
Db	1081	GCAAAATCATCGTGTGTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTGATCACAG	1140
Qy	1158	CCAGCCGCGTGTGTTGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCTCT	1217
Db	1141	CCAGCCGCGTGTGTTGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCTCT	1200
Qy	1218	TCCTTCCCTCAGCCATTGAGAGGGTGTAGAGGCAATCGTCAGNCATCCGAAGAATCCAGA	1277

Db	1201	TCTTCC	CCCTCAGCC	ATTGAGAGG	GTGTGAGAGG	CAATCGTCAGCAT	CCGAGAAATCC	GAGA	1260
QY	1278	CC	TTTTTGGCTACTTGATGAGATATC	CACAGCCGCAACCGTCA	CGTCA	CGTCCGCTG	CAGATG	GTAAAA	1337
Db	1261	CC	TTTTTGGCTACTTGATGAGATATC	CACAGCCGCAACCGTCA	CGTCCGCTG	CAGATG	GTAAAA	1320	
QY	1338	AGAT	TG	TGTCATGTGCAGGATTTT	ACTGCTTTTTTGGGAT	TAAGGCAT	CAGAGACCCCA	CTC	1397
Db	1321	AGAT	TG	TGTCATGTGCAGGATTTT	ACTGCTTTTTTGGGAT	TAAGGCAT	CAGAGACCCCA	CTC	1380
QY	1398	TACA	AGGCCCTT	CCTTTTACTGTGCAGACCTG	CGCGAATTTT	TAGCTGTGGT	CGGCCCGGTG		1457
Db	1381	TACA	AGGCCCTT	CCTTTTACTGTGCAGACCTG	CGCGAATTTT	TAGCTGTGGT	CGGCCCGGTG		1440
QY	1458	GAGC	AGGAAAGTCATCACTGTT	TAGTGCCGTGCTCGGGGAAT	TGCCCCCAAGTCAC	GGC			1517
Db	1441	GAGC	AGGAAAGTCATCACTGTT	TAGTGCCGTGCTCGGGGAAT	TGCCCCCAAGTCAC	GGC			1500
QY	1518	TGGT	CA	GC	GTGCATGGAAGAAATTC	CGCTATGTGTC	CAGAGCCCTGGGTG	TTCTCGGAA	1577
Db	1501	TGGT	CA	GC	GTGCATGGAAGAAATTC	CGCTATGTGTC	CAGAGCCCTGGGTG	TTCTCGGAA	1560
QY	1578	CTCT	GAGGAGTAATATTTT	TTTATTTGGGAAAGAAAT	TGAAAAGAA	ACGATATG	AAAAAGTCA		1637
Db	1561	CTCT	GAGGAGTAATATTTT	TTTATTTGGGAAAGAAAT	TGAAAAGAA	ACGATATG	AAAAAGTCA		1620
QY	1638	TAAAG	CTGTGCTCTG	AAAAAGGATTTACAGCTGTT	TGGAGGATG	TGACTG	ACTGTA		1697
Db	1621	TAAAG	CTGTGCTCTG	AAAAAGGATTTACAGCTGTT	TGGAGGATG	TGACTG	ACTGTA		1680
QY	1698	TAGG	GATCGGGAA	CCACGCTGAGTGGAGGGCAG	AAAGCACGGGTAA	ACCTTGC	CAAGAG		1757
Db	1681	TAGG	GATCGGGAA	CCACGCTGAGTGGAGGGCAG	AAAGCACGGGTAA	ACCTTGC	CAAGAG		1740
QY	1758	CAGT	GTATCAAGATGCTG	ACATCTCTCTG	CAGCATCTCTC	TGAGTGCAGT	AGTGC	CGG	1817
Db	1741	CAGT	GTATCAAGATGCTG	ACATCTCTCTG	CAGCATCTCTC	TGAGTGCAGT	AGTGC	CGG	1800
QY	1818	AA	GTTAGCAGACACTT	GTGTTTCCGA	ACTGTGATTTTGTCA	AAATTTTGCATG	AGAAATCACA		1877
Db	1801	AA	GTTAGCAGACACTT	GTGTTTCCGA	ACTGTGATTTTGTCA	AAATTTTGCATG	AGAAATCACA		1860
QY	1878	TTTT	AGTACTCATCACTAGTT	TGCAGTACCTCAA	AGCTGCAAGT	TCAGATCTCTGAT	ATTGAAAG		1937
Db	1861	TTTT	AGTACTCATCACTAGTT	TGCAGTACCTCAA	AGCTGCAAGT	TCAGATCTCTGAT	ATTGAAAG		1920
QY	1938	ATGG	TAAATGTTGCAGAGGGG	ACATCTACTGAGTT	CTCTAAATCTG	GTATAGATTT	GTG		1997
Db	1921	ATGG	TAAATGTTGCAGAGGGG	ACATCTACTGAGTT	CTCTAAATCTG	GTATAGATTT	GTG		1980
QY	1998	GCT	CCCTTTTAAAGAA	AGGATTAATGAGGAA	GTGTAATGCAAC	ACCTCCAGTTC	CAGGAAC	TC	2057
Db	1981	GCT	CCCTTTTAAAGAA	AGGATTAATGAGGAA	GTGTAATGCAAC	ACCTCCAGTTC	CAGGAAC	TC	2040
QY	2058	CAC	TAAAGAAATCGTAC	CTTCTCAGAGTCTTC	GGTTTGGTCTCA	AAATCTCTCTAG	ACCCT		2117
Db	2041	CAC	TAAAGAAATCGTAC	CTTCTCAGAGTCTTC	GGTTTGGTCTCA	AAATCTCTCTAG	ACCCT		2100
QY	2118	CC	TGAAAGATGGT	GTCTCGGAGAGCC	ACAGATATGCC	AGTTACACTAT	PCAG		2177
Db	2101	CC	TGAAAGATGGT	GTCTCGGAGAGCC	ACAGATATGCC	AGTTACACTAT	PCAG		2160
QY	2178	AGG	AAACCGTCTG	TGAAGAAAGTTGGTTT	TTCAGGCCCTAT	TAAGAAAT	TACTT	CAGAGCTG	2237
Db	2161	AGG	AAACCGTCTG	TGAAGAAAGTTGGTTT	TTCAGGCCCTAT	TAAGAAAT	TACTT	CAGAGCTG	2220
QY	2238	GTG	CTCACTGG	ATGCTTCATTTTCC	TTATTTCTTCA	TAACAC	ACTGCAGCT	TCAGGTTGC	2297
Db	2221	GTG	CTCACTGG	ATGCTTCATTTTCC	TTATTTCTTCA	TAACAC	ACTGCAGCT	TCAGGTTGC	2280
QY	2298	ATG	TGCTTCAAGAT	TGGTGGCTTTCAT	CTGCGCAAC	AAACAAAG	ATGCTAA	ATGTC	2357
Db	2281	ATG	TGCTTCAAGAT	TGGTGGCTTTCAT	CTGCGCAAC	AAACAAAG	ATGCTAA	ATGTC	2340

QY	2358	CTGTAATGAGGAGGAAATGTAACCGAGAACTAGATCTTAACTGGTACTTAGGAATTT	2417
Db	2341	CTGTAATGAGGAGGAAATGTAACCGAGAACTAGATCTTAACTGGTACTTAGGAATTT	2400
QY	2418	ATTGAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGTAATCT	2477
Db	2401	ATTGAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGTAATCT	2460
QY	2478	ACGTCCCTGTTAACTCTTCACAAACTTTGCACAACAAATGTTTCAGTCAATCTGAAAG	2537
Db	2461	ACGTCCCTGTTAACTCTTCACAAACTTTGCACAACAAATGTTTCAGTCAATCTGAAAG	2520
QY	2538	CTCGGTATTAATCTTTTGATAGAAATCCAATPAGGAAGAAATTTAAATCGTTTCTCCAAG	2597
Db	2521	CTCGGTATTAATCTTTTGATAGAAATCCAATPAGGAAGAAATTTAAATCGTTTCTCCAAG	2580
QY	2598	ACATTGGACACTTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTTCATCCAGACATTCG	2657
Db	2581	ACATTGGACACTTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTTCATCCAGACATTCG	2640
QY	2658	TACAAGTGGTGGTGTTGCTCTGTGGGTGGGCGGTGATTCCTTGGATCGCAATACCCCT	2717
Db	2641	TACAAGTGGTGGTGTTGCTCTGTGGGTGGGCGGTGATTCCTTGGATCGCAATACCCCT	2700
QY	2718	TGGTTCGCCCTTGGAAATCAATTTTCATTTTCTTCGGCGGATATTTTTTGGAAACGTCAAGG	2777
Db	2701	TGGTTCGCCCTTGGAAATCAATTTTTCATTTTCTTCGGCGGATATTTTTTGGAAACGTCAAGG	2760
QY	2778	ATGTGAAGCGCCTTGGAAATCTACAACCTCGAGTCCAGTCTTTTCCCACTTGTCACTTCCTC	2837
Db	2761	ATGTGAAGCGCCTTGGAAATCTACAACCTCGAGTCCAGTCTTTTCCCACTTGTCACTTCCTC	2820
QY	2838	TCAGGGGCTCTGGACCATCCGGGCATACAAGCAGAAGAGGTGTCAGAACTGTTTG	2897
Db	2821	TCAGGGGCTCTGGACCATCCGGGCATACAAGCAGAAGAGGTGTCAGAACTGTTTG	2880
QY	2898	ATGCACAC - CAGGATTACATTCAGAGGCTTGGTCTTTGTTTTTGACACGTCGCCGTGG	2956
Db	2881	ATGCACACGAGGATTTACATTCAGAGGCTTGGTCTTTGTTTTTGACACGTCGCCGTGG	2940
QY	2957	TTGCGGTCGCTCGATGCCATCTGTGCGCATGTTTTCATCATCTGTTGCCCTTTGGGTCC	3016
Db	2941	TTGCGGTCGCTCGATGCCATCTGTGCCATGTTTGTCACTCATCTGTTGCCCTTTGGGTCC	3000
QY	3017	CTGATCTGCAAAAACACTCTGATCCGGGCAGGTGGTTTGGGCACCTGTCTCTATGCCCTC	3076
Db	3001	CTGATCTGCAAAAACACTCTGATCCGGGCAGGTGGTTTGGGCACCTGTCTCTATGCCCTC	3060
QY	3077	ACGCTCATGGGATGTTTCAGTGGTGTCTGCACAAAGTCTGAAGTTGAGATATATGATG	3136
Db	3061	ACGCTCATGGGATGTTTCAGTGGTGTCTGCACAAAGTCTGAAGTTGAGATATATGATG	3120
QY	3137	ATCTAGTAGAAGGTCATTTGAATACAGACCTTGAAAAGAACACCTTTGGGAATAT	3196
Db	3121	ATCTAGTAGAAGGTCATTTGAATACAGACCTTGAAAAGAACACCTTTGGGAATAT	3180
QY	3197	CAGAAAGCCCAACCCAGCCTGGCCCCATGAGAGTGATATCTTTGACAATGTGAAC	3256
Db	3181	CAGAAAGCCCAACCCAGCCTGGCCCCATGAGAGTGATATCTTTGACAATGTGAAC	3240
QY	3257	TTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCATCTGACGACATCAATAATCA	3316
Db	3241	TTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCATCTGACGACATCAATAATCA	3300
QY	3317	CAGAAAAAGTTGGCATTTGGGAAGAACCGGAGCTGAAAAAGTTCCCTCATCTCAGCC	3376
Db	3301	CAAGAAAAAGTTGGCATTTGGGAAGAACCGGAGCTGAAAAAGTTCCCTCATCTCAGCC	3360
QY	3377	CTTTTATGATTTGTCAGAACCCGAGGTAAAATTTTGGATGATAGATCTTTGACAACTGAA	3436
Db	3361	CTTTTATGATTTGTCAGAACCCGAGGTAAAATTTTGGATGATAGATCTTTGACAACTGAA	3420

QY	3437	ATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTGTTC	3499
DB	3421	ATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTGTTC	3480
QY	3497	ACTGGAAACAATGAGGAAAACCTGGATCCCTTTAAAGGACACACGATGAGGAACCTGTGG	3556
DB	3481	ACTGGAAACAATGAGGAAAACCTGGATCCCTTTAAATGAGCACACGATGAGGAACCTGTGG	3540
QY	3557	AATGCCCTTACAAGAGGTACAACCTTAAAGAAAACCATTTGAAGATCTTCCCTGGTAAAAATGGAT	3616
DB	3541	AATGCCCTTACAAGAGGCACAACCTTAAAGAAAACCATTTGAAGATCTTCCCTGGTAAAAATGGAT	3600
QY	3617	ACTGAATTAGCAGATCAGGATCCCAATTTTAGTGTGGACAAGACAACCTGGTGTGCCTT	3676
DB	3601	ACTGAATTAGCAGATCAGGATCCCAATTTTAGTGTGGACAAGACAACCTGGTGTGCCTT	3660
QY	3677	GCCAGGGCAATTCCTCAGGAAAATCAGATATTGATTATTGATCAAGCGACGGCAAAATGTG	3736
DB	3661	GCCAGGGCAATTCCTCAGGAAAATCAGATATTGATTATTGATCAAGCGACGGCAAAATGTG	3720
QY	3737	GATCCAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAAATTTGCCCACTGCACC	3796
DB	3721	GATCCAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAAATTTGCCCACTGCACC	3780
QY	3797	GTGCTTAACCATTTGCACACAGATTGAACACCATATTATGACAGCGACAAGATAATGGTTTTA	3856
DB	3781	GTGCTTAACCATTTGCACACAGATTGAACACCATATTATGACAGCGACAAGATAATGGTTTTA	3840
QY	3857	GATTCAGGAAGACTGAAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAAGAGAGC	3916
DB	3841	GATTCAGGAAGACTGAAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAAGAGAGC	3900
QY	3917	CTATTTTACAAGATGGTGCAACAACCTGGCAAGGCAAGACGGCTGCCCTCACTGAAACA	3976
DB	3901	CTATTTTACAAGATGGTGCAACAACCTGGCAAGGCAAGACGGCTGCCCTCACTGAAACA	3960
QY	3977	GC AAAACAGGTACTTCAAAAAGAAATATCCACATATTGGTTCACACTGACCCACATGGTT	4036
DB	3961	GC AAAACAGGTACTTCAAAAAGAAATATCCACATATTGGTTCACACTGACCCACATGGTT	4020
QY	4037	ACAACACTTCCAATGGACAGCCCTGACCTTAACATATTTTCGAGACAGACCTGTGAATC	4096
DB	4021	ACAACACTTCCAATGGACAGCCCTGACCTTAACATATTTTCGAGACAGACCTGTGAATC	4080
QY	4097	CAACCAAAATGTCAAGTCGGTCCGAAGGCATTTCCCACTAGTTTTGGACACTGTGTAAC	4156
DB	4081	CAACCAAAATGTCAAGTCGGTCCGAAGGCATTTCCCACTAGTTTTGGACACTGTGTAAC	4140
QY	4157	CACATTTGACTTTTTTTTTACTTTGGCAACAAAATTTATACATACAAGATGCTAGTTTCAT	4216
DB	4141	CACATTTGACTTTTTTTTTACTTTGGCAACAAAATTTATACATACAAGATGCTAGTTTCAT	4200
QY	4217	TTGAATATTTCTCC	4231
DB	4201	TTGAATATTTCTCC	4215

RESULT	9
ABV24188	
ID	ABV24188 standard; cDNA; 4515 BP.
XX	
AC	ABV24188;
XX	
DT	16-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker cDNA 24179.
XX	
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200160860-A2.

XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX PS Claim 1; Page 4506-4507; 11750pp; English.
 XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;
 Query Match 99.2%; Score 4196.6; DB 23; Length 4515;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 18 GGAGCCCGCAGCATCCCTGCTTGGAGTCCAGGAGCGGAGCCCGCCGACCGCCGCTGTAT 77
 DB 1 GGAGCCCGCAGCATCCCTGCTTGGAGTCCAGGAGCGGAGCCCGCCGACCGCCGCTGTAT 60
 QY 78 CAGCGCGACCCCGCCGCGCCGCGCCGCGCCGCGGCAAGATGCTGCCGCTGTACCGAGG 137
 DB 61 CAGCGCGACCCCGCCGCGCCGCGCCGCGCCGCGGCAAGATGCTGCCGCTGTACCGAGG 120
 QY 138 TGAAGCCCAACCCGCTGCAGACCGGACATCTGCTCAGCGGTGTCTTCGGTGGCTCA 197
 DB 121 TGAAGCCCAACCCGCTGCAGACCGGAACTCTGCTCAGCGGTGTCTTCGGTGGCTCA 180
 QY 198 ATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATGATTTCAGTGC 257
 DB 181 ATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATGATTTCAGTGC 240
 QY 258 TGCAGAGACCGCTCAGACACCTTGGAGAGGAGTTGCAAGGTTCTGGGATAAAGAG 317
 DB 241 TGCAGAGACCGCTCAGACACCTTGGAGAGGAGTTGCAAGGTTCTGGGATAAAGAG 300
 QY 318 TTTTAAAGAGCTGAAATGACCCAGACAGCCCTCTTTTAAAGAGCAATATCAAGTGT 377
 DB 301 TTTTAAAGAGCTGAAATGACCCAGACAGCCCTCTTTTAAAGAGCAATATCAAGTGT 360
 QY 378 ACTGGAATCTTATTAGTTTGGGAATTTTACGTTAAATGAGGAAGTCCCAAGTAA 437
 DB 361 ACTGGAATCTTATTAGTTTGGGAATTTTACGTTAAATGAGGAAGTCCCAAGTAA 420

QY 438 TCCAGCCCATATTTTGGGAAAAATTTATTTATTTTGAATAATATCATCCATGGATT 497
 DB 421 TCCAGCCCATATTTTGGGAAAAATTTATTTATTTTGAATAATATCATCCATGGATT 480
 QY 498 CTGTGGCTTTTGAACACACAGCGTACGCCTATGCCACGGTCTGACTTTTTCGACGCTCATTT 557
 DB 481 CTGTGGCTTTTGAACACACAGCGTACGCCTATGCCACGGTCTGACTTTTTCGACGCTCATTT 540
 QY 558 TGGCTATACATCATCACTTATTTTATCATCGTTTCACTGTGCTGGGATGAGGTTACGAG 617
 DB 541 TGGCTATACATCATCACTTATTTTATCATCGTTTCACTGTGCTGGGATGAGGTTACGAG 600
 QY 618 TAGCCATGTGCCATATGATTTATCGAAGGCACCTTCGCTTTAGTAAACATGCCATGGGA 677
 DB 601 TAGCCATGTGCCATATGATTTATCGAAGGCACCTTCGCTTTAGTAAACATGCCATGGGA 660
 QY 678 AGACAACACACAGCGCCAGATAGTCAATCTGCTGTCCAAATGATGTGAACAAGTTTGTATCAGG 737
 DB 661 AGACAACACACAGCGCCAGATAGTCAATCTGCTGTCCAAATGATGTGAACAAGTTTGTATCAGG 720
 QY 738 TGACAGTGTCTTACACTTCTCTGTGGGAGGACCACTGCAGGCGATCGCACTGACTGCC 797
 DB 721 TGACAGTGTCTTACACTTCTCTGTGGGAGGACCACTGCAGGCGATCGCACTGACTGCC 780
 QY 798 TACTCTGGATGGAGATAGGAATATCGTCCCTTGTGGGATGGGAGTCTATATCTCTCC 857
 DB 781 TACTCTGGATGGAGATAGGAATATCGTCCCTTGTGGGATGGGAGTCTATATCTCTCC 840
 QY 858 TGCCCTTGGCAAGCTGTTTGGGAAAGTTGTTCTCATCTCAGGAGTAAACTGCAACTT 917
 DB 841 TGCCCTTGGCAAGCTGTTTGGGAAAGTTGTTCTCATCTCAGGAGTAAACTGCAACTT 900
 QY 918 TCAGGATGCCAGATCAGGACCAATGAAGTTATTAAGTATTAAGGATAATAAAA 977
 DB 901 TCAGGATGCCAGATCAGGACCAATGAAGTTATTAAGTATTAAGGATAATAAAA 960
 QY 978 TGTACGCTGGGAAAGTCAATTTTCAATCTTATTTCAATTTTGAAGAAGAGAGATT 1037
 DB 961 TGTACGCTGGGAAAGTCAATTTTCAATCTTATTTCAATTTTGAAGAAGAGAGATT 1020
 QY 1038 CCAAGATTCTGAGAAGTTCTGCTCAGGGGATGAATTTGGCTTCGTTTTTTCAGTGCAA 1097
 DB 1021 CCAAGATTCTGAGAAGTTCTGCTCAGGGGATGAATTTGGCTTCGTTTTTTCAGTGCAA 1080
 QY 1098 GCAAAATCATCTGTTTGTACCTTCAACACTCAGTGTCTCGGGCAGTGTGATCACAG 1157
 DB 1081 GCAAAATCATCTGTTTGTACCTTCAACACTCAGTGTCTCGGGCAGTGTGATCACAG 1140
 QY 1158 CCAGCCCGCTGTTCGTTGGCAGTCACTGTATGGGGCTGTGGCTGACCGTTACCTCTCT 1217
 DB 1141 CCAGCCCGCTGTTCGTTGGCAGTCACTGTATGGGGCTGTGGCTGACCGTTACCTCTCT 1200
 QY 1218 TCTTCCCTCAGCCATTGAGAGGTTGTAGAGGCAATTCGTCAGCATCCGGAAGATCCAGA 1277
 DB 1201 TCTTCCCTCAGCCATTGAGAGGTTGTAGAGGCAATTCGTCAGCATCCGGAAGATCCAGA 1260
 QY 1278 CTTTTTGTCTACTGTATGATATACAGGCAACCGTCAAGTGTGCTGAGTGGTAAAA 1337
 DB 1261 CTTTTTGTCTACTGTATGATATACAGGCAACCGTCAAGTGTGCTGAGTGGTAAAA 1320
 QY 1338 AGATGTCATGTGTCAGGATTTTACTGCTTTTGGGATAGGATAGGATAGGATAGGATAGGAT 1397
 DB 1321 AGATGTCATGTGTCAGGATTTTACTGCTTTTGGGATAGGATAGGATAGGATAGGATAGGAT 1380
 QY 1398 TACAAGGCTTTTCTTTTACTGTGTCAGACCTGGCGAATTTTGTAGTGTGGTGGCGCGTGG 1457
 DB 1381 TACAAGGCTTTTCTTTTACTGTGTCAGACCTGGCGAATTTTGTAGTGTGGTGGCGCGTGG 1440
 QY 1458 GAGCAGGAGTCACTGTTTAAAGTGGCGTGTCTGGGGAATTTGGCCCCAAGTACAGGCG 1517
 DB 1441 GAGCAGGAGTCACTGTTTAAAGTGGCGTGTCTGGGGAATTTGGCCCCAAGTACAGGCG 1500

QY 1518 TGGTCAGCGTCGATGAAGAATTCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAA 1577
Db 1501 TGGTCAGCGTCGATGAAGAATTCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAA 1560
QY 1578 CTCTGAGGAGTAATATTTATTTGGGAAGAAATATGAAAAGGAACGATATGAAAAGTCA 1637
Db 1561 CTCTGAGGAGTAATATTTATTTGGGAAGAAATACGAAAAGGAACGATATGAAAAGTCA 1620
QY 1638 TAAAGGCTGTGTCTCTGAAAAGGATTTACAGCTGTGTGGAGGATGGTGATCTGACTGTGA 1697
Db 1621 TAAAGGCTGTGTCTCTGAAAAGGATTTACAGCTGTGTGGAGGATGGTGATCTGACTGTGA 1680
QY 1698 TAGGAGATCGGGAAACCGCTCAGCTGGAGGCGAGAAAGCACGGGTAAACCTTGCRAAG 1757
Db 1681 TAGGAGATCGGGAAACCGCTCAGCTGGAGGCGAGAAAGCACGGGTAAACCTTGCRAAG 1740
QY 1758 CAGTGATCAAGATGCTGACATCTATCTCTCTGGACGATCTCTCAGTGCAAGTAGATCGG 1817
Db 1741 CAGTGATCAAGATGCTGACATCTATCTCTCTGGACGATCTCTCAGTGCAAGTAGATCGG 1800
QY 1818 AAGTTAGCAGACACTTGTTCGAACTGTGATTTGTCAAAATTTTGCATGAGAAGATCACAA 1877
Db 1801 AAGTTAGCAGACACTTGTTCGAACTGTGATTTGTCAAAATTTTGCATGAGAAGATCACAA 1860
QY 1878 TTTTAGTACTCATCAGTTGCAGTACTCTCAAAGCTGCAAGTCAAGTCAAGTATGAAAG 1937
Db 1861 TTTTAGTACTCATCAGTTGCAGTACTCTCAAAGCTGCAAGTCAAGTCAAGTATGAAAG 1920
QY 1938 ATGGTAAATGGTGCAAGAGGAGCTTACACTGAGTTCCTTAAATCTGGTATAGATTTTG 1997
Db 1921 ATGGTAAATGGTGCAAGAGGAGCTTACACTGAGTTCCTTAAATCTGGTATAGATTTTG 1980
QY 1998 GTCCTCTTTAAAGAAAGTAATAGGAAAGTGAACAACCTCCAGTTCAGGAACCTCCCA 2057
Db 1981 GTCCTCTTTAAAGAAAGTAATAGGAAAGTGAACAACCTCCAGTTCAGGAACCTCCCA 2040
QY 2058 CACTAAGGAATCGTACTCTCAGAGTCTTCGTTTGGTCTCAACAATCTTCTAGACCT 2117
Db 2041 CACTAAGGAATCGTACTCTCAGAGTCTTCGTTTGGTCTCAACAATCTTCTAGACCT 2100
QY 2118 CTTGAAAGATGGTCTCTGGAGAGCAAGATACAGAGATGTCCTCAGTTCACACTATCAG 2177
Db 2101 CTTGAAAGATGGTCTCTGGAGAGCAAGATACAGAGATGTCCTCAGTTCACACTATCAG 2160
QY 2178 AGGAGAACCGTCTCTGAAGAAAGTTGGTTTTCAGGCTTATAAGAAATTAATTCAGAGCTG 2237
Db 2161 AGGAGAACCGTCTCTGAAGAAAGTTGGTTTTCAGGCTTATAAGAAATTAATTCAGAGCTG 2220
QY 2238 GTGCTCACTGGATGTCTTCATTTCTTATTTCTCTTAACACTGCAGCTCAGGTTGCCT 2297
Db 2221 GTGCTCACTGGATGTCTTCATTTCTTATTTCTCTTAACACTGCAGCTCAGGTTGCCT 2280
QY 2298 ATGTGCTTCAAGATGGTGGCTTCTACTGGGCAACAAACAAAGTATGCTAAATGTCA 2357
Db 2281 ATGTGCTTCAAGATGGTGGCTTCTACTGGGCAACAAACAAAGTATGCTAAATGTCA 2340
QY 2358 CTGTAATGGAGAGAAATGTAACCGAGAGCTAGATCTTAAGTGGTACTTAGGAATTT 2417
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QY 2418 ATTCAGGTTTAACTGTAGCTACCGTCTTTTGGCATACAGATCTCTATTTGGTATCT 2477
Db 2401 ATTCAGGTTTAACTGTAGCTACCGTCTTTTGGCATACAGATCTCTATTTGGTATCT 2460
QY 2478 AGCTCCTGTTAACTCTTCAACAACTTTCACAAACAAATGTTTGGTCAATTTCTGAAAG 2537
Db 2461 AGCTCCTGTTAACTCTTCAACAACTTTCACAAACAAATGTTTGGTCAATTTCTGAAAG 2520
QY 2538 CTCGGGTATATCTTTGTATAGAAATCCAAATAGGAAGATTTTAAATCGTTTCTCCAAAG 2597
Db 2521 CTCGGGTATATCTTTGTATAGAAATCCAAATAGGAAGATTTTAAATCGTTTCTCCAAAG 2580
QY 2598 ACATGGACACTTGGATGATTTGCTGCCCTGACGTTTTTAGATTTTCATCCAGACATTCG 2657

Db 2581 ACATGGACACTTGGATGATTTGCTGCCCTGACGTTTTTAGATTTTCATCCAGACATTCG 2640
QY 2658 TACAAGTGGTGGTGGTCTCTCTGCTGGCTGGCCGTCGATTCCTTGGATCCCAATACCT 2717
Db 2641 TACAAGTGGTGGTGGTCTCTCTGCTGGCTGGCCGTCGATTCCTTGGATCCCAATACCT 2700
QY 2718 TGGTTCCTTGGGAATCATTTTTCATTTTCTCGCGGATATTTTGGGAAACGTCAGAG 2777
Db 2701 TGGTTCCTTGGGAATCATTTTTCATTTTCTCGCGGATATTTTGGGAAACGTCAGAG 2760
QY 2778 ATGTGAAGCGCTCGGAATCTACAACTCGAGTCCAGTGTTTTCCCACTTGTCTCTCTC 2837
Db 2761 ATGTGAAGCGCTCGGAATCTACAACTCGAGTCCAGTGTTTTCCCACTTGTCTCTCTC 2820
QY 2838 TCCAGGGGCTCTGACACCTCCGGGCATACAAAGCAGAGAGAGGTGTCCAGAACTGTTG 2897
Db 2821 TCCAGGGGCTCTGACACCTCCGGGCATACAAAGCAGAGAGAGGTGTCCAGAACTGTTG 2880
QY 2898 ATGCACAC - CAGGATTTACATTCAGAGCTTGGTCTTGTGTTTGGACAACTCCGCTGG 2956
Db 2881 ATGCACACGAGGATTTACATTCAGAGCTTGGTCTTGTGTTTGGACAACTCCGCTGG 2940
QY 2957 TCCGCCCTCCCTCTGGATGCCATCTGTGCCATGTGTTCATCATCTGTTGGGTCC 3016
Db 2941 TCCGCCCTCCCTCTGGATGCCATCTGTGCCATGTGTTCATCATCTGTTGGGTCC 3000
QY 3017 CTGATTCCTGCAAAACTCTGGATGCCGGCAGGTTGGTTGGCACTGTCTATGCCCTC 3076
Db 3001 CTGATTCCTGCAAAACTCTGGATGCCGGCAGGTTGGTTGGCACTGTCTATGCCCTC 3060
QY 3077 ACCTCATGCGGATGTTTTCAGTGGTGTTCGACAAAGTGTGAAAGTGAAGTATGATG 3136
Db 3061 ACCTCATGCGGATGTTTTCAGTGGTGTTCGACAAAGTGTGAAAGTGAAGTATGATG 3120
QY 3137 ATCTCAGTAGAAGGTCATTTGAATACACAGACCTTGAAAGAAAGCACTTGGGAATAT 3196
Db 3121 ATCTCAGTAGAAGGTCATTTGAATACACAGACCTTGAAAGAAAGCACTTGGGAATAT 3180
QY 3197 CAGAAAGCCACACACAGCTGCCCCCATGAGAGTGAATCTTTGACAAATGTGAC 3256
Db 3181 CAGAAAGCCACACACAGCTGCCCCCATGAGAGTGAATCTTTGACAAATGTGAC 3240
QY 3257 TTCTATGACAGTCCAGTGGGCTCTGCTGTAAGAGCATCTGACAGCACTCATTTAAATCA 3316
Db 3241 TTCTATGACAGTCCAGTGGGCTCTGCTGTAAGAGCATCTGACAGCACTCATTTAAATCA 3300
QY 3317 CAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTCCCTCATCTCAGCC 3376
Db 3301 CAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTCCCTCATCTCAGCC 3360
QY 3377 CTTTTAGATTTGACAAAGGTAATTTGGGATGATAGATCTTTGACAACTGAA 3436
Db 3361 CTTTTAGATTTGACAAAGGTAATTTGGGATGATAGATCTTTGACAACTGAA 3420
QY 3437 ATTTGACCTTCAAGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTTC 3496
Db 3421 ATTTGACCTTCAAGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTTC 3480
QY 3497 ACTGGAAACATGAGGAAACCTTGGATCCCTTTAAGGACACAGGATGAGGAACTGTGG 3556
Db 3481 ACTGGAAACATGAGGAAACCTTGGATCCCTTTAAGGACACAGGATGAGGAACTGTGG 3540
QY 3557 AATGCCCTTACAAGAGTACAACTTAAAGAAACCATTTCAAGATCTTCTGGTAAATGGAT 3616
Db 3541 AATGCCCTTACAAGAGGACAACTTAAAGAAACCATTTCAAGATCTTCTGGTAAATGGAT 3600
QY 3617 ACTGAATTAGCAGAACTCAGGATCCAAATTTTAGTGTGGCAAAAGCACTGGTGTGCTT 3676
Db 3601 ACTGAATTAGCAGAACTCAGGATCCAAATTTTAGTGTGGCAAAAGCACTGGTGTGCTT 3660
QY 3677 GCCAGGCAATCTCAGGAAAAATCAGATATGATTAATGATGAAGCAGCGCAATGTG 3736

Db 3661 GCAGGGCAATTCAGGAAATCAGATATTCATTATTGATGAAGCGACGCAATATG 3720
QY 3737 GATCCAGAACTGATGAGTTAATACAAAAAATCCGGGAGAAATTTGCCCACTGCACC 3796
Db 3721 GATCCAGAACTGATGAGTTAATACAAAAAATCCGGGAGAAATTTGCCCACTGCACC 3780
QY 3797 GTGCTAACCATTCACACAGATTTGACACCATATTTAGACAGGACAGATATGTTTA 3856
Db 3781 GTGCTAACCATTCACACAGATTTGACACCATATTTAGACAGGACAGATATGTTTA 3840
QY 3857 GATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTGTGCTGCAAAATAAAGAGAGC 3916
Db 3841 GATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTGTGCTGCAAAATAAAGAGAGC 3900
QY 3917 CTATTTTACAAGATGGTGAACAATCGGCAAGGAGGAGCGGCTGCCCTCACTGAAACA 3976
Db 3901 CTATTTTACAAGATGGTGAACAATCGGCAAGGAGGAGCGGCTGCCCTCACTGAAACA 3960
QY 3977 GCAAAACAGGTATCTTCAAAAGAAATATCCACATATTTGTCACACTGACCATGTT 4036
Db 3961 GCAAAACAGGTATCTTCAAAAGAAATATCCACATATTTGTCACACTGACCATGTT 4020
QY 4037 ACAAACTTCCATGAGACAGCCCTCGACCTTAATCTATTTTCGAGACAGCACTGTGAATC 4096
Db 4021 ACAAACTTCCATGAGACAGCCCTCGACCTTAATCTATTTTCGAGACAGCACTGTGAATC 4080
QY 4097 CAACCAAAATGTCAAGTCCGTTCCGAAGGCAATTTTCCACTAGTTTGGACTATGTAAC 4156
Db 4091 CAACCAAAATGTCAAGTCCGTTCCGAAGGCAATTTTCCACTAGTTTGGACTATGTAAC 4140
QY 4157 CACATTGTACTTTTTTTTACTTTGGCAACAATATTTATACATAACAAGATGCTAGTTCAT 4216
Db 4141 CACATTGTACTTTTTTTTACTTTGGCAACAATATTTATACATAACAAGATGCTAGTTCAT 4200
QY 4217 TTGAATATTTCTCC 4231
Db 4201 TTGAATATTTCTCC 4215

RESULT 10

ABV24580
ID ABV24580 standard; cDNA; 4515 BP.

XX AC ABV24580;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 24571.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US051171.

XX 17-FEB-2000; 2000US-183319P.

XX 16-MAR-2000; 2000US-189862P.

XX 25-MAY-2000; 2000US-207454P.

XX 09-JUN-2000; 2000US-211314P.

XX 18-JUL-2000; 2000US-219007P.

XX 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX

PS Claim 1; Page 4662-4663; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX

SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;

Query Match

Best Local Similarity 99.2%; Score 4196.6; DB 23; Length 4515;

Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 18 GGAGCCCCAGCATCCCTGCTTGGAGTCCAGAGCGGAGCCCGGGCCACCGCCCTGAT 77

Db 1 GGAGCCCCAGCATCCCTGCTTGGAGTCCAGAGCGGAGCCCGGGCCACCGCCCTGAT 60

QY 78 CAGCGCGACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 137

Db 61 CAGCGCGACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 120

QY 138 TGAAGCCCCAACCGCTGCGAGGACGCGAACAATCTGCTCACGCGTGTCTTCTGCTGCTCA 197

Db 121 TGAAGCCCCAACCGCTGCGAGGACGCGAACAATCTGCTCACGCGTGTCTTCTGCTGCTCA 180

QY 198 ATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATATATGATTCAGTGC 257

Db 181 ATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATATATGATTCAGTGC 240

QY 258 TGCCAGAACCGCTCACAGACACCTTTGGAGAGGAGTTGCAAGGGTCTGGGATAAAGAG 317

Db 241 TGCCAGAACCGCTCACAGACACCTTTGGAGAGGAGTTGCAAGGGTCTGGGATAAAGAG 300

QY 318 TTTTAAGAGCTGAGATGACGACAGAGCGCTTCTTTTAAACAGAGCAATCATATAAGTGT 377

Db 301 TTTTAAGAGCTGAGATGACGACAGAGCGCTTCTTTTAAACAGAGCAATCATATAAGTGT 360

QY 378 ACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTAAATGAGGAAAGTCCAAAGTAA 437

Db 361 ACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTAAATGAGGAAAGTCCAAAGTAA 420

QY 438 TCCAGCCCATATTTTGGGAAAATTTAAATATTTTGAATAATATGATCCCATGGATT 497

Db 421 TCCAGCCCATATTTTGGGAAAATTTAAATATTTTGAATAATATGATCCCATGGATT 480

QY 498 CTGTGGCTTTGAACACAGCGTACGGCTATGCGACGCTGCTGACTTTTTCACGCTCATTT 557

Db 481 CTGTGGCTTTGAACACAGCGTACGGCTATGCGACGCTGCTGACTTTTTCACGCTCATTT 540

QY 558 TGGCTATACATGACATATATTTTATACGTTTCACTGCTGCTGGATGAGGTACAGAG 617

Db 541 TGGCTATACATGACATATATTTTATACGTTTCACTGCTGCTGGATGAGGTACAGAG 600

QY 618 TAGCCATGTCATATGATTATTCGGAAGGCACTTCGCTTATAGTAACATGGCCATGGGA 677

Db 601 TAGCCATGTCATATGATTATTCGGAAGGCACTTCGCTTATAGTAACATGGCCATGGGA 660

QY 678 AGACAACCACAGGCCAGATAGTCAATCTGCTGCCAATCATGTGAACAAGTTTGATCAGG 737

Db 661 AGACACACAGGCCAGATAGTCAATCTGCTCCATGATGTAACAGTTGATCAGG 720
Qy 738 TGACAGTGTGTTACACTTCCGTGGCAGACCACTGCAGCGCATCGCACTGCCCC 797
Db 721 TGACAGTGTGTTACACTTCCGTGGCAGACCACTGCAGCGCATCGCACTGCCCC 780
Qy 798 TACTCTGGATGGAGATAGGATATCGTGCCTTGGTGGATGGGAGTTCTAATCATTTCC 857
Db 781 TACTCTGGATGGAGATAGGATATCGTGCCTTGGTGGATGGGAGTTCTAATCATTTCC 840
Qy 858 TGCCCTTGCAAGCTGTTTGGGAAGTGTCTCATCACTGAGGAGTAAACTGCACTT 917
Db 841 TGCCCTTGCAAGCTGTTTGGGAAGTGTCTCATCACTGAGGAGTAAACTGCACTT 900
Qy 918 TCACGGATGCCAGGATCAGGACCACTGAATGAAGTTAATCACTGATGAAGTAATAAAA 977
Db 901 TCACGGATGCCAGGATCAGGACCACTGAATGAAGTTAATCACTGATGAAGTAATAAAA 960
Qy 978 TGTACGCTGGGAAAGTCAATTTCAATCTTATACCAATTTGAGAAAGAGATTT 1037
Db 961 TGTACGCTGGGAAAGTCAATTTCAATCTTATACCAATTTGAGAAAGAGATTT 1020
Qy 1038 CCAAGATCTTGAGAAGTTCCTGCTCAGGGGATGAATTTGGCTTCCTTTTTCAGTGCAA 1097
Db 1021 CCAAGATCTTGAGAAGTTCCTGCTCAGGGGATGAATTTGGCTTCCTTTTTCAGTGCAA 1080
Qy 1098 GCAAAATCATCGTGTGTTGTGACCTTCCACCCTACGCTGCTCCGCGCAGTGTATCACAG 1157
Db 1081 GCAAAATCATCGTGTGTTGTGACCTTCCACCCTACGCTGCTCCGCGCAGTGTATCACAG 1140
Qy 1158 CCAGCCGCTGTTGCTGGCAGTGAACGCTGTATGGGCTGTGGGCTGACGGTTACCCCTCT 1217
Db 1141 CCAGCCGCTGTTGCTGGCAGTGAACGCTGTATGGGCTGTGGGCTGACGGTTACCCCTCT 1200
Qy 1218 TCTTCCCTCAGCCATGAGAGGTTGTCAGAGGCAATCTGACATCCGGAAGATCCAGA 1277
Db 1201 TCTTCCCTCAGCCATGAGAGGTTGTCAGAGGCAATCTGACATCCGGAAGATCCAGA 1260
Qy 1278 CTTTTTGTCTACTGTAGATATACAGCGCAACCGTCAGCTGCCGTGAGATGGTAAAA 1337
Db 1261 CTTTTTGTCTACTGTAGATATACAGCGCAACCGTCAGCTGCCGTGAGATGGTAAAA 1320
Qy 1338 AGATGTCATGTGCAGGATTTTACTGCTTTTGGGATAGGATACAGACCCCACTC 1397
Db 1321 AGATGTCATGTGCAGGATTTTACTGCTTTTGGGATAGGATACAGACCCCACTC 1380
Qy 1398 TACAAGCCCTTCCCTTACTGTGACAGCTGGCGAATTTGTTAGCTGTGGTGGCCCGCTGG 1457
Db 1381 TACAAGCCCTTCCCTTACTGTGACAGCTGGCGAATTTGTTAGCTGTGGTGGCCCGCTGG 1440
Qy 1458 GAGCAGGAAGTCACTACTGTTAAAGTCCGTGCTCGGGGAATTTGGCCCAAGTCACGGGC 1517
Db 1441 GAGCAGGAAGTCACTACTGTTAAAGTCCGTGCTCGGGGAATTTGGCCCAAGTCACGGGC 1500
Qy 1518 TGCTCAGCTGCAATGGAAGATTTGCTATGCTGCTCAGACGCCCTGGGTTCTCGGGAA 1577
Db 1501 TGCTCAGCTGCAATGGAAGATTTGCTATGCTGCTCAGACGCCCTGGGTTCTCGGGAA 1560
Qy 1578 CTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAAAAGGAACGATATGAAAAGTCA 1637
Db 1561 CTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAAAAGTCA 1620
Qy 1638 TAAAGCTGTGCTCTGAAAAGGATTTTACAGCTGTGGAGGATGGTACTGACTGTGA 1697
Db 1621 TAAAGCTGTGCTCTGAAAAGGATTTTACAGCTGTGGAGGATGGTACTGACTGTGA 1680
Qy 1698 TAGGAGATCGGGGAACCACTGAGTGGAGGCGAGAAAGCACCGGTTAAACCTTGCAGAG 1757
Db 1681 TAGGAGATCGGGGAACCACTGAGTGGAGGCGAGAAAGCACCGGTTAAACCTTGCAGAG 1740
Qy 1758 CAGTGTATCAAGATGTGACATCTATCTCTGACCATCTCTCAGTGCAGTATGATCCGG 1817
Db 1821 TCAGGGGCTCTGGACCATCCGGGCATACAAAGCAAGAGAGAGGTGTGAGGAACTGTTG 2880

Db 1741 CAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTAGATCGG 1800
Qy 1818 AAGTTAGCAGACACTGTTTCGAACTGTGTATTTGTCAAAATTTTGCATGAGAAGATCACAA 1877
Db 1801 AAGTTAGCAGACACTGTTTCGAACTGTGTATTTGTCAAAATTTTGCATGAGAAGATCACAA 1860
Qy 1878 TTTTAGTGACTCATCAGTTGCGAGTACCTCAAGCTGCAAGTGCAGATTTCTGATATTGAAAG 1937
Db 1861 TTTTAGTGACTCATCAGTTGCGAGTACCTCAAGCTGCAAGTGCAGATTTCTGATATTGAAAG 1920
Qy 1938 ATGTTAAATGTTGCAGAGGGGACTTACACTGAGTTCCTTAAATCTGGTATAGATTTTG 1997
Db 1921 ATGTTAAATGTTGCAGAGGGGACTTACACTGAGTTCCTTAAATCTGGTATAGATTTTG 1980
Qy 1998 GCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAACAACCTCCAGTTCGAGGAATCCCA 2057
Db 1981 GCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAACAACCTCCAGTTCGAGGAATCCCA 2040
Qy 2058 CACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTCCTCAACAATCTTCTAGACCT 2117
Db 2041 CACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTCCTCAACAATCTTCTAGACCT 2100
Qy 2118 CCTTGAAGATGGTCTCTGAGAGCCCAAGATACAGAGAATGTCCAGTTTACACTATCAG 2177
Db 2101 CCTTGAAGATGGTCTCTGAGAGCCCAAGATACAGAGAATGTCCAGTTTACACTATCAG 2160
Qy 2178 AGGAGAACCGTCTGAAAGAAAGTGTGTTTTCAGGCTTATAAGAAATTTACTTTCAGAGCTG 2237
Db 2161 AGGAGAACCGTCTGAAAGAAAGTGTGTTTTCAGGCTTATAAGAAATTTACTTTCAGAGCTG 2220
Qy 2238 GTGCTCAGTGGATGTCTTCAATTTTCCCTTATTTCTTAAACACTGCAGCTCAGGTTGCT 2297
Db 2221 GTGCTCAGTGGATGTCTTCAATTTTCCCTTATTTCTTAAACACTGCAGCTCAGGTTGCT 2280
Qy 2298 ATGTCCTTCAAGATTTGTCGCTTTCATCTGCGGCAACAAAGATGTCTAAATGTCA 2357
Db 2281 ATGTCCTTCAAGATTTGTCGCTTTCATCTGCGGCAACAAAGATGTCTAAATGTCA 2340
Qy 2358 CTGTAATTTGAGGAGGAAATGTAACCGAGAGCTAGATCTTAACTGGTACTTAAAGAAATTT 2417
Db 2341 CTGTAATTTGAGGAGGAAATGTAACCGAGAGCTAGATCTTAACTGGTACTTAAAGAAATTT 2400
Qy 2418 ATTACAGTTTAACTGTAGCTTACCTTCTTTTGGCATAGCAAGATCTCTATTTGATTTCT 2477
Db 2401 ATTACAGTTTAACTGTAGCTTACCTTCTTTTGGCATAGCAAGATCTCTATTTGATTTCT 2460
Qy 2478 AGTCCCTTGTAACTCTTCAAACTTTCACAACTTTCGACAACTTTTTCAGTCAATTTCTGAAG 2537
Db 2461 AGTCCCTTGTAACTCTTCAAACTTTCGACAACTTTTTCGACAACTTTTTCGAGTCAATTTCTGAAG 2520
Qy 2538 CTCGGTATTATTCTTTTGTAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTTCCAAAG 2597
Db 2521 CTCGGTATTATTCTTTTGTAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTTCCAAAG 2580
Qy 2598 ACATTGACACTTGGATGATTTGCTGCGCTGACGTTTGTAGATTTTTCATCAGACATTCG 2657
Db 2581 ACATTGACACTTGGATGATTTGCTGCGCTGACGTTTGTAGATTTTTCATCAGACATTCG 2640
Qy 2658 TACAAGTGGTGGTGTGCTCTGCTGCTGCTGCGCTGATTCCTTGGATCGCAATACCT 2717
Db 2641 TACAAGTGGTGGTGTGCTCTGCTGCTGCTGCGCTGATTCCTTGGATCGCAATACCT 2700
Qy 2718 TGGTTCCTTCTTGAATCATTTTTCATTTTCTTCCGCGATATTTTTCGAAACGTCGAAG 2777
Db 2701 TGGTTCCTTCTTGAATCATTTTTCATTTTCTTCCGCGATATTTTTCGAAACGTCGAAG 2760
Qy 2778 ATGTGAAGCCCTTGGAAATCTACAACTCGAGTCCAGTGTGTTTTCCTACTGTGCTTCTC 2837
Db 2761 ATGTGAAGCCCTTGGAAATCTACAACTCGAGTCCAGTGTGTTTTCCTACTGTGCTTCTC 2820
Qy 2838 TCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAAGAGAGAGGTGTGAGGAACTGTTG 2897
Db 2821 TCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAAGAGAGAGGTGTGAGGAACTGTTG 2880

QY	2898	ATGCACAC-CAGGATTTACATTCAGAGGCTTGCTTCTTGTGTTTTGACAACTGCCGCTGG	2955
DB	2881	ATGCACACGACGAGTTTACATTCAGAGGCTTGCTTCTTGTGTTTTGACAACTGCCGCTGG	2940
QY	2957	TTGCGCGTCCGCTTGATGCGCAATCTGCGCATGTTTGTGCATCATCGTTGCTTTGGGTGTC	3016
DB	2941	TTGCGCGTCCGCTTGATGCGCAATCTGCGCATGTTTGTGCATCATCGTTGCTTTGGGTGTC	3000
QY	3017	CTGATTTCTGGCAAAACTCTGGATGCCGGCAGTTGGTTTGGCACTGTCTATGCCCTC	3076
DB	3001	CTGATTTCTGGCAAAACTCTGGATGCCGGCAGTTGGTTTGGCACTGTCTATGCCCTC	3060
QY	3077	ACGCTCATGGGATGTTTCAGTGGTGTTCGACAAAGTCTGAACTTGAGATATGATG	3136
DB	3061	ACGCTCATGGGATGTTTCAGTGGTGTTCGACAAAGTCTGAGTGTGAGATATGATG	3120
QY	3137	ATCTCAGTAGAAGGTCATTAATACACAGACCTTTGAAAAAGAACACCTTTGGGAATAT	3196
DB	3121	ATCTCAGTAGAAGGTCATTAATACACAGACCTTTGAAAAAGAACACCTTTGGGAATAT	3180
QY	3197	CAGAAAGCCCAACCAACAGCTGGCCCATGAAGGAGTGATTAATCTTTGACAACTGTAAC	3256
DB	3181	CAGAAAGCCCAACCAACAGCTGGCCCATGAAGGAGTGATTAATCTTTGACAACTGTAAC	3240
QY	3257	TTCTATGATCAGTCCAGTGGGCTCTGGTACTGAAGCATCTGACAGCACTCAATTAATCA	3316
DB	3241	TTCTATGATCAGTCCAGTGGGCTCTGGTACTGAAGCATCTGACAGCACTCAATTAATCA	3300
QY	3317	CAAGAAAAGTTGGCATTTGGGGAAGAACCCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC	3376
DB	3301	CAAGAAAAGTTGGCATTTGGGGAAGAACCCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC	3360
QY	3377	CTTTTTCAGATGTCAGAACCCGAGGTAAATTTGGATTGATAAGATCTTTGACAACTGAA	3436
DB	3361	CTTTTTCAGATGTCAGAACCCGAGGTAAATTTGGATTGATAAGATCTTTGACAACTGAA	3420
QY	3437	ATTGACTTCAGATTTAAGGAAGAAAAATGTCAATCATACCTTCAGGAACCTGTTTGTTC	3496
DB	3421	ATTGACTTCAGATTTAAGGAAGAAAAATGTCAATCATACCTTCAGGAACCTGTTTGTTC	3480
QY	3497	ACTGGACAATGAGGAAAAACCTTGGATCCCTTTAAGGAGCACACGGATGAGGAACCTGG	3556
DB	3481	ACTGGACAATGAGGAAAAACCTTGGATCCCTTTAATGAGCACACGGATGAGGAACCTGG	3540
QY	3557	AATGCCTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCCCTGGTAAATGGAT	3616
DB	3541	AATGCCTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCCCTGGTAAATGGAT	3600
QY	3617	ACTGAATTAGCAGATCAGGATCCAAATTTTAGTGTGGACAAAGACAACTGGTGTGCCCTT	3676
DB	3601	ACTGAATTAGCAGATCAGGATCCAAATTTTAGTGTGGACAAAGACAACTGGTGTGCCCTT	3660
QY	3677	GCCAGGGCAATCTCAGAAAAATCAGATATTGATTATGATGAAGCAGCGCAAAATGTG	3736
DB	3661	GCCAGGGCAATCTCAGAAAAATCAGATATTGATTATGATGAAGCAGCGCAAAATGTG	3720
QY	3737	GATCCAAAGACTGATGAGTTAAATACAAAAAATCCGGAGAAATTTGCCCACTGCACC	3796
DB	3721	GATCCAAAGACTGATGAGTTAAATACAAAAAATCCGGAGAAATTTGCCCACTGCACC	3780
QY	3797	GTGCTAACCAATTCACACAGATTGAACACCAATTTATGACAGCGACAGATTAATGGTTTTA	3856
DB	3781	GTGCTAACCAATTCACACAGATTGAACACCAATTTATGACAGCGACAGATTAATGGTTTTA	3840
QY	3857	GATTCAGGAAGACTGAAGAATATGATGAGCCGATGTTTGTCTGCAAAATAAAGAGAGC	3916
DB	3841	GATTCAGGAAGACTGAAGAATATGATGAGCCGATGTTTGTCTGCAAAATAAAGAGAGC	3900
QY	3917	CTATTTTACAAAGATGGTGCACAACTGGCGAAGCAGAGCCGCTGCCTCAGTGAACA	3976
DB	3901	CTATTTTACAAAGATGGTGCACAACTGGCGAAGCAGAGCCGCTGCCTCAGTGAACA	3960

QY	3977	GC	AAACAGGTATAC	TTCAAAAGAAAT	TTCACATAT	TGGTCACAC	TGACCATGGTT	4036
Db	3961	GC	AAACAGGTATAC	TTCAAAAGAAAT	TTCACATAT	TGGTCACAC	TGACCATGGTT	4020
QY	4037	AC	AAACACAT	TCCAAATGG	CAGCCCTCG	ACCTTAACTAT	TTTCGACAGCAGCTGTGAATC	4096
Db	4021	AC	AAACACAT	TCCAAATGG	CAGCCCTCG	ACCTTAACTAT	TTTCGACAGCAGCTGTGAATC	4080
QY	4097	CA	ACCAAAATG	TCAAGTCGG	TCCGAAGSCAT	TTTCCACTAG	TTTTTGGCACTATGTAAAC	4156
Db	4081	CA	ACCAAAATG	TCAAGTCGG	TCCGAAGSCAT	TTTCCACTAG	TTTTTGGCACTATGTAAAC	4140
QY	4157	CAC	ATTGTACT	TTTTTTTACT	TTGGCAACAAT	TATTTATACAT	ACAGATGCTAGTTCAT	4216
Db	4141	CAC	ATTGTACT	TTTTTTTACT	TTGGCAACAAT	TATTTATACAT	ACAGATGCTAGTTCAT	4200
QY	4217	TT	GAATAT	TTCTCC				4231
Db	4201	TT	GAATAT	TTCTCC				4215

RESULT 11.

ABV26511	
ID	ABV26511 standard; cDNA: 4515 BP.
XX	
AC	ABV26511;
XX	
DT	16-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker cDNA 26502.
XX	
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200160860-A2.
XX	
PD	23-AUG-2001.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 5356-5357; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

- (a) assessing whether a patient is afflicted with prostate cancer;
- (b) monitoring the progression of prostate cancer in a patient;
- (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

- (e) selecting a composition for inhibiting prostate cancer in a patient;
- (f) assessing the prostate cell carcinogenic potential of a compound;
- (g) determining whether prostate cancer has metastasized in a patient;

Db 4201 TTGAATATTTCTCCC 4215

RESULT 12
ABV28224
ID ABV28224 standard; cDNA; 4515 BP.
XX
AC ABV28224;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 28215.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 5861-5862; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;
SQ

Query Match 99.2%; Score 4196.6; DB 23; Length 4515;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1

QY 18 GGAGCCCGACCATCCCTCTGAGTCCAGAGCGGAGCCCGCCGCCACCGCGCGCTGAT 77
Db 1 GGAGCCCGACCATCCCTCTGAGTCCAGAGCGGAGCCCGCCGCCACCGCGCGCTGAT 60
QY 78 CAGCGGACCCCGCCGCCCGCCGCCCGCCGCAAGATGTCGCCGTGTACCGAGGAG 137
Db 61 CAGCGGACCCCGCCGCCCGCCGCCCGCCGCAAGATGTCGCCGTGTACCGAGGAG 120

Db	1201	TC	TTTTCCCTCAGCCATTGAGAGGGTGTACAGAGCAATCGTCAGCATCCGAGGATCCAGA	1260
Qy	1278	CC	TTTTTGTCTACTTGATGAGATATCACAGCGCAACCGTCAGCTCGCGTCAGATGGTAAAA	1337
Db	1261	CC	TTTTTGTCTACTTGATGAGATATCACAGCGCAACCGTCAGCTCGCGTCAGATGGTAAAA	1320
Qy	1338	AG	ATGATGTCATGTCAGGATTTTACTGCTTTTGGATAAGGCATCAGAGACCCCAACTC	1397
Db	1321	AG	ATGATGTCATGTCAGGATTTTACTGCTTTTGGATAAGGCATCAGAGACCCCAACTC	1380
Qy	1398	TACA	AGGCCCTTCCCTTACTGTCTCAGACCTTGGCGAAATTTTACGTGTGTCGGCCCGTGG	1457
Db	1381	TACA	AGGCCCTTCCCTTACTGTCTCAGACCTTGGCGAAATTTTACGTGTGTCGGCCCGTGG	1440
Qy	1458	GAGC	AGGGAAGTCATCACCTGTTAAAGTCCCGTGTCTCGGGAAATTTGGCCCCCAAGTCACGGGC	1517
Db	1441	GAGC	AGGGAAGTCATCACCTGTTAAAGTCCCGTGTCTCGGGAAATTTGGCCCCCAAGTCACGGGC	1500
Qy	1518	TGGT	CAGCGTCATGGAAGAAATTTGCTATGTCTCAGCAGCCCTGGGTGTTCTCGGGAA	1577
Db	1501	TGGT	CAGCGTCATGGAAGAAATTTGCTATGTCTCAGCAGCCCTGGGTGTTCTCGGGAA	1560
Qy	1578	CTCT	CAGGAGTAATATTTTATTTGGGAAGAAATATGAAAGAACATATGAAAAAGTCA	1637
Db	1561	CTCT	CAGGAGTAATATTTTATTTGGGAAGAAATACGAAAGAACATATGAAAAAGTCA	1620
Qy	1638	TAA	AGCTTGTCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGCTGATCTGACTGTGA	1697
Db	1621	TAA	AGCTTGTCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGCTGATCTGACTGTGA	1680
Qy	1698	TAGG	AGATCGGGGAACACGCTGAGTGGAGGCGAGAAACGCGGTAAACCTTTGCAAGAG	1757
Db	1681	TAGG	AGATCGGGGAACACGCTGAGTGGAGGCGAGAAACGCGGTAAACCTTTGCAAGAG	1740
Qy	1758	CAGT	CTATCAAGATCCTGACATCTATCTCTCGAGCATCCTCTCAGTCGAGTAGATCGCG	1817
Db	1741	CAGT	CTATCAAGATCCTGACATCTATCTCTCGAGCATCCTCTCAGTCGAGTAGATCGCG	1800
Qy	1818	AAGT	TAGCAGACACTTGTTCGAACCTGTGTATTGTTCAAATTTTGCATGAGAAAGTACAAA	1877
Db	1801	AAGT	TAGCAGACACTTGTTCGAACCTGTGTATTGTTCAAATTTTGCATGAGAAAGTACAAA	1860
Qy	1878	TTTT	TAGTCATCATCAGTTTGCAGTACCTCAAGCTGCAAGTCAGATCTTGATTTGAAAG	1937
Db	1861	TTTT	TAGTCATCATCAGTTTGCAGTACCTCAAGCTGCAAGTCAGATCTTGATTTGAAAG	1920
Qy	1938	ATGT	TAATAATGGTCAGAGGGGACTTACACTGAGTTCCTTAAATCTCGTATAGATTTTG	1997
Db	1921	ATGT	TAATAATGGTCAGAGGGGACTTACACTGAGTTCCTTAAATCTCGTATAGATTTTG	1980
Qy	1998	GCTC	CCCTTTTAAAGAAGGATAATGAGGAAGTGAACAACTCCAGTTCGAGGAATCCCA	2057
Db	1981	GCTC	CCCTTTTAAAGAAGGATAATGAGGAAGTGAACAACTCCAGTTCGAGGAATCCCA	2040
Qy	2058	CACT	TAAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTCTAGACCT	2117
Db	2041	CACT	TAAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTCTAGACCT	2100
Qy	2118	CCTT	GAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGTCCAGTTACACTATCAG	2177
Db	2101	CCTT	GAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGTCCAGTTACACTATCAG	2160
Qy	2178	AGGA	AACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCATATAAGAAATTTACTTCAGAGCTG	2237
Db	2161	AGGA	AACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCATATAAGAAATTTACTTCAGAGCTG	2220
Qy	2238	GTGC	TACTGGATTTCTTCAATTTTCCCTTATCTCTTAAACACTGCAGCTCAGGTTGCT	2297
Db	2221	GTGC	TACTGGATTTCTTCAATTTTCCCTTATCTCTTAAACACTGCAGCTCAGGTTGCT	2280
Qy	2298	ATGT	GCTTCAAGATTTGGTGGCTTTTCATACTCGGCAACAAACAAAGTATGCTAATGTCA	2357

Db	2281	ATGTGCTTCAAGATTGGTGGCTTTTCATACTGGGCAACAAACAAGATGCTAAATGCTCA	234
QY	2358	CTGTAAATGGAGGAGGAATGTACCAGAAAGCTAGATCTTTAACTGGTACTTTAGGAATTT	2417
Db	2341	CTGTAAATGGAGGAGGAATGTACCAGAAAGCTAGATCTTTAACTGGTACTTTAGGAATTT	2400
QY	2418	ATTTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGGTATTCT	2477
Db	2401	ATTTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGGTATTCT	2460
QY	2478	ACGTCTCTGTGTTAACTCTTCAACAACTTTGCACACAAAAATCTTTGAGTCAATCTGAAAG	2537
Db	2461	ACGTCTCTGTGTTAACTCTTCAACAACTTTGCACACAAAAATCTTTGAGTCAATCTGAAAG	2520
QY	2538	CTCCGGTATTATCTCTTTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTCCAAG	2597
Db	2521	CTCCGGTATTATCTCTTTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTCCAAG	2580
QY	2598	ACATTGGACACTTGGATGATTGTCGCGCTGAGCTTTTATAGATTTTCATCCAGACATGTC	2657
Db	2581	ACATTGGACACTTGGATGATTGTCGCGCTGAGCTTTTATAGATTTTCATCCAGACATGTC	2640
QY	2658	TACAAGTGGTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATACCCCT	2717
Db	2641	TACAAGTGGTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATACCCCT	2700
QY	2718	TGGTTCCCTTTGGAATCATTTTTCATTTTCTTCTGGCGATATTTTGGAAACGTCGAAGAG	2777
Db	2701	TGGTTCCCTTTGGAATCATTTTTCATTTTCTTCTGGCGATATTTTGGAAACGTCGAAGAG	2760
QY	2778	ATGTGAAGCCCTTGGAAATCTACAACCTCGGAGTCCAGTGTTTTCCCACTTCTCATCTTCTC	2837
Db	2761	ATGTGAAGCCCTTGGAAATCTACAACCTCGGAGTCCAGTGTTTTCCCACTTCTCATCTTCTC	2820
QY	2838	TCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGGTGTCAGGAACCTGTTTG	2897
Db	2821	TCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGGTGTCAGGAACCTGTTTG	2880
QY	2898	ATGCACAC - CAGGATTTACATTCAGAGCTTGGTCTTGTGTTCATCATCGTTCGCTCCCTGG	2956
Db	2881	ATGCACACGAGGATTTACATTCAGAGCTTGGTCTTGTGTTCATCATCGTTCGCTCCCTGG	2940
QY	2957	TTCGCCGCTCCGCTCGGATGCCATCTGTGCCATCTTTTGTTCATCATCGTTCGCTTCGGTCC	3016
Db	2941	TTCGCCGCTCCGCTCGGATGCCATCTGTGCCATCTTTTGTTCATCATCGTTCGCTTCGGTCC	3000
QY	3017	CTGATTCCTGCAAAAACCTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCTATGCCCTC	3076
Db	3001	CTGATTCCTGCAAAAACCTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCTATGCCCTC	3060
QY	3077	ACGCTCATGGGATGTTTCAGTGGTCTGTTCGACAAGTGCCTCAAGTTGAGATATGATG	3136
Db	3061	ACGCTCATGGGATGTTTCAGTGGTCTGTTCGACAAGTGCCTCAAGTTGAGATATGATG	3120
QY	3137	ATCTCAGTAGAAGGCTCATTTGAATACACAGACCTTTGAAAAAGAACGACCTTTGGGAATAT	3196
Db	3121	ATCTCAGTAGAAGGCTCATTTGAATACACAGACCTTTGAAAAAGAACGACCTTTGGGAATAT	3180
QY	3197	CAGAAACGCCACCCACCCAGCTTGGCCCAATGAGGAGTGATTAATCTTTGACAATGTGAAC	3256
Db	3181	CAGAAACGCCACCCACCCAGCTTGGCCCAATGAGGAGTGATTAATCTTTGACAATGTGAAC	3240
QY	3257	TTTCATGTACAGTCCAGTGGGGCTCTGGTACGTAAGCATCTCACAGCACTCAATTAATCA	3316
Db	3241	TTTCATGTACAGTCCAGTGGGGCTCTGGTACGTAAGCATCTCACAGCACTCAATTAATCA	3300
QY	3317	CAAGAAAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC	3376
Db	3301	CAAGAAAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC	3360
QY	3377	CTTTTTCATGCTCAGACCCCGAAGGTAAAAATTTGGATGTGTAAGATCTTGACAACTGAA	3436
Db	3361	CTTTTTCATGCTCAGACCCCGAAGGTAAAAATTTGGATGTGTAAGATCTTGACAACTGAA	3420

the diagnosis and treatment of cancer, especially prostate cancer -
Claim 1; Page 412-414; 579pp; English.
The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.

Sequence 6140 BP; 1737 A; 1260 C; 1353 G; 1780 T; 10 other;

Query Match 92.4%; Score 3910.2; DB 22; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

QY 189 GGTGGCTCAATCCCTGTTTAAATGGCCATAAACGAGAGATTAGAGGAAGATATATGT 248
DB 233 GGTGGCTCAATCCCTGTTTAAATGGCCATAAACGAGAGATTAGAGGAAGATATATGT 292
QY 249 ATTCAGTCTCCAGAGACCGCTCACAGACCTTGGAGAGAGTTGCAAGGTTCTGGG 308
DB 293 ATTCAGTCTCCAGAGACCGCTCACAGACCTTGGAGAGAGTTGCAAGGTTCTGGG 352
QY 309 ATAAGAAGTTTAAAGAGCTGAGATGACGACAGACCTTCTTTAAAGAGCAATCA 368
DB 353 ATAAGAAGTTTAAAGAGCTGAGATGACGACAGACCTTCTTTAAAGAGCAATCA 412
QY 369 TAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAAATGAGGAAAGTG 428
DB 413 TAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAAATGAGGAAAGTG 472
QY 429 CCAAGTAATCCAGCCCATATTTTGGGAAATTTTACGTTAAATGAGGAAATGATC 488
DB 473 CCAAGTAATCCAGCCCATATTTTGGGAAATTTTACGTTAAATGAGGAAATGATC 532
QY 489 CCATGGATTCTGTGGCTTTGAACACAGCGTACGCGCTATGCCACGCTGCTGACTTTTGGCA 548
DB 533 CCATGGATTCTGTGGCTTTGAACACAGCGTACGCGCTATGCCACGCTGCTGACTTTTGGCA 592
QY 549 CGCTCATTTTGGCTATCTAGCATCACTATATTTTATFCAGTTTCAGTGTCTGGGATGA 608
DB 593 CGCTCATTTTGGCTATCTAGCATCACTATATTTTATFCAGTTTCAGTGTCTGGGATGA 652
QY 609 GGTTCAGATAGCCATGCGCATATGATTTATCGAAGGCACTTCGCTTAGTACATGG 668
DB 653 GGTTCAGATAGCCATGCGCATATGATTTATCGAAGGCACTTCGCTTAGTACATGG 712
QY 669 CCATGGGGAAGACAAACACAGGCGAGATAGTCAATCTGCTCAATGATGATGAACAGT 728
DB 713 CCATGGGGAAGACAAACACAGGCGAGATAGTCAATCTGCTCAATGATGATGAACAGT 772
QY 729 TTGATCAGGTGACAGTGTCTTACATCTTCCTGCTGGGAGGACCACTGCAGCGCATCGCAG 788
DB 773 TTGATCAGGTGACAGTGTCTTACATCTTCCTGCTGGGAGGACCACTGCAGCGCATCGCAG 832
QY 789 TGACTGCCCTACTCTGATGGAGATAGGAATATCGTCTGCTGGGATGGCACTTCTAA 848
DB 833 TGACTGCCCTACTCTGATGGAGATAGGAATATCGTCTGCTGGGATGGCACTTCTAA 892
QY 849 TCATTCCTCCCTGCTCAAGCTGTTTGGGAAAGTTGTTCTCATCACTCAGGAGTAAA 908
DB 893 TCATTCCTCCCTGCTCAAGCTGTTTGGGAAAGTTGTTCTCATCACTCAGGAGTAAA 952
QY 909 CTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTTAACTGGTATAAGGA 968

DB 953 CTCCACTTTCACGGATGCCAGATCAGGACCATGAATGAAGTTTAACTGGTATAAGGA 1012
QY 969 TAATAAAATGTACGCTGGGAAAAGTCAATTTCAATCTTATTAACAATTTGAGAAGA 1028
DB 1013 TAATAAAATGTACGCTGGGAAAAGTCAATTTCAATCTTATTAACAATTTGAGAAGA 1072
QY 1029 AGGAGATTTCCAGAGATCTCAGAGATTCCTGCTCAGGCGGATGAATTTGGCTTCGTTT 1088
DB 1073 AGGAGATTTCCAGAGATCTCAGAGATTCCTGCTCAGGCGGATGAATTTGGCTTCGTTT 1132
QY 1089 TCAGTCAAGCAAAATCATCGTGTGTGACCTTTCACCACTACGCTCCTCGCGAGTG 1148
DB 1133 TCAGTCAAGCAAAATCATCGTGTGTGACCTTTCACCACTACGCTCCTCGCGAGTG 1192
QY 1149 TGATCACAGCCAGCCGCTGTTCTGCGAGTGACGCTGATGCGGCTGTGCGGCTCAGCG 1208
DB 1193 TGATCACAGCCAGCCGCTGTTCTGCGAGTGACGCTGATGCGGCTGTGCGGCTCAGCG 1252
QY 1209 TTACCCCTCTTCTCCCTCAGCCATTTGAGAGGCTGTGAGAGGCAATCGTCAGCATCCGAA 1268
DB 1253 TTACCCCTCTTCTCCCTCAGCCATTTGAGAGGCTGTGAGAGGCAATCGTCAGCATCCGAA 1312
QY 1269 GAATCCAGACCTTTTGTGCTACTTGTAGATATACAGCGCAACCGCTCAGCTCCGCTCAG 1328
DB 1313 GAATCCAGACCTTTTGTGCTACTTGTAGATATACAGCGCAACCGCTCAGCTCCGCTCAG 1372
QY 1329 ATGGTAAAAGATGGTGCATGTGACGAGATTTTACTGCTTTTGGGATAAGGCATCAGAGA 1388
DB 1373 ATGGTAAAAGATGGTGCATGTGACGAGATTTTACTGCTTTTGGGATAAGGCATCAGAGA 1432
QY 1389 CCCCACTCTACAGGCCCTTCTTCTTACTGTACAGACTGCGGCAATTTGTAGCTGTGGTGC 1448
DB 1433 CCCCACTCTACAGGCCCTTCTTCTTACTGTACAGACTGCGGCAATTTGTAGCTGTGGTGC 1492
QY 1449 GCCCGTGGAGCAGGGAAGTCACTACTGTTAAGTCCCGTGTGCGGGGAATTTGGCCCAAA 1508
DB 1493 GCCCGTGGAGCAGGGAAGTCACTACTGTTAAGTCCCGTGTGCGGGGAATTTGGCCCAAA 1552
QY 1509 GTACGGCTGTGACGCTGCGATGGAAGATTTGCCCTATGCTCTCAGCAGCCCTGGGTGT 1568
DB 1553 GTACGGCTGTGACGCTGCGATGGAAGATTTGCCCTATGCTCTCAGCAGCCCTGGGTGT 1612
QY 1569 TCTCGGAACTCTGAGGAGTAAATTTTATTTGGGAAAGATTTACAGCTGTTGGAGGATGGTATC 1628
DB 1613 TCTCGGAACTCTGAGGAGTAAATTTTATTTGGGAAAGATTTACAGCTGTTGGAGGATGGTATC 1672
QY 1629 AAAAACTATAAGGCTTGTGCTCTGAAAAAGATTTACAGCTGTTGGAGGATGGTATC 1688
DB 1673 AAAAACTATAAGGCTTGTGCTCTGAAAAAGATTTACAGCTGTTGGAGGATGGTATC 1732
QY 1689 TGACTGTGATAGGATCGGGGAACACCGCTGAGTGGAGGCGAGAAACACGGGTAAACC 1748
DB 1733 TGACTGTGATAGGATCGGGGAACACCGCTGAGTGGAGGCGAGAAACACGGGTAAACC 1792
QY 1749 TTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGCAAGCATCTCTCAGTGCAG 1808
DB 1793 TTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGCAAGCATCTCTCAGTGCAG 1852
QY 1809 TAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTTGTCAAAATTTTGCATGAGA 1868
DB 1853 TAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTTGTCAAAATTTTGCATGAGA 1912
QY 1869 AGATCACAAATTTTAGTGACTCATCATGTTGCACTTCAAGCTCAAGTCAAGTTCGA 1928
DB 1913 AGATCACAAATTTTAGTGACTCATCATGTTGCACTTCAAGCTCAAGTCAAGTTCGA 1972
QY 1929 TATTGAAAGATGGTAAAATGGTGCAGAGGGGACTTACACTGAGTTCCTTAAATCTGGTA 1988
DB 1973 TATTGAAAGATGGTAAAATGGTGCAGAGGGGACTTACACTGAGTTCCTTAAATCTGGTA 2032
QY 1989 TAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGAAAGTCAACAACTCCAGTTCAG 2048

Db 2033 TAGATTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAACCTCCAGTTCAG 2092
 QY 2049 GAATCTCCACACTAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGTGCTCAACAATCTT 2108
 Db 2093 GAATCTCCACACTAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGTGCTCAACAATCTT 2152
 QY 2109 CTAGACCTCTCTTGAAGATGGTCTCTGAGAGCCAAAGATACAGAGAATGTCCAGTTA 2168
 Db 2153 CTAGACCTCTCTTGAAGATGGTCTCTGAGAGCCAAAGATACAGAGAATGTCCAGTTA 2212
 QY 2169 CACTATCAGAGAGAACCCCTTCTGAAGAAAGTTGGTTTTCAGGCCATATAAGAAATTA 2228
 Db 2213 CACTATCAGAGAGAACCCCTTCTGAAGAAAGTTGGTTTTCAGGCCATATAAGAAATTA 2272
 QY 2229 TCAGAGCTGGTGTCTACTGGATGTCTTCATTTTCCTTATTCCTTAAACACTGCAGCTC 2288
 Db 2273 TCAGAGCTGGTGTCTACTGGATGTCTTCATTTTCCTTATTCCTTAAACACTGCAGCTC 2332
 QY 2289 AGCTTCCCTATGTCTCAAGATTGGTCTTTCATAGTGGGCAACAAACAAGTATGC 2348
 Db 2333 AGCTTCCCTATGTCTCAAGATTGGTCTTTCATAGTGGGCAACAAACAAGTATGC 2392
 QY 2349 TAAATGTCTACTGTAAATGGAGGAGGAAATGTAAACGAGAGCTAGATCTTAACTGGTACT 2408
 Db 2393 TAAATGTCTACTGTAAATGGAGGAGGAAATGTAAACGAGAGCTAGATCTTAACTGGTACT 2452
 QY 2409 TAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATATGCAAGATCTCTAT 2468
 Db 2453 TAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATATGCAAGATCTCTAT 2512
 QY 2469 TGGTATTTCTACGTCCTGTAACTCTTCAAACTTTGACAACTTTGACAACTTTTGAAGTCAA 2528
 Db 2513 TGGTATTTCTACGTCCTGTAACTCTTCAAACTTTGACAACTTTTGAAGTCAA 2572
 QY 2529 TTCTGAAAGCTCGGTATTAATCTTTGATAGAAATCCAATAGGAAGAAATTTAAATCGTT 2588
 Db 2573 TTCTGAAAGCTCGGTATTAATCTTTGATAGAAATCCAATAGGAAGAAATTTAAATCGTT 2632
 QY 2589 TCTCCAAAGACATTTGACACTTGGATGTATGCTGCGGTGAGCTTTTATGATTTCATCC 2648
 Db 2633 TCTCCAAAGACATTTGACACTTGGATGTATGCTGCGGTGAGCTTTTATGATTTCATCC 2692
 QY 2649 AGACATTTGCTACAAGTGGTGGTGTGCTCTGCTGCTGCTGCGCGTATTCCTTGGATCG 2708
 Db 2693 AGACATTTGCTACAAGTGGTGGTGTGCTCTGCTGCTGCTGCGCGTATTCCTTGGATCG 2752
 QY 2709 CAATACCCCTTGGTTCCTCCCTTGGAAATCAATTTTCTTCCGCGATATTTTTTGGAAA 2768
 Db 2753 CAATACCCCTTGGTTCCTCCCTTGGAAATCAATTTTCTTCCGCGATATTTTTTGGAAA 2812
 QY 2769 CGTCAAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGT 2828
 Db 2813 CGTCAAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGT 2872
 QY 2829 CATCTTCTCTCCAGGGCTCTGACCATCCGGCATACAAAGCAGAGAGAGTGTCAAG 2888
 Db 2873 CATCTTCTCTCCAGGGCTCTGACCATCCGGCATACAAAGCAGAGAGAGTGTCAAG 2932
 QY 2889 AACTGTTTGTATGCACACACAGGATTTACATTCAGAGGCTTGGTTCTTGTGTTTGGACAACTG 2948
 Db 2933 AACTGTTTGTATGCACACACAGGATTTACATTCAGAGGCTTGGTTCTTGTGTTTGGACAACTG 2992
 QY 2949 CCGCTGGTTCGGCTCGCTGGATGGCATCTGTGCCATGTTTGTTCATCATCGTTGGCT 3008
 Db 2993 CCGCTGGTTCGGCTCGCTGGATGGCATCTGTGCCATGTTTGTTCATCATCGTTGGCT 3052
 QY 3009 TTGGGTTCCTGATTTCTGGCAAAACTCTGATGTCGGGCGAGCTTGGTTGGCAGCTGCT 3068
 Db 3053 TTGGGTTCCTGATTTCTGGCAAAACTCTGATGTCGGGCGAGCTTGGTTGGCAGCTGCT 3112
 QY 3069 ATGCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCCAGAAAGTGTGAAGTTGAGA 3128
 Db 3113 ATGCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCCAGAAAGTGTGAAGTTGAGA 3172

QY 3129 ATATGATGATCTCAGTAGAAAGGCTCATTTGAATACACAGACCTTGAAAAAGAACACCTT 3188
 Db 3173 ATATGATGATCTCAGTAGAAAGGCTCATTTGAATACACAGACCTTGAAAAAGAACACCTT 3232
 QY 3189 GGGAAATATCAGAAAGCCACACAGCCTGGCCCCATGAAGAGAGTGATAATCTTTTGACA 3248
 Db 3233 GGGAAATATCAGAAAGCCACACAGCCTGGCCCCATGAAGAGAGTGATAATCTTTTGACA 3292
 QY 3249 ATGTGAATCTCATGTACAGTCCAGTGGCTCTGGTACTGAAGCATCTGACAGCATCA 3308
 Db 3293 ATGTGAATCTCATGTACAGTCCAGTGGCTCTGGTACTGAAGCATCTGACAGCATCA 3352
 QY 3309 TTAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCA 3368
 Db 3353 TTAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCA 3412
 QY 3369 TCTCAGCCCTTTTAGATTTGTGACAAACCGGAAGTAAATTTGGATTGATGAAGATCTTGA 3428
 Db 3413 TCTCAGCCCTTTTAGATTTGTGACAAACCGGAAGTAAATTTGGATTGATGAAGATCTTGA 3472
 QY 3429 CAATGAAATTTGGACTTCAGSATTAAAGGAGAAATGTCAATCATACCTCAGGAACCTG 3488
 Db 3473 CAATGAAATTTGGACTTCAGSATTAAAGGAGAAATGTCAATCATACCTCAGGAACCTG 3532
 QY 3489 TTTTGTCTACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGATGAGG 3548
 Db 3533 TTTTGTCTACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGATGAGG 3592
 QY 3549 AACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCTCGTA 3608
 Db 3593 AACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCTCGTA 3652
 QY 3609 AAATGGAATCTGAATTAGCAGAAATCAGSATTCCAAATTTAGTGTGGCAAGAACACTGG 3668
 Db 3653 AAATGGAATCTGAATTAGCAGAAATCAGSATTCCAAATTTAGTGTGGCAAGAACACTGG 3712
 QY 3669 TGTGCTCTGCGAGGCAATTTCTCAGGAAAAATCAGATATTGATTATTGATGAAGACGCG 3728
 Db 3713 TGTGCTCTGCGAGGCAATTTCTCAGGAAAAATCAGATATTGATTATTGATGAAGACGCG 3772
 QY 3729 CAATGTGGATTCAGAACTGATGATTATACAAAAAAATCCGGGAGAAATTTGCGCC 3788
 Db 3773 CAATGTGGATTCAGAACTGATGATTATACAAAAAAATCCGGGAGAAATTTGCGCC 3832
 QY 3789 ACTGCAACCTGCTTAACCATTTGCACACAGATTGAACACCATTTATTGACAGCGCACAGATA 3848
 Db 3833 ACTGCAACCTGCTTAACCATTTGCACACAGATTGAACACCATTTATTGACAGCGCACAGATA 3892
 QY 3849 TGTGTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTGTGCTGCAAAATA 3908
 Db 3893 TGTGTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTGTGCTGCAAAATA 3952
 QY 3909 AAGAGAGCTTATTTTACAAGATGGTGCACAACTGGGCAAGGAGGAGCGCTGCCCTCA 3968
 Db 3953 AAGAGAGCTTATTTTACAAGATGGTGCACAACTGGGCAAGGAGGAGGAGCGCTGCCCTCA 4012
 QY 3969 CTGAAACAGCAAAACAG----- 3985
 Db 4013 CTGAAACAGCAAAACAGAGATGGGTTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCT 4072
 QY 3986 ----- 3985
 Db 4073 GACCTCAAGTGATCCACCTTGCCCTTGCCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCA 4132
 QY 3986 -----GTATACTTCAAAAGAAATATCCACATATTTGCTCAGCTGACCCAC 4030
 Db 4133 CCACGCCAGCCTGAGTATACTTCAAAAGAAATTTATCCACATATTTGCTCAGCTGACCCAC 4192
 QY 4031 ATGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATTTTCGAGACAGCACTG 4090
 Db 4193 ATGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATTTTCGAGACAGCACTG 4252

QY 4091 TGAATCAACCAAAATGTCAGTCCTCGGAAGGCATTTTCACACTAGTTTGGACTAT 4150
|||||
Db 4253 TGAATCCACCAAAATGTCAGTCCTCGGAAGGCATTTTCACACTAGTTTGGACTAT 4312
|||||
QY 4151 GTAACCAACATGTTACTTTTACTTTGGCAACAAATATTTATACATACAAAGATGCTA 4210
|||||
Db 4313 GTAACCAACATGTTACTTTTACTTTGGCAACAAATATTTATACATACAAAGATGCTA 4372
|||||
QY 4211 GTTCATTTGAATATTTCTCCC 4231
|||||
Db 4373 GTTCATTTGAATATTTCTCCC 4393
|||||

RESULT 15

AAH93829
ID AAH93829 standard; cDNA; 6140 BP.

XX AC
AAH93829;

XX 04-OCT-2001 (first entry)

XX Human prostate-specific 2nd full length cDNA sequence for P510S.

DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.

XX Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US01574.

XX 14-JAN-2000; 2000US-0483672.

XX (CORI-) CORIYA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -

XX Claim 1; Page 412-414; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I). (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX Sequence 6140 BP; 1737 A; 1260 C; 1353 G; 1780 T; 10 other;

XX Query Match 92.4%; Score 3910.2; DB 22; Length 6140;
XX Best Local Similarity 97.1%; Pred. No. 0;
XX Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

QY 189 GGTGGCTCAATCCCTCTTTAAATTTGGCCATAACGGAGATTAGAGCAAGATATATGT 248
|||||

Db 233 GGTGGCTCAATCCCTCTTTAAATTTGGCCATAACGGAGATTAGAGCAAGATATATGT 292
QY 249 ATTCAAGTGTGCCAGAGACCGCTCACAGCACCTTTGGAGAGGAGTTCACAGGGTTCGGG 308
|||||
Db 293 ATTCAAGTGTGCCAGAGACCGCTCACAGCACCTTTGGAGAGGAGTTCACAGGGTTCGGG 352
|||||
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Search completed: December 18, 2002, 07:46:31
Job time : 554.063 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:10 ; Search time 6968.22 Seconds
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Title: US-09-647-140A-1

Perfect score: 4231

Sequence: 1 ggcacagcgtggcgccgga.....ttcatttgattttctccc 4231

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hgt:*

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6: gb_pat:*

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32: em_hgt_other:*

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41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	4231	100.0	4231	9	AF071202 Homo sapi
3	4211	99.5	6082	6	AX141045 Sequence
4	4211	99.5	6082	6	AX200905 Sequence
5	4211	99.5	6082	6	AX267561 Sequence
6	4125.8	97.5	5759	9	AX081219 Homo sapi
7	3910.2	92.4	6140	6	AX141046 Sequence
8	3910.2	92.4	6140	6	AX200906 Sequence
9	3910.2	92.4	6140	6	AX267562 Sequence
10	2875	68.0	2940	9	AF071203 Homo sapi
11	1045.4	24.7	1074	6	AX201051 Sequence
12	1045.4	24.7	1074	6	AX267850 Sequence
13	651.8	15.4	2275	6	AX046474 Sequence
14	611.8	14.5	176082	3	AC007144 Drosophil
15	611.8	14.5	267284	3	AE003668 Drosophil
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17	563.6	13.3	170546	3	AC011756 Drosophil
18	563.6	13.3	265010	3	AE003661 Drosophil
19	555.8	13.1	76095	2	AC012753 Drosophil
20	537.2	12.7	4377	3	AY118336 Drosophil
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33	452	10.7	4909	10	RNCMRP X96393 R.norvegicu
34	450.6	10.6	5744	10	AB020209 Rattus no
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45	437.4	10.3	4847	6	AR099619 Sequence

ALIGNMENTS

RESULT 1

AX210645

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AX210645 Sequence 287 from Patent WO0157058. linear PAT 31-AUG-2001

AX210645

AX210645.1 GI:15424905

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4231)

Rosenthal,A., Hinzmann,B., Schaefer,R., Zuber,J., Tchernitsa,O.,

Grips,M., Hellriegel,M., Schmitz,A.C. and Sers,C.

Detection of differential gene expression

JOURNAL Patent: WO 0157058-A 287 09-AUG-2001:

Metagen Gesellschaft fuer Genomforschung mbH (DE)

Location/Qualifiers

1. 4231

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 1170 a 895 c 1015 g 1151 t

ORIGIN

Query Match 100.0%; Score 4231; DB 6; Length 4231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	GGCCACCGCGCTGATCAGCGCGACCCCGCGCGCGCGCGCGCGCGCGCAAGATGCT	120
Db	61	GGCCACCGCGCTGATCAGCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCAAGATGCT	120
Qy	121	GCCCGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTACGGGT	180
Db	121	GCCCGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTACGGGT	180
Qy	181	GTTCTTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAACCGGAGATTAGAGGAAGA	240
Db	181	GTTCTTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAACCGGAGATTAGAGGAAGA	240
Qy	241	TGATATGTATTCAGTGTGCGCAGAGACCGCTCAGCAGCACCTTGGAGAGGAGTTCGAAGG	300
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Qy	301	GTTCTGGGATAAAGAAGTTTAAAGAGCTGAGAATGACACAGAGCCCTCTTTAAACAG	360
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Qy	1321	GCCGTCAGATGTGTAAGAGATGTCATCTGAGAGTTTACTGCTTTTGGGATAGGC	1380
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Qy	1381	ATCAGAGACCCCAACTCTACAAGGCGCTTCTTCTTACTGTGACAGCTGGGAAATTTAGC	1440
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Qy	1441	TGTGTCGCGCCCGTGGGAGGAGGAAATCATCTGTTAAGTGCCTGCTCGGGAAAT	1500
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ACCESSION AF071202
VERSION AF071202.1 GI:3335172
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Lee,K., Belinsky,M.G., Bell,D.W., Testa,J.R. and Kruh,G.D.
TITLE Isolation of MOAT-B, a widely expressed multidrug
resistance-associated protein/canicular multispecific organic
anion transporter-related transporter
JOURNAL Cancer Res. 58 (13), 2741-2747 (1998)
MEDLINE 98324262
PUBMED 9661885
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AUTHORS Lee,K., Belinsky,M.G., Bell,D.W., Testa,J.R. and Kruh,G.D.
TITLE Direct Submission
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7701 Burholme Ave., Philadelphia, PA 19111, USA
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AX141045

LOCUS

DEFINITION Sequence 535 from Patent WO0134802.

AX141045 6082 bp DNA linear PAT 31-MAY-2001

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ACCESSION AX141045
VERSION AX141045.1 GI:14281100
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6082)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
Skelky, Y.A. and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 535 17-MAY-2001;
CORIXA CORPORATION (US)
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ORGANISM Homo sapiens
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RESULT 5
AX267561
LOCUS AX267561 6082 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 535 from Patent WO0173032.
ACCESSION AX267561
VERSION AX267561.1 GI:16516283
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H.,
Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A., Hepler, W. T.
and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 535 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1. 6082
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BASE COUNT 1721 a 1249 c 1357 g 1755 t
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Query Match 99.5%; Score 4211; DB 6; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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RESULT 6
AY081219
LOCUS
DEFINITION
ACCESSION
VERSION

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AY081219.1 GI:21655122

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linear
PRI 01-JUL-2002

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KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1 (bases 1 to 5759)
AUTHORS     Adachi, M., Sampath, J., Sun, D. and Schuetz, J.D.
TITLE       Isolation of human ATP-binding cassette, sub-family C (CFTR/MRP),
            member 4 (ABCC4)
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 5759)
AUTHORS     Adachi, M., Sampath, J., Sun, D. and Schuetz, J.D.
TITLE       Direct Submission
JOURNAL     Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude
            Children's Research Hospital, 332 North Lauderdale St., Memphis, TN
            38105-2794, USA
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RESULT 7
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LOCUS AX141046 6140 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 536 from Patent WO0134802.
ACCESSION AX141046
VERSION AX141046.1 GI:14281101
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6140)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 536 17-MAY-2001;
CORIXA CORPORATION (US)
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BASE COUNT 1737 a 1260 c 1353 g 1780 t 10 others
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Query Match 92.4%; Score 3910.2; DB 6; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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Db	2213	CACATTCAGGAGAACCCCTCTGAAGGAAAGTTGGTTTTCAGGCCCTATAAGAATTA	2272
Qy	2229	TCAGAGCTGGTCTCACTGGATGTCTTCAATTTTCTTATCTCTTAAACACTGCAGCTC	2288
Db	2273	TCAGAGCTGGTCTCACTGGATGTCTTCAATTTTCTTATCTCTTAAACACTGCAGCTC	2332
Qy	2289	AGTTTGCCTATGTGCTTCAAGATGGTGGCTTTCATCTAGTGGGCAACCAACAAGTATGC	2348

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RESULT 8
LOCUS AX200906 6140 bp DNA Linear PAT 29-AUG-2001
DEFINITION Sequence 536 from Patent WO0151633.
ACCESSION AX200906
VERSION AX200906.1 GI:15390773
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 6140)
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 536 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1737 a 1260 c 1353 g 1780 t 10 others
ORIGIN
Query Match 92.4%; Score 3910.2; DB 6; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
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Qy	1089	TCAGTGCACGCAAAATCATCGTTGTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTG	1148
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Qy	1149	TGATCAGCAGCCGCGGTTCCTGCGGAGTGACGCTGTATGGGGCTGTGCGGTGACGG	1208
Db	1193	TGATCAGCAGCCGCGGTTCCTGCGGAGTGACGCTGTATGGGGCTGTGCGGTGACGG	1252
Qy	1209	TTACCTCTCTTCCCTCAGCCATTGAGAGGGTGTACAGAGCAATCGTCAGCATCCGAA	1268
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Qy	1269	GAATCCAGACCTTTTGTGCTACTTGATGAGATATCACAGCAACCGTCAGTCGCCGTAC	1328
Db	1313	GAATCCAGACCTTTTGTGCTACTTGATGAGATATCACAGCAACCGTCAGTCGCCGTAC	1372
Qy	1329	ATGTTAAAGATGGTGATGTGCAGGATTTTACTGCTTTTGGGATTAAGCATCAGAGA	1388
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Qy	1389	CCCCAACTCTACAAGGCTTTTCCCTTACTGTACAGCTTGGGGAATTTTACTGTGGTGTG	1448
Db	1433	CCCCAACTCTACAAGGCTTTTCCCTTACTGTACAGCTTGGGGAATTTTACTGTGGTGTG	1492
Qy	1449	GCCCCGTGGGAGCAGGGAAGTCATCACCTGTTAAAGTGCCGTCTCGGGGAATTTGGCCCCAA	1508
Db	1493	GCCCCGTGGGAGCAGGGAAGTCATCACCTGTTAAAGTGCCGTCTCGGGGAATTTGGCCCCAA	1552
Qy	1509	GTCAAGGCTGTGTACGCTGCATGGAAGAATTTGCTATGTCTCAGCAGCCCTGGGTGT	1568
Db	1553	GTCAAGGCTGTGTACGCTGCATGGAAGAATTTGCTATGTCTCAGCAGCCCTGGGTGT	1612
Qy	1569	TCCTGGGAATCTGAGGAGTAATATTTTATTTGGGAAGAATATGAAGAAGACGATATG	1628
Db	1613	TCCTGGGAATCTGAGGAGTAATATTTTATTTGGGAAGAATATGAAGAAGACGATATG	1672
Qy	1629	AAAAAGTCATAAAGGCTTGCTCTGTAAGGAGATTTTACAGCTGTTCGAGGATGGTGATC	1688
Db	1673	AAAAAGTCATAAAGGCTTGCTCTGTAAGGAGATTTTACAGCTGTTCGAGGATGGTGATC	1732
Qy	1689	TGACTGTGATAGGATCGGGGAACACCGCTGAGTGGAGGSGCAAGACGCGGTAAACC	1748
Db	1733	TGACTGTGATAGGATCGGGGAACACCGCTGAGTGGAGGSGCAAGACGCGGTAAACC	1792
Qy	1749	TTGCAAGACGAGTGATCAGATGCTGCATCTATCTCTCGGACGATCTCTCAGTGCAG	1808
Db	1793	TTGCAAGACGAGTGATCAGATGCTGCATCTATCTCTCGGACGATCTCTCAGTGCAG	1852
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QY	2049	GA	ACTCCCAC	ATAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTT	2108
DB	2093	GA	ACTCCCAC	ATAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTT	2152
QY	2109	CT	AGACCCCT	CTTTGAAGATGGTGCTCTGGAGAGCCAAAGATACAGAGAAATGTCCACGTTA	2168
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DB	2213	CAC	TATCAGAGGAGA	ACCGGTTCTGAAGGAAAAGCTTGTTTTTCAGGCCCTATAAGAAATTA	2272
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QY	2349	TAA	ATGCTCACTGTA	ATGAGGAGGAAAAGTGAACCCGAGAAAGCTAGATCTTTAACTGGTACT	2408
DB	2393	TAA	ATGCTCACTGTA	ATGAGGAGGAAAAGTGAACCCGAGAAAGCTAGATCTTTAACTGGTACT	2452
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DB	2453	TAG	GAATTTATTCAG	GTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTAT	2512
QY	2469	TG	TATCTACGTCCT	TGTTAACTCTTCAACAACCTTTGCACAACAANAATGTTTGAGTCAA	2528
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RESULT 9
LOCUS AX267562 6140 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 536 from Patent WO0173032.
ACCESSION AX267562
VERSION AX267562.1 GI:16516284
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
AUTHORS Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 536 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1. 6140
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1737 a 1260 c 1353 g 1780 t 10 others
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Query Match 92.4%; Score 3910.2; DB 6: Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;
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REFERENCE 1 (bases 1 to 2940)
AUTHORS Lee K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.
TITLE Isolation of MOAT-B, a widely expressed multidrug
resistance-associated protein/canalicular multispecific organic
anion transporter-related transporter
Cancer Res. 58 (13), 2741-2747 (1998)
JOURNAL 98324262
MEDLINE 9661885
PUBMED
REFERENCE 2 (bases 1 to 2940)
AUTHORS Lee, K. and Kruh, G.D.
TITLE Isolation of another form of MOAT-B
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2940)
AUTHORS Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center,
7701 Burholme Ave., Philadelphia, PA 19111, USA
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LOCUS
DEFINITION Sequence 681 from Patent WO0151633.
ACCESSION AX201051
VERSION AX201051.1 GI:15390859
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 681 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
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PAT 24-NOV-2000			

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DEFINITION      Sequence 10 from Patent WO0058471.
ACCESSION       AX046474
VERSION         AX046474.1 GI:11344431
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
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                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 2275)
AUTHORS       Schuetz, J. and Fridland, A.
TITLE         Multidrug resistance associated proteins and uses thereof
JOURNAL       Patent: WO 0058471-A 10 05-OCT-2000;
                ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
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DEFINITION      Drosophila melanogaster, chromosome 2L, region 38F-39A, BAC clone
ACCESSION       BACR06G10, complete sequence.
VERSION         AC007144
KEYWORDS
SOURCE         HTG.
                AC007144.13 GI:13702789
ORGANISM       Drosophila melanogaster.
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                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 176082)
AUTHORS       Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
                Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
                Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
                Carlson, J.W., Center, A., Chapple, M., Davenport, L.B., Dietz, S.M.,
                Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
                Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
                Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
                Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A.,
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                Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
                Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
                Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                Sequencing of Drosophila chromosome 2L, region 38F-39A
                Unpublished
                2 (bases 1 to 176082)
                Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
                Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
                Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
                Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
                Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
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                Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                Rubin, G.M.
                Direct Submission
                Submitted (24-MAR-1999) Drosophila Genome Center, Lawrence Berkeley
                Laboratory, MS 64-121, Berkeley, CA 94720, USA
                On Apr 21, 2001 this sequence version replaced gi:7264767.
                Sequence submitted by:
                Lawrence Drosophila Genome Project
                Berkeley National Laboratory
                Berkeley, CA 94720
                This sequence was assembled using end sequences from a whole genome
                shotgun and from subclones of this BAC and its neighboring clones.
                For further information about this sequence, including its location
                and relationship to other sequences, please visit our sequence
                archive web site (http://www.fruitfly.org/sequence/) or send email
                to bdg@fruitfly.berkeley.edu.
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REFERENCE
AUTHORS
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COMMENT
FEATURES
source

267284 bp DNA linear INV 11-OCT-2000
Drosophila melanogaster genomic scaffold 14200001386055 section 61
of 63, complete sequence.
AE003668 AE002690
AE003668.3 GI:10799497
HTG.
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 267284)
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
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Brandon,R.C., Rogers,Y.H., Blazey,R.G., Champe,M., Pfeiffer,B.D.,
Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor
Miklos,G.L., Abriil,J.F., Aqbayani,A., An,H.J.,
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McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
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Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
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The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
20196006
10731132
2. (bases 1 to 267284)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000)
Rockville, MD, USA
On Oct 12, 2000 this sequence version replaced gi:10728900.
Location/Qualifiers
1. 267284

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COMPARISONS

Result No.	Query Match	Score	Length	DB	ID	Description
1	99.5	4211	6082	4	US-09-605-785-535	Sequence 535, Appl
2	99.5	4211	6082	4	US-09-439-313-535	Sequence 535, Appl
3	92.4	3910.2	6140	4	US-09-605-785-536	Sequence 536, Appl
4	92.4	3910.2	6140	4	US-09-439-313-536	Sequence 536, Appl
5	1045.4	24.7	1074	4	US-09-605-785-824	Sequence 824, Appl
6	437.4	10.3	4781	2	US-09-001-273-1	Sequence 1, Appl
7	437.4	10.3	4781	4	US-08-843-459A-1	Sequence 1, Appl
8	437.4	10.3	4847	3	US-09-061-400-1	Sequence 1, Appl
9	390.4	9.2	5011	1	US-08-141-893-1	Sequence 1, Appl
10	390.4	9.2	5011	1	US-08-463-092B-1	Sequence 1, Appl
11	390.4	9.2	5011	2	US-08-462-109A-1	Sequence 1, Appl
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13	390.4	9.2	5011	3	US-08-463-179A-1	Sequence 1, Appl
14	390.4	9.2	5011	3	US-08-461-384B-1	Sequence 1, Appl
15	390.4	9.2	5011	3	US-08-407-207A-1	Sequence 1, Appl
16	388.8	9.2	5011	3	US-08-463-092B-3	Sequence 3, Appl
17	388.8	9.2	5011	2	US-08-462-109A-3	Sequence 3, Appl
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26	363.8	8.6	5232	4	US-08-972-927-1	Sequence 1, Appl
27	356.2	8.4	5175	4	US-08-972-927-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-605-785-535
; Sequence 535, Application US/09605785
; Patent No. 6321716

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QY 1021 GAGAAAGAGGAGATTTCCAAGATTTCTGAGAAGTTCCCTGCCCTCAGGGGATGAATTTGGC 1080
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; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-535

Query Match          99.5%; Score 4211; DB 4; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 661 TAACATGGCCATGGGGAAGACACCAACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGT 720
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Db 731 TAACATGGCCATGGGGAAGACACCAACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGT 790

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QY 841 AGTTCTTAATCTTCTCCCTTGCAGAGCTGTTTGGGAGGAGTTGTTCTCATCACTGAG 900
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RESULT 3
US-09-605-785-536
; Sequence 536, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4535)
; OTHER INFORMATION: n=A,T,C or G
US-09-605-785-536

Query Match 92.4%; Score 3910.2; DB 4; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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QY	1749	TTGCAAGACAGTGTATCAAGATGCTTGACATCTATCTCCTGGAGCATCTCTCAGTGCAG	1808
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QY	3729	CAAAATGTGGATCCAAAGACTGATGAGTTTAATACAAAAAAATCCGGGAGAAATTTGCC	3788
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RESULT 4

US-09-439-313-536
; Sequence 536, Application US/09439313
; Patent No. 6329505

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqul
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 536

; LENGTH: 6140

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (4535)

; OTHER INFORMATION: n=A,T,C or G

US-09-439-313-536

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Query Match 92.4%; Score 3910.2; DB 4; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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QY 2889 AACTGTTTCATGCACACAGAGATTTACATTCAGAGCTTGGTCTTGTGTTTTCACACAGT 2948
Db 2933 AACTGTTTCATGCACACAGAGATTTACATTCAGAGCTTGGTCTTGTGTTTTCACACAGT 2992
QY 2949 CCCGTGTTCCCGTCCGCTCTGGATGCCATCTGTGCCATGTTTGTTCATCATCTGTCCT 3008
Db 2993 CCCGTGTTCCCGTCCGCTCTGGATGCCATCTGTGCCATGTTTGTTCATCATCTGTCCT 3052
QY 3009 TTGGGTCCCTGATTTCTGGCAAAACTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCT 3068
Db 3053 TTGGGTCCCTGATTTCTGGCAAAACTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCT 3112
QY 3069 ATGCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAAGTGTGAGTTGAGA 3128
Db 3113 ATGCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAAGTGTGAGTTGAGA 3172
QY 3129 ATATGATGATCTCAGTAGAAGGGTTCATTGAATACACAGACCTTGAAAAGAGACCTT 3188
Db 3173 ATATGATGATCTCAGTAGAAGGGTTCATTGAATACACAGACCTTGAAAAGAGACCTT 3232
QY 3189 GGAATATCAGAAACGCCACCCAGCCCTGCCCATGAAGAGTGTGATACTTTGAGA 3248
Db 3233 GGAATATCAGAAACGCCACCCAGCCCTGCCCATGAAGAGTGTGATACTTTGAGA 3292
QY 3249 ATGTGAACCTCATGTACAGTCCAGTGGCCCTCTGGTACTGAAGCATGTGACAGACTCA 3308
Db 3293 ATGTGAACCTCATGTACAGTCCAGTGGCCCTCTGGTACTGAAGCATGTGACAGACTCA 3352
QY 3309 TTAATCAACAAGAAAGTTGGCATTGTTGGGAAGAACCGGAGCTGGAAGAACTTCCCTCA 3368
Db 3353 TTAATCAACAAGAAAGTTGGCATTGTTGGGAAGAACCGGAGCTGGAAGAACTTCCCTCA 3412
QY 3369 TCTCAGCCCTTTTATAGATTGTACAGAACCCGAAAGTAAATTTGGATTGATAAGATCTTGA 3428
Db 3413 TCTCAGCCCTTTTATAGATTGTACAGAACCCGAAAGTAAATTTGGATTGATAAGATCTTGA 3472
|||||

QY	3429	CAACTGAAATTGGACTTTCAGATTTTAAGGAAGAAATGTCAATCATCTCAGGAACCTG	3448
DB	3473	CAACTGAATTTGGACTTTCAGATTTTAAGGAAGAAATGTCAATCATCTCAGGAACCTG	3532
QY	3489	TTTTTGTCTACTGGAACAATGAGGAAAAACCTTGGATCCCTTTAAAGGAGCACACGGATGAGG	3548
DB	3533	TTTTTGTCTACTGGAACAATGAGGAAAAACCTTGGATCCCTTTAAAGGAGCACACGGATGAGG	3592
QY	3549	AACGTGCGAATGCTTTCACAAAGAGGTACAACCTTAAAGAAACCATTTGAAGATCTTCTCGGTA	3608
DB	3593	AACGTGCGAATGCTTTCACAAAGAGGTACAACCTTAAAGAAACCATTTGAAGATCTTCTCGGTA	3652
QY	3609	AAATGGATCTGAAATTTAGCAGAAATCAGGATCCAAATTTTAAAGTGTGGACAAAGACAACCTG	3668
DB	3653	AAATGGATCTGAAATTTAGCAGAAATCAGGATCCAAATTTTAAAGTGTGGACAAAGACAACCTG	3712
QY	3669	TGTGCTTGGCCAGGCGCAATCTCAGGAAAAATTCAGATATTGATTAATTTGATGAAGCAGCAGG	3728
DB	3713	TGTGCTTGGCCAGGCGCAATCTCAGGAAAAATTCAGATATTGATTAATTTGATGAAGCAGCAGG	3772
QY	3729	CAAAATGTGGATCAAGAACTGATGAGTTTAATACAAAAAATAATCCGGGAGAAATTTGCC	3788
DB	3773	CAAAATGTGGATCAAGAACTGATGAGTTTAATACAAAAAATAATCCGGGAGAAATTTGCC	3832
QY	3789	ACTGCACCGTGTCAACCATTTGCACACAGATTTGAACACCATTTATTGACAGCGGACAAGATAA	3848
DB	3833	ACTGCACCGTGTCAACCATTTGCACACAGATTTGAACACCATTTATTGACAGCGGACAAGATAA	3892
QY	3849	TGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCCGTATGTTTTGCTGCAAAATA	3908
DB	3893	TGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCCGTATGTTTTGCTGCAAAATA	3952
QY	3909	AAGAGAGCCCTATTTTACAGATGGTGCAACACTGGGCAAGGCAAGCCGCTGCCCTCA	3968
DB	3953	AAGAGAGCCCTATTTTACAGATGGTGCAACACTGGGCAAGGCAAGCCGCTGCCCTCA	4012
QY	3969	CTGAAACAGCAAAACAG-----	3985
DB	4013	CTGAAACAGCAAAACAGAGATGGGTTTCAACCATGTTGGCCAGCTGGTCTCAAACTCCT	4072
QY	3986	-----	3985
DB	4073	GACCTCAAGTGATCCACCTTGGCCCTCCCAACTGCTGAGATTACAGGTGTGAGCCA	4132
QY	3986	-----GTATACCTTCAAAAGAAATATCCACATATTGCTACACTGACCAC	4030
DB	4133	CCAGGCCAGCCGTAGATACCTTCAAAAGAAATATCCACATATTGCTACACTGACCAC	4192
QY	4031	ATGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG	4090
DB	4193	ATGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG	4252
QY	4091	TGAATCCAAACCAAAATGTCAAGTCGGTTCGAGGCAATTTTCCACTAGTTTTTGGACTAT	4150
DB	4253	TGAATCCAAACCAAAATGTCAAGTCGGTTCGAGGCAATTTTCCACTAGTTTTTGGACTAT	4312
QY	4151	GTAACCCACATTTGACTTTTTTTTACTTTTGGCAACAATATTTATACATACAAGATGCTTA	4210
DB	4313	GTAACCCACATTTGACTTTTTTTTACTTTTGGCAACAATATTTATACATACAAGATGCTTA	4372
QY	4211	GTTTCATTTGAATTTTCTCCC	4231
DB	4373	GTTTCATTTGAATTTTCTCCC	4393

; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C16
 ; CURRENT APPLICATION NUMBER: US/09/605,785
 ; CURRENT FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 835
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 824
 ; LENGTH: 1074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-605-785-824

Query Match	24.7%	Score 1045.4	DB 4	Length 1074	
Best Local Similarity	99.9%	Find. No. 7e-292			
Matches 1046	Conservative	0	Mismatches 1	Indels 0	Gaps 0
QY 1226	TCAGCCATTGAGAGGGTGTTCAGAGGCAATCGTCAGCATCCGGAAGATCCAGACCTTTTGG	1285			
DB 4	TCAGCCATTGAGAGGGTGTTCAGAGGCAATCGTCAGCATCCGGAAGATCCAGACCTTTTGG	63			
QY 1286	CTACTTGATGAGATATCATACGGCAACCGTCAGCTGCCGTTCAGATGGTAAAAAGATGGTG	1345			
DB 64	CTACTTGATGAGATATCATACGGCAACCGTCAGCTGCCGTTCAGATGGTAAAAAGATGGTG	123			
QY 1346	CATGTGCAGGATTTTACATGCTTTTTGGGATAGGCATCAGACACCCCAACTCTACAAGGC	1405			
DB 124	CATGTGCAGGATTTTACATGCTTTTTGGGATAGGCATCAGACACCCCAACTCTACAAGGC	183			
QY 1406	CTTCTCTTTACTGTCAGACCTGGGAAATGTTAGCTGTGGTGGCCCGTGGGAGCAGGG	1465			
DB 184	CTTCTCTTTACTGTCAGACCTGGGAAATGTTAGCTGTGGTGGCCCGTGGGAGCAGGG	243			
QY 1466	AAGTCATCACATGTTAAGTGGCCGTGCTCGGGGAATGGCCCCCAAGTCAGGGCTGTGCAGC	1525			
DB 244	ARGTCATCACATGTTAAGTGGCCGTGCTCGGGGAATGGCCCCCAAGTCAGGGCTGTGCAGC	303			
QY 1526	GTGCATGGAAGAAATGGCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGG	1585			
DB 304	GTGCATGGAAGAAATGGCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGG	363			
QY 1586	AGTAATATTTTATTTGGGAAGAAATATGAAAGGAACGATATGAAAAAGTCATAAAGCT	1645			
DB 364	AGTAATATTTTATTTGGGAAGAAATATGAAAGGAACGATATGAAAAAGTCATAAAGCT	423			
QY 1646	TGTGCTCTGAAAAAGGATTTACAGCTGTGGAGGATGGTGATCTGACTGTGATAGGAGAT	1705			
DB 424	TGTGCTCTGAAAAAGGATTTACAGCTGTGGAGGATGGTGATCTGACTGTGATAGGAGAT	483			
QY 1706	CGGGGAACCGCTGAGTGGAGGGCAGAAACGACGGGTAAACCTTTGCAAGAGCAGTGTAT	1765			
DB 484	CGGGGAACCGCTGAGTGGAGGGCAGAAACGACGGGTAAACCTTTGCAAGAGCAGTGTAT	543			
QY 1766	CAAGATGTCACATCTATCTCTCGAGCATCCTCTCAGTCGAGTAGATGCCGAAGTTAGC	1825			
DB 544	CAAGATGTCACATCTATCTCTCGAGCATCCTCTCAGTCGAGTAGATGCCGAAGTTAGC	603			
QY 1826	AGACACTTGTTCGAACCTGTGTATTTGTTCAAAATTTTGCATGAGAAGATCACAAATTTTAGTG	1885			

|||||
Db 604 AGACACTGTTCCAGCTGATGATTTGTCAAATTTTGATGAGAAGATCAAAATTTTAGTG 663
QY 1886 ACTCATCAGTTGCAAGCTCAAGCTGCAAGCTGCAAGCTGATGATTTGAAAGATGTTAA 1945
Db 664 ACTCATCAGTTGCAAGCTCAAGCTGCAAGCTGCAAGCTGATGATTTGAAAGATGTTAA 723
QY 1946 ATGGTCCAGAAAGGACTTACACTGAGTTCCCTAAATCTGGGTATAGATTTGGCTCCCT 2005
Db 724 ATGGTCCAGAAAGGACTTACACTGAGTTCCCTAAATCTGGGTATAGATTTGGCTCCCT 783
QY 2006 TTAAGAAAGATTAATCAGGAAAGTGAACACCTCCAGTTCCAGTTCCAGGAACTCCACACTAAG 2065
Db 784 TTAAGAAAGATTAATCAGGAAAGTGAACACCTCCAGTTCCAGTTCCAGGAACTCCACACTAAG 843
QY 2066 AATCGTACCTTCTCAGAGCTTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCTTGAA 2125
Db 844 AATCGTACCTTCTCAGAGCTTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCTTGAA 903
QY 2126 GATGGTCTCTGAGAGCCCAAGATACAGAGAATGTCCTCCAGTTACACTATCAGAGGAGAAC 2185
Db 904 GATGGTCTCTGAGAGCCCAAGATACAGAGAATGTCCTCCAGTTACACTATCAGAGGAGAAC 963
QY 2186 CTTCTGAGGAAAGTTGGTTTTCAGGCTTATAGAAATTTACTTACAGAGCTGGTCTCAC 2245
Db 964 CTTCTGAGGAAAGTTGGTTTTCAGGCTTATAGAAATTTACTTACAGAGCTGGTCTCAC 1023
QY 2246 TGGATGTCTTCATTTTCTTCTTATTC 2272
Db 1024 TGGATGTCTTCATTTTCTTATTC 1050

RESULT 6

US-09-001-273-1
; Sequence 1, Application US/09001273
; Patent No. 5994130
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/001.273
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON, Gillian M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..4360

US-09-001-273-1

Query Match 10.3% Score 437.4; DB 2; Length 4781;
Best Local Similarity 48.8%; Pred. No. 9.4e-116;
Matches 1244; Conservative 0; Mismatches 1296; Indels 9; Gaps 2;
QY 1394 ACTCTACAAGSCCTTCTCTTACTGTCTCAGACCTGGCGAAATTTGTTAGCTGTGGTCGGGCC 1453
Db 1778 ACACGTGACAGATCGATCTGGAGATCCAAGAGGGTAAACTGTTGGAATCTCGGGCAGT 1837
QY 1454 GTGGGACAGGAAGTCACTCACTGTTAAGTGCCGTGTCGGGGAATTTGGCCCCAAGTCAC 1513
Db 1838 GTGGGAAGTGGAAACCTCTCTCATTTAGCCCAATTTTAGGCCAGATGACGCTCTTAGAG 1897
QY 1514 GGCTGTCTCAGCGTGCATGGAAGATTTCCCTATGTCTCTCAGACGCTGGGTGTTCTCG 1573
Db 1898 GGCAGCATTCGATTCAGTGGAACTTCGCTTATGTGCCCCAGAGGCTGGATCTCAAT 1957
QY 1574 GGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATATGAAAGGAACGATATGAAAA 1633
Db 1958 GCTACTCTGAGACACACTCTCTTTTGGGAAGGAATATGATGAAGAAAGATACAATCT 2017
QY 1634 GTCATAAGCGTTGTGCTCTCAAAAAGGATTTACAGCTGTTGGAGGATGTTGATCTGACT 1693
Db 2018 GTGCTGAACAGCTGCTGCTGAGGCCCTGACCTGSCCATTTCTTCCACAGCAGCTGACG 2077
QY 1694 GTGATAGGAGATCGGGGAACCCAGCTGAGTGGAGGGCAGAAAGCAGCGGTAAACCTTGCA 1753
Db 2078 GAGATTGGAGAGCGAGGAGCCAACTGAGCGGTGGCGAGGCCAGAGAGTACAGCTTGCC 2137
QY 1754 AGACAGTGTATCAAGATGCTGACATCTATCTCTGACGATCTCTCAGTGCAGTATAGT 1813
Db 2138 CGGSCCTTGTATGATGACAGGAGCATCTACATCTCTGACGACCCCTCTGATCTTATAG 2197
QY 1814 GCGGAAGTTAGACAGACTTGTTCGAACTGTGATTTGTCATAATTTTGCATGAGAAATC 1873
Db 2198 GCGCATGTGGCAACCACTCTTCAATAGTGTCTATCGGAACATCTCAAGTCCCAAGACA 2257
QY 1874 ACAATTTTGTAGTCACTCATGATGCTGAGTGTTCGAACTGTGATTTGTCATAATTTTGCATGAGAAATC 1933
Db 2258 GTTCTGTTGTTACCCACCAGTTTACAGTACCTGTTGATGATGATGATGATGATGATGATG 2317
QY 1934 AAAGATGTTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGGTATAGAT 1993
Db 2318 AAAGAGGCTGTATTACGGAAGAGGCCACCCATGAGGAATGATGATGATGATGATGATG 2377
QY 1994 TTTGGCTCCCTTTTAAAGAAAGGATAATAGGAAAGTGAACAACTCCAGTTCAGGAACT 2053
Db 2378 TATGCTTACCATTTTTAAATACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATCA 2437
QY 2054 CCCACACTAAGGAATCGTACCTTCTCAGAGTCTTGGTGTGCTCAACAACTTCTTACA 2113
Db 2438 AAAAGGAACCAAGTGTTCACAGAAGAAGTCAACAAGAAAGGTTCTTAAACAGGATCA 2497
QY 2114 CCCTCTCTGAAAGATGGTCTCTGAGAGCCAAAGATACAGAGATGTCCTGATGATGATG 2173
Db 2498 ATAAGAAAGAAAGCAGTAAAGCCAGAGGAAGGCGAGCTTGTGAGCTGGGAAGAA 2557
QY 2174 TCAGAGGAGAAACGGTTCTGAAGGAAAGTTGGTTTTTCAGGCCCTTATAGAAATTTACTTACA 2233
Db 2558 GGGCAGGGTTCAGTGCCCTGGTCAATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2617
QY 2234 GCTGTGCTCACTGGATTTGTTCTTCAATTTTCTTATTTCTTCTTCTTCTTCTTCTTCTTCT 2293
Db 2618 TTGGCATTCCTGTTTATTTATGCCCCCTTTTCTATGCTGAATGTAGGACGACCCGCTTCAGC 2677
QY 2294 GCCTATGTGCTTCAAGATTGGTGGCTTTTCATCTGCGCAACAAACAAAGTATGCTTAAAT 2353
Db 2678 ACCTGGTGTGATGTTACTGGATCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2737
QY 2354 GTCACTGTAAATGGAGGAGGAATGTAAACGAGAACTAGATCTTAACTGTTACTTACTAGGA 2413
Db 2738 AACGAGACCTCGTGTGATGACACGATGAGGAGCAATCTCTCATATGATGATGATGATGATG 2797

LOCATION: 2..4360
US-08-843-459A-1

Query Match 10.3%; Score 437.4; DB 4; Length 4781;
Best Local Similarity 48.8%; Pred. No. 9.4e-116;
Matches 1244; Conservative 0; Mismatches 1296; Indels 9;

2;

Qy	1394	ACTCTACAAGGCCCTTCTTTACTGTCTCAGACCTGGCGAAATTTAGCTGTGTGGTGGGCCCC	1493
Db	1778	ACATGCAACAGATCGATCTGGAGATCCAAAGAGGGTAAACTGGTTGGAATCTGCGGCAGT	1837
Qy	1454	GTGGGACAGGGAGTCAACACTGTTAAAGTGCCGTCTCGGGGAATTTGGCCCCAAGTCAC	1513
Db	1838	GTGGGAAGTGGAAAAACCTCTCTCATTTTCAGCGCATTTTAGGCCAGATGACGCTTCTTAG	1897
Qy	1514	GGGCTGCTCAGCGGTGCATGGAAAGAAATGGCTATGTCTCTCAGCAGCCCTGGGTGTCTCG	1573
Db	1898	GGCAGCATTCGAATCAGTGGAACTTCGCTTATGTGGCCACAGCGCTTGATCCTCAAT	1957
Qy	1574	GGAACTCTGAGGAGTAAATATTTTATTTGGGAAGAAATATGAAAGGAACGATATCAAAA	1633
Db	1958	GCTACTCTGAGAGCAACATCTCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCT	2017
Qy	1634	GTCAATAAGGCTTGTCTCTGAAAAAGGATTTTACAGCTGTGTGGAGGATGGTGAATCTGACT	1693
Db	2018	GTGCTGAACAGCTGTGCTCTGAGGCGTGAACCTGGCCATCTCTCCACGACGCGACCTGACG	2077
Qy	1694	GTGATAGGAGATCGGGGAACCAACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTTGCA	1753
Db	2078	GAGATTGGACGACGAGGACCAACCTGACGGGTGGCAGGCCAGAGGATCATGCGCTTGCC	2137
Qy	1754	AGACAGCTGTATCAAGATGCTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGAT	1813
Db	2138	CGGCGCTTGTATAGTGACAGGAGCATCTACATCTCTGGACGACCCCTCAGTGCCTTAGAT	2197
Qy	1814	GCGGAAGTTAGCAGACACTTGTTCGAACCTGCTATTTCTCAAAATTTGCCATGAGAAATC	1873
Db	2198	GCCCATGTGGCAACCACTCTTCAATAGTGCTATCCGGGAACATCTCAAGTCCAGACA	2257
Qy	1874	ACAAATTTAGTGACTCATCTGGACTGACCTTCAAGCTGCAAGTGCAGATCTCGATATTG	1933
Db	2258	GTCTGTGTTCTTACCCACCAGTTACAGTACCTGGTGTGACTGTGATGAGTCACTTCATG	2317
Qy	1934	AAAGATGGTAAATGTGACAGAGGGACTTACACTGAGTTCCTTAAATCTGGTATAGAT	1993
Db	2318	AAAGAGGGCTGTATATACGGAAGAGGACCCCATGAGGAACATGATGAATTTAAATGGTGAC	2377
Qy	1994	TTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACTCCAGTTCAGGNACT	2053
Db	2378	TATGCTACCAATTTTAAATTAACCTGTGTGGAGAGACACCGCCAGTTGAGATCAATCA	2437
Qy	2054	CCACACTAAGGAATCGTACCTTCTCAGAGCTTCGCTTGGTCTCAACAATCTTCTAGA	2113
Db	2438	AAAAAGGAACACAGTGGTTCACAGAAGAAGTCAACAAGACAGGGTCTTAAACAGGATCA	2497
Qy	2114	CCCTCTCTGAAGATGGTCTCTGAGAGGCCAAGATACAGAGATGTCCAGAGTTACATTA	2173
Db	2498	ATAAGAAGGAAGAAAGCAGTAAGCCAGAGGAGGGCAGCTTGTGCACTGGGAAGAGAAA	2557
Qy	2174	TCAGAGGAAGAACCGTTCTCAAGGAAAAGTTGGTTTTCAGGGCTATAAGAAATTACTTCAGA	2233
Db	2558	GGCAGGGTTAGTGCCCTGGTTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCC	2617
Qy	2234	GTGTGTCTACTGGATGTCTTTCATTTTCCCTTAAACACTGCAGCTCAGGTT	2293
Db	2618	TTGGCATCTCGTATATATGCCCCCTTTTCATGTGTAATGTAGCAGCACCGCCTTCAGC	2677
Qy	2294	GCCTATGTGCTCAAGATTTGGTGTCTTCACTACCTGGGCAACAAACAAATATGCTAAAT	2353
Db	2678	ACCTGGTGGTTACTTGATTCAGCAAGCAAGCAAGCGGGAACCACTGTGACTCGAGGG	2737
Qy	2354	GTCACTGTAAATGGAGGAGGAATCTAACCGAAGCTAGATCTTACTTGCTACTTAGGA	2413

D	b	2738	AAGCAGACCTCGGTTAGTGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGC	2797
Q	y	2414	ATTATATCAAGGTTTAAGCTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTGGTA	2473
D	b	2798	ATCTACGCCCTCTCCATGGCAGTCATGCTGATCTCTGAAAGCCATTCGAGGAGTGTCCTTT	2857
Q	y	2474	TTCAGCTCTCTGTTTAACCTCTCACAAACTTTTCACAACAAAATGTTTGAGTCAAATTCGT	2533
D	b	2858	GTCAAAGGCGACGCTCGGAGCTTCTCCGGCTGCATGACGAGCTTTTCCGAGGATCCTTT	2917
Q	y	2534	AAAGCTCCGGTATATATCTTTTGATAGAAATCCAATAGGAAGAATTTTAAATCTGTTCTCC	2593
D	b	2918	CGAAGCCCTATGAAGTTTTTTGACAGACCCCCACAGGGAGAGTTCTCAACAGGTTTTTC	2977
Q	y	2594	AAAGACATTGGACACTTGGATGATTTGCTGCCCTGACGTTTTTAGATTTCATCCACAGA	2653
D	b	2978	AAAGACATGATGAAGTTGACGTGCGCTGCCGTTCAGGCCGAGAGTTTCATCCAGAAC	3037
Q	y	2654	TTGCTACAAGTGGTGTGGTCTCTGTGGCTGTGGCCGTGATCTCCTTGGATCGCAATA	2713
D	b	3038	GTTATCTCGTGTCTTCTGTGTGGGAATGATCGCAGGAGCTCTCCCGTGGTTCCTGTG	3097
Q	y	2714	CCCTTGGTTCCTCTGGAATCATTTTCAATTTTTTCTTCGGGGATATTTTTTGGAAACGTCA	2773
D	b	3098	GGAGTGGGGCCCCCTGTCACTCTCTTTTTCAGTCTCTGCACATTTCTCTCCAGGGTCTGATT	3157
Q	y	2774	AGAGATGTGAAGCGCTGGAATCTACAACCTCGGAGTCCAGTGTTTTCCCACITTTGTCTATCT	2833
D	b	3158	CGGGAGCTGAGCGCTGTGACAAATATCAGCATCACTTTTCTCTCTCCACATCAGCTCC	3217
Q	y	2834	TCTCTCCAGGGGCTCTGACCATTCCGGGCATACAAAGCAGAGAGAGTGTCAGGAAC TG	2893
D	b	3218	AGCATACAGGGGCTTCCCAACCATCCACGCCTACAATAAAGGCGCAGGATTTCTGACAGA	3277
Q	y	2894	TTTGATGCACACAGAGATTTACATTCAGAGGCTTGTTGTTGTTTGTGACAGCTCCCGC	2953
D	b	3278	TACCAGGAGCTGTGGATGACAACCAAGCTCTTTTTTTTTTTTGTACGTGTGCGATGCGG	3337
Q	y	2954	TGGTGGCCGCTCGCTGATGCCATCTGCGCATTTTGTCTATCATCTGTGCTTTGGG	3013
D	b	3338	TGGCTGGCTGTGGCTGACCTCATCAGCATGCGCCTCATCACACACAGGGGCTGATG	3397
Q	y	3014	TCCTGTATTTCTGGCAAAACTCTGGATGCGGGCAGTTGGTTTGGCACTGTCTCTATGCC	3073
D	b	3398	ATCGTCTTTATGCACGGGCAGATTCGCCACGCCTATCGGGTCTCGCCATCTCTTATGCT	3457
Q	y	3074	CTCAGCTCATGGGATGTTTTCAGTGGTGTGTCGACAAAGTCTGCAAGTTGAGAAATATG	3133
D	b	3458	GTCCAGTTNACGGGGCTGTTCAGTTTACGGTTCAGACTGGCATCTGAGACAGAAGCTCGA	3517
Q	y	3134	ATGATCTCAGTAGAAGGCTATTGAATACACAGACCTT-----GAAAAAGAGCACCT	3187
D	b	3518	TTCACTCGGTGAGAGGATCAATCACATTTAAGACTCTGTCTTTGAGCACCTGGC	3577
Q	y	3198	TGGGAATATCAGAAAGCCCCACACAGCTGGCCCCATFGAAGGATGATAATCTTTGAC	3247
D	b	3578	AGAATTAAAGAAACAGGCTCTCTCCCTGACTGGCCCCAGAGGGAGAGGTGACCTTTGAG	3637
Q	y	3248	AATGTGAATCTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCATCTGCACGACTC	3307
D	b	3638	RACGCAGATGAGGTACGGAAGAACCTTCTCTGCTCTTAAAGAAAGTATCTTCTCAG	3697
Q	y	3308	ATTAATACAGAAAGGTTTGGCATTTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTC	3367
D	b	3698	ATCAAACTTAAGAGAAGATTGGCATTTGTGGGCGGACAGGATCAGGNAAGTCTCTCGTG	3757
Q	y	3368	ATCTCAGCCCTTTTATGATGTFCAG---ACCCGAGGTFAAAATTTGGATGTGATAAGATC	3424
D	b	3758	GGGATGGCCCTCTTCCGCTCTGGTGAGTTATCTGAGGGCTGCATCAAGATTGATGAGTG	3817
Q	y	3425	TTGACAAC TGAATTTGGACTTCACCAATTTAAGGAAGAAATGTCATCATCTCAGGAA	3484
D	b	3818	AGAATCAGTGATATTGGGCTTGGCCACCTCCGAAGCAACTCTCATCTCATCTCCCAAG	3877

Db 2804 AACGAGACCTCGGTGAGTCACACCATGAAGGACAACTCCATATGACAGTACTATGCCAGC 2863
QY 2414 ATTTATTCAGGTTTAACTAGTACCTACCGTCTCTTTTGGCATGCAAGATCTCTATTGGTA 2473
Db 2864 ATCTAGCCCTCTCCATGCGAGTCATGCTGATCTCTGAAAGCCATTGCGAGGAGTGTCTTT 2923
QY 2474 TTCTAGGCTCTTGTAACTCTTCACAAACTTTGACACAAATAATGTTTGAAGTCAATCTG 2533
Db 2924 GTCAAGGACACGCTGCGAGCTTCTCCCGGCTGCAATGACGAGCTTTTCCGAAGGATCTT 2983
QY 2534 AAAGTCTCCGGTATTATCTTTCATAGAAATCCAATAGGAAGAATTTAAATCGTTTCTCC 2593
Db 2984 CGAAGCCCTATGAAGTTTTCACAGGCCCCACAGGAGGAGTCTCAACAGGTTTTC 3043
QY 2594 AAAGACATTTGGACACTTGGATGATTGCTGCGCTGACGCTTTTATAGATTTCATCCAGACA 2653
Db 3044 AAAGACATGGATGAAGTTGACGTGCGCTGCGTTCAGGCCGAGATGTTTCATCCAGAAC 3103
QY 2654 TTGCTTACAAGTGGTGGTGTCTCTGTGGCTGTGGCGGTGATTCCTTGGATCGCAATA 2713
Db 3104 GTATCTCTGGTGTCTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGTCTCTTGTG 3163
QY 2714 CCCTTGGTTCCTTGGAAATCATTTTCTTCTGCGGATATTTTTCGAAACGTCA 2773
Db 3164 GCAGTGGGCCCCCTGTCTATCTCTTTTTCAGTCTGACATGCTCCAGGCTCTGATT 3223
QY 2774 AGAGATGTGAAGCGCTCGAATCTAACAACCTGGAGTCCAGTGTCTTCCACTTGTCTACT 2833
Db 3224 CGGAGCTGAAGCGCTCGAATAATATCAGGAGTCACTTCTCTCCACATCAGTCC 3283
QY 2834 TCTCTCAGGCGCTGACACCATCGGCGCATACAAGCAGAGAGAGTGTCCAGAACTG 2893
Db 3284 AGCATACAGGCGCTTGGCACCATCCAGCTTACATAAAGGCGAGAGTTTCTGCACAGA 3343
QY 2894 TTTGATGCACACCATGATTTACATTCAGAGCTGTGTTCTTGTCTTTCACAACTGCCG 2953
Db 3344 TACCAGGAGCTGTGGATGACAAACCACTCTCTTTTGTGTTTACGTGTGCGATGCGG 3403
QY 2954 TGGTTCGCGCTGCTGCTGAGTGCATCTGCGCATCTGCTGCTGCTGCTGCTGCTGCTG 3013
Db 3404 TGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3463
QY 3014 TCCCTGATCTGCGAAGAACTCTGATGCGCGGAGGTTGTTGGCACTGCTCTATGCC 3073
Db 3464 ATCTGTTTATGACGCGGAGATTTCCCGCAGCTATGCGGCTCGCCATCTCTTATGCT 3523
QY 3074 CTCACGCTCATGGGATGTTTCACTGTGTGTTGACAAAGTGTGAAGTTGAGATATG 3133
Db 3524 GTCCAGTTAAGGCGCTGTTCCAGTTTACGGTCAAGTGGCATCTGACAGAGAGCTCGA 3583
QY 3134 ATGATCTAGTAGAAGGGTCAATGAATACACAGACCTT-----GAAAGAGAGCACT 3187
Db 3584 TTCACCTCGGTGAGAGGATCAATCACTACATTAAGACTCTGCTTGGAGAGCACTGCC 3643
QY 3188 TGGGAATATCAGAAACCCACACCACTGCTGCGCCATGAGAGAGTGAATCTTTGAC 3247
Db 3644 AGAATTAGAACAGAGCTCTCCCTGACTGCGCGGAGGAGGAGTGAACCTTTGAG 3703
QY 3248 AATGTGAATCTATGATGCTCAGTTCAGGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTG 3307
Db 3704 AACGCAGAGATGAGTACCGAGAAACCTCCCTCTGCTCTAAAGAAATCTCTTCAAG 3763
QY 3308 ATTAATCACAAGAAAGTTGGATTTGGGAAGAACCGAGCTGGAAAGTTCCCTC 3367
Db 3764 ATCAAACTTAAGAGAGATTTGGATTTGGGCGGAGAGGATCAGGAAAGTCTCGCTG 3823
QY 3368 ATCTACGCCCTTTTAGATTGTGAGA---ACCGAAGGTAAATTTGGATTGATAAGATC 3424
Db 3824 GGGATGCCCTCTTCCGCTGTGGTGTGAGTTATCTGAGGCTGTCATCAAGATTGATGAGTG 3883
QY 3425 TTGCAACTGAATTTGACATTCAGATTTTAAGGAAGAAATGTCATCATCTACCTCAGAA 3484

Db 3884 AGAATCAGTGATATTGGCCTTGGCGACCTCGAAGCAAACTCTCTATCATTTCTCTCAAGAG 3943
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Db 3944 CCGTGTCTGTTTCTAGTGGCACTGTCAGTCAAAATTTGACCCCTTCAACCACTACACTGAA 4003
QY 3545 GAGAACTGTGGAATGCTTTACAGAGAGTACAACTTAAAGAAACCAATTGAAGATCTTCTCT 3604
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QY 3605 GGTAAATGATGATCTGAATTTAGCAGATCAGGATCCAAATTTTGTGTTGGACAAAGACAA 3664
Db 4064 CTGAAACTTGAATCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4123
QY 3665 CTGCTGCTGCTTCCAGGCAATCTCAGGAAATTCAGAGAAATCAGATATTTGATGAAGCG 3724
Db 4124 CTCTTGTGATAGTCTGAGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4183
QY 3725 ACGGCAATTTGATCCAGAACTGATGATTAATACAAAAAATAATCCGCGGAGAAATTT 3784
Db 4184 ACAGCTGCCATGACACAGAGACAGACTTATTGATTCAGAGACCATCCGAGAGCAATTT 4243
QY 3785 GCCACTGACCTGCTTAACCATTTGACACAGATTTGAACACCATTTATTTGACAGCGACAAG 3844
Db 4244 GCAGACTGTACCTGCTGACCATTTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4303
QY 3845 ATAAATGTTTTAGATTCAGAACTGAAAGAAATATGATGAGCGGTATGTTTGTCTGCTCAA 3904
Db 4304 ATATGCTGCTGCGCCAGGACAGGTGCTGAGTTTGAACACCCCATCGGCTCTCTGCTGC 4363
QY 3905 AATAAGAGAGCTTATTTTACAAGATGGT 3933
Db 4364 AACGACAGTTCGCGATTCTATGCCATGTT 4392

RESULT 9
US-08-141-893-1
; Sequence 1, Application US/08141893
; Patent No. 5489519
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,893
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923; 08/029,340
; FILING DATE: 27-OCT-1992; 8-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: POI-002
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5149
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-141-893-1

Query Match.          9.2%; Score 390.4; DB 1; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

QY 518 TAGCGCTATGCCACGGTGTGACTTTTGCACGCTCATTTTGGCTATPACTGCACTTA 577
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Db 1285 TACTTCTACACCGTGTGCTGTTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1344

QY 578 TATTTTATCAGTTCAGTGTGCTGGATGAGGTTAGGATAGCCATGTCCTATGATT 637
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Db 1345 TACTTCCACATCTGCTTCGTGATGATGATGATGATGATGATGATGATGATGAT 1404

QY 638 TATCGGAAGCACTTCGCTTACTAGTAACTAGCCATGGGAGGAGACACACAGCCAGATA 697
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Db 1405 TATCGGAAGCCCTCGTGATGATGATGATGATGATGATGATGATGATGATGAT 1464

QY 698 GTCAATCTGCTGCCAATGATGTGAACAAGTTTGTATGATGATGATGATGATGATGAT 757
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Db 1465 GTCAACCTCATGCTGTGGACGCTCAGAGGTTTATGATGATGATGATGATGATGAT 1524

QY 758 CTGTGGGAGGACCACTGACAGGCGATGCGAGTGTGCTGCTGCTGCTGCTGCTGCTG 817
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Db 1525 ATCTGTGACGCCCCCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1584

QY 818 ATATCGTCTGCTGGGATGCGAGTTCTAAATCATCTCTGCTGCTGCTGCTGCTGCT 877
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Db 1585 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1644

QY 878 GGGAGTGTCTCTCATCTAGGAGTAAACTGCAACTTTCACGGATGCCAGGATCAGG 937
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Db 1645 GCGATGAAGACCAAGACGTATCAGGTGGCCACATCAGAGGACAAAGACAAATCG 1704

QY 938 ACCATGAATGAAGTATACTGGTAAAGATTAATAAATGTACGCTGGGAAAGTCA 997
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Db 1705 CTGATGAAGAAATCTCAATGGATCAAGTGTCAAGTCTTATGCTGGGAGCTGGCA 1764

QY 998 TTTTCAAAATCTTATTAACCAATTTGAGAAAGAGGATTTCCAAAGATTTCTGAGA 1057
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1765 TTCAAGGACAAAGTGTGCGCCATCAGGAGGAGGAGCTGAAGTGTGAGAAAGTCTGC 1824

QY 1058 TGCCCTAGGGGATGAATTTGGCTTCGTTTTTTCAGTGAAGCAAAATCATCGTTTGTG 1117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1825 TACCTGTACGCGTGGGCACCTTCACCTGGGTCTGACGCGCTTTCTGTTGGCTTGTG 1884

QY 1118 ACCTTCACCACTACGTGCTCTCGGATGTGATCAGACCGCGGCTGTCGTGGCA 1177
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Db 1885 ACATTTGCGCTAGCTGACCATTTGACGAGAAACAACTCCTGGATGCCAGACGCTTC 1944

QY 1178 GTGACGCTGTATGGGCTGTGGGCTGACGGTTACCCCT---CTTCTTCCCTCAGCCATT 1234
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Db 1945 GTGTCTTTGGCCCTTGTTCACATCTCTCCGCTTCCCTGAACATCTCCCATGGTCA 2004

QY 1235 GAGAGGGTGTACAGGCAATCTGACATCCGAAAGAAATCCAGACCTTTTGTACTTGTAT 1294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2005 AGCAGCATGTGCAGCGAGTGTCTCCCTCAAAGCGCTGAGGATCTTCTCTCCCATGAG 2064

QY 1295 GAGATATCACAGCGCAACCGTACGTCGCTGATGGTAAAGATGTCATGTCATGTCAG 1354
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Db 2065 GAGCTGGAACCTGCACAGCATCGAGC--GACGGGCTGTCAAAGAGCGGGGCGACGACAG 2123

QY 1355 GATTTTACTGCTTTTGGGATA-----AGGCATCAGAGACCCCAACTCTACAAG 1404
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2124 CATCACCGTGAGGAATGCCACATTCACCTGGGCGAGGAGCCCTCCCACTGAATGG 2183
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QY 1405 CCTTTCCTTTACTGTCTCAGACCTTGCAGAAATTTAGCTGTGTGTCGCCCCCGTGGAGCAGG 1464
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2184 CATCACCTTCTCCATCCCGAAGGTGCTTTGGTGGCCGTGTGGCCAGGTGGGCTGCGG 2243

QY 1465 GAAGTCACTACTGTTAAGTCCCGTGTGCGGGAATTTGCCCCCAAGTACAGGGCTGGTCTAG 1524
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Db 2244 AAGTTGTCCCTGCTCTCAGGCCCTTGGCTGAGATGGACAAAGTGGAGGGCGACGTGGC 2303

QY 1525 CGTCATGGAAGAAATTCCTATGTCTCAGCAGCCCTGGGTGTTCTCGGGAACCTCTCAG 1584
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Db 2304 TATCAAGGGCTCCCTGCGCTATGTGCCACAGCAGCCCTGGATTCAGATGATTCTCTCCG 2363

QY 1585 GAGTAATATTTATTTTGGGAGAAATATGAAAAGAACAGATATGAAAAGTATCAAAAGGC 1644
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Db 2364 AGAAAACATCTTTTGGATGTGACGTGGAGGACCATATTTACAGGTCGCTGATACAGGC 2423

QY 1645 TTGTGCTCTGAAAAGAGATTTACAGCTGTGGAGATGGTGTATCTGACTGTGATAGGAGA 1704
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2424 CTGTGCCCTCTCCACAGCCTGGAATCTGCCAGTGGGATCGGACAGAGATTTGGCGA 2483

QY 1705 TCGGGGAACCAAGCTGAGTGGAGGGCAGAAAGCAGGTAACCTTGCACAGCAGTCTA 1764
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2484 GAGGGCGTGAACCTGTCTGGGGACAGAGACGCGGTGAGCCTGGCCCGGCGGTGTA 2543

QY 1765 TCAAGATGCTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGATGCGGAAGTTAG 1824
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2544 CTCCAACGCTGACATTTACCTTCTCGATGATCCCTCTCAGCAGTGGATGCCATGTGGG 2603

QY 1825 CAGACACTTGTGCACTGTGATTTGTCAA-----ATTTTGCATGAGAAGTACACAAT 1878
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Db 2604 AAAACACATCTTTGAAAATGTGATTTGGCCCCCAAGGGATGCTGAAGAACAAGCCGGAT 2663

QY 1879 TTTAGTGACTCATCAGTTGAGTACCTCAAGCTCAAGTCAAGTCTGATTTGAAAGA 1938
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Db 2664 CTTGGTCACCCACAGATGAGCTACTTGGCCAGGTGGACGCTCATCTGCTCATGAGTGG 2723

QY 1939 TGGTAAATGTCAGAAAGGGACTTACACTGAGTTCTTAAATCTGCTATAGATTTTGG 1998
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2724 CGCAAGATCTCTGAGATGGCTCTACCAGAGCTGTGGCTCGAGAGCGCGCTTCGC 2783

QY 1999 CTCCCTTTTA-----AAGAAGGATATGAGGAAAGTGAACAACCTC 2039
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2784 TGAGTTCTCTCGTACCTATGCCACAGCAGAGCAGGACAGGATCGAGAGAGACGGGT 2843

QY 2040 CAGTTCAGGAAGTCCACACTAAGGAATCGTACCTCTCAGAGCTTCGCTGGTGGTCTC 2099
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2844 CACGGGCTCAGCGGTCAGGAGGAGCAACAATGGAGAAATGGCATGCTGCTGCTGAC 2903

QY 2100 ACAAATCTTCTAGACCTCTTGAAGATGGTCTGAGAGAGCCAAAGATACAGAGATG 2159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2904 GGACAGTGCAGGAAGCAACTGCAGAGACAGCTCAGCAGCTCTCTCTCTATAGTGGGA 2963

QY 2160 TCCAG-----TTACACTATCAGAGGAGAACCTGTTCTGA----AGGAAAGTTGGTTTT 2209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2964 CATCAGCAGCACCACACAGCAGCCGAGCACTCGAAGAGCTGAGGCCAAGAGGAGGA 3023

QY 2210 CAGGCTATAAAGAAATTTACTTCAGAGCTGGTGTCTCAGTGGATTTCTTCTATTTCTTATT 2269
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Db 3024 GACTGGAAGCTGATGGAGCTGACAGGGCGACAGAGGCGAGGCTCAAGCTTTCCGTGTA 3083

QY 2270 CTCTAAACACTCAGCTCAGGTTGGCTATGTGTTCA-----AGATTGGTGGCTTTTCA 2324
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3084 CTGGGACTACATGAAGCCATCGGACTTCTCATCTCTCTCTCAGCATCTTCTCTTTTCA 3143

QY 2325 ACTGGGCAACAACAAGATGCTAAATGTCTGTAATGAGAGGAGGAAATGTAACCG 2384
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3144 GTGTAACCATGTGTCGCGCTGGCTTCAACTATTTGGCTCAGCCTCTGAGCTGTAGTACC 3203

QY 2385 AGAAGCTAGATCTTAAGTGTACTTAGGAATTTATTAGGTTTAACTGAGTACCGTTC 2444
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3204 CATCGTCAACGGGACTCAGGAGCACACGAAGTCCGCGTGAAGCTCTATGAGGCCCTGGG 3263

QY 2445 TTTTGGCATAGCAAGATCTCTATTG-----GTATTCTACGCTCTTGTTAA 2490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 3264 CATTTTCAAGAGTCCGCTGTTGGCTACTCCATGCGCGTGTCTCATCGGGGATCTTT 3323
QY 2491 CTCCTTCAAACTTTGCAACAATAATGTTGAGTCAATCTGAAAGTCCCGTATTAAT 2550
Db 3324 GGCCTCCCGCTGCTGCAAGTGGAGCTGCTGACAGCATCTCGGCTACCCATGAGCTT 3383
QY 2551 CTTTGTATGAATCAATAGGAGAAATTTAATCGTTTCTCCAAGACATTTGGACACTT 2610
Db 3384 CTTTGAAGGAGCCCGAGTGGAACTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGT 3443
QY 2611 GGATGATTTGCTGCGCGTGCACCTTTTATGATTTTCATCCAGACATTCCTACAAAGTGGTGG 2670
Db 3444 GGACTCCATGATCCCGGAGGTATCAAGATGTTCAATGGCTCCCTGTTCAACGTCATTTGG 3503
QY 2671 TGTGCTCTGTTGGCTGTGGCGTGATTCCTTGGATCGCAATACCCCTTGGTTCCCGCTTGG 2730
Db 3504 TGCCTGTCATGTTATCTCTGCTGGCCACGCCATCCCGCATCATCCCGCCCTTGG 3563
QY 2731 AATCATTTTCAATTTTCTTCCGCGATATTTTGTGAAAGCTCAAGAGATGTAAGCGCT 2790
Db 3564 CTTCACTACATCTTCTGCTGAGAGTCTACGTGCTTCTCCCGGAGCTGAAGCGCT 3623
QY 2791 GGAATCTACAATCGGAGTCCAGTCTTTTCCACTTGTCTCTCTCCAGGGCTCTG 2850
Db 3624 CGAGTCTGCTACCGCTCCCGCTCTATTCCTTCAACAGACTTGTCTGGGGGTGAG 3683
QY 2851 GACCATCCGGGATACAAAGAGAGAGGTGTGAGAACTGTTTGTATGCACACAGGA 2910
Db 3684 CGTCAATCGAGCTTCGAGGAGCAGAGCGCTTCAACACAGAGTGAACGTGGA 3743
QY 2911 TTTACATTCAGAGCTTGGTCTTCTTTTTCACACGTCCTCGCTGGTTCGCGCTCCGCT 2970
Db 3744 CGAAGCAGAGAGGCTTATACCCAGCATCTGGCCCAACAGGTGGCTGGCGCTGCGCT 3803
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Db 3804 GGAGTGTGTGGCACTGCATCTGTTCTGTTGCTGCCCTGTTGGGTGATCTCCAGCA 3863
QY 3031 AACTCTGATCCGGGAGGTGTTGGCTACTGTCTTATCCCTCAGCTCATGGGAT 3090
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Db 4044 GCCCAGAGCTGGCCCATGAGTGGCGAGTGGAAATCCGGAATCTGCTGCTGCTACCG 4103
QY 3268 TCCAGTGGGCTCTGTTGTTGAGTGTGACAGACTCATTAATCAACAGAAAGGT 3327
Db 4104 AGAGGACTGGACTTCTGTCAGGACATCAATGTCAAGATCAATGGGGAGAAAGGT 4163
QY 3328 TGGCAATTTGGGAGAACCCGAGCTGGAAAGATTCCTCTATCTCAGCCCTTTTAGATT 3387
Db 4164 CGGCATCTGGGGGAGGAGCTGGAAGTCTGCTCCCTGACCTGGCTTATTTTCGAT 4223
QY 3388 GTCAGA---ACCCGAGGTAAATTTGGATGTGATAAGATCTTGACAACTGAAATTTGACT 3444
Db 4224 CAACGAGTCTGCCGAGGAGATCATCTGATGGCATCAACATCCCAAGATCGGCT 4283
QY 3445 TCAGATTTAAGGAGAAATGTCATCATCTCAGGAACCTGTTTGTCTACTGGAAAC 3504
Db 4284 GCAGGACTCTGGCTTCAAGATCAACATCACTCCCGGAGGCTGTTTGTCTCGGGTTC 4343
QY 3505 AATGAGAAACCTGATCCCTTAAAGAGCAGCAGGATGAGAACTGGAATGCTT 3564

Db 4344 CTCCGAAATGAACCTGGACCCATTCAGCCAGTACTCGATGAAGAGCTCTGGAGCTCCCT 4403
QY 3565 ACAAGAGGTACAATTAAGAAACCACTTGAAGATCTTCCCTGGTAAATGATGATGATTAAT 3624
Db 4404 GGAGCTGGCCCACTGAGGACTTGTGTGAGCCCTTCTTGACAAAGTAGACCATGAATG 4463
QY 3625 AGCAGATCAGGATCCAAATTTTGTGTGACAAAGACAACTGTTGCTTGGCCCTGGCCAGGC 3684
Db 4464 TGCAGAGGCGGGAGAACCTCAGTGTGCGGAGCGCCAGCTTGTGTGCTAGCCCGGC 4523
QY 3685 AATTCACGAGAAATTCAGATATTTATGATGAAGCAGCGCAATGTGATCCAAG 3744
Db 4524 CTTGCTGAGGAGAACGAGATCTTGTGTGATGAGGCCAGCCAGCTGACCTGGA 4583
QY 3745 AACTGATGAGTTAATCAAAATAATCGGAGAAATTTGCCCACTGACCCGTGCTAAC 3804
Db 4584 AAGGAGGAGCTTCCAGTCCACCATCGGACACAGTTCGAGGACTGACCCGTCTCAC 4643
QY 3805 CATTCACACAGATTTGAACACCATTTATGACAGCGACAGATTAATGTTTAGATTCAAG 3864
Db 4644 CATCGCCACCGCTCAACACCATCATGAGTACACAGGCTGATCTTGGACAAAG 4703
QY 3865 AAGACTGAAGATATGATGAGCCGTATGTTTGTGCAAAATAAAGAGAGCTATTTTA 3924
Db 4704 AGAATCCAGGAGTACGGCGCCCATCGGACCTCTCTGACAGAGAG---GTCTTTTCTA 4760
QY 3925 CAAGATGTGCAACAACTGGCAAGCAGACGCGCTGCCCT 3966
Db 4761 CAGCATGGCCAAAGACGCGCTTGTGTGAGCCCCAGAGCT 4802

RESULT 10

US-08-463-092B-1
; Sequence 1, Application US/08463092B
; Patent No. 5766880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Delevy, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,092B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196...4788
US-08-463-092B-1

Query Match 9.2%; Score 390.4; DB 1; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

QY 518 TACGCCATGCCACGCTGCTGACTTTTGCACGCTCATTTTGGCTATACATCACTTA 577
DB 1285 TACTTCTACACCGTGTGCTGTTTGTCACTGCTGCTGCAGACCCCTCGTGCACACAG 1344
QY 578 TATTTTATCACGCTTTCAGTGTGCTGGGATGAGGTACGAGTACGATGTCATGGGCTGTC 1404
DB 1345 TACTTCCACATCTGCTTCGTCAGTGCATGAGGATCAAGACCCGCTGTCATGGGCTGTC 1404
QY 638 TATCGGAAGCAGCTTCTGTTAGTACATGGCCATGGGGAAGACACACAGCCAGGCGATA 697
DB 1405 TATCGGAAGGCCCTGCTGTATCAACAATTCAGCCAGAAAATCTCCACGGCTCGGGGAGAT 1464
QY 698 GTCAATCTGCTGCCAATGATGTAACAAGTTTGTGATCAGGTGACAGTGTCTTACACTTC 757
DB 1465 GTCAACTCATGCTGTGACGCTCAGAGTTTCATGGATGTCGACGATACATTAACATG 1524
QY 758 CTGTGGGAGGACCACTGACGGCGATGCGAGTGAAGTCCCTACTCTGAGTGGAGTAGGA 817
DB 1525 ATCTGTGACGCCCTCCCAAGTCATCTTCTGCTCTACCTGCTGGCTGAATCTGGGC 1584
QY 818 ATATCTGCTCTGCTGGATGAGTTCATATCATTTCTCTGCTGCTTGCCTGCTGCTGCTG 877
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QY 878 GGAAGTCTGCTCATCACTGAGGAGTAAACTGCAACTTTCACGATGCCAGGATCAGG 937
DB 1645 GCGATGAAGACCAAGACGTATCAGGTGGGCCACATGAAGAGCAACATCGGATCAAG 1704
QY 938 ACCATGAATGAAGTTATACTGGTATPAGGATTAATAAATGTACGCTGGGAAAAGTCA 997
DB 1705 CTGATGAACGAATTTCTCAATGGATCAAGTCAAGTCTAAGCTTTATGCTGGAGCTGGCA 1764
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DB 1765 TTCAAGGACAAGTGCTGCCATCAGGAGGAGGAGCTGAAGGTGCTGAAGAAAGTCTGCC 1824
QY 1058 TGCTCAGGGGGATGAATTTGGCTTCTGTTTTCAGTGAAGCAAAATCATCGTTTGTG 1117
DB 1825 TACCTGTACGCGTGGGACCTTCACCTGGGTCTGACGCCCTTTCTGGTGGCTGTGC 1884
QY 1118 ACCTTACACCACTAGTGTCTCGGCTGAGTGTATCAGACCCAGCGCGTGTTCGTGGCA 1177
DB 1885 ACATTTGGCGTCTACGTGACCATTTGACGAGAACAACATCTGGATGCCAGACAGCCTTC 1944
QY 1178 GTGACCTGTATGGGCTGTGGGCTGAGCGTTACCTCTTCTTCTCCCTCAGCCAT 1234
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QY 1295 GAGATATCACAGCGCAACCCGTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1354
DB 2065 GAGCTGGAACTGACAGCATGCTGAGC-GACGGCTGCTCAAAGACGCGGGGCGACGAACAG 2123
QY 1355 GATTTTACTGCTTTTGGGATA-----AGGCATCAGAGACCCCACTCTACAAGG 1404
DB 2124 CATCAGCTGAGGAATGCCATTTACCTGGCCAGGAGGACCTCCACACATGAATGG 2183
QY 1405 CCTTTCCTTTACTGTCAGACCTGCGGAATTTAGTGTGCTGGCCCGCTGGGAGCAGG 1464
DB 2184 CATCAGCTTCTCCATCCCGAAGGTGCTTTGGTGGCGGTGGTGGGCGAGGTGGCTGGCG 2243
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DB 2724 CGCAGATCTCTGAGATGGCTCTACCAGGAGCTGCTGGCTCGAGAGCGGCTTTCGC 2783
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DB 2784 TGAGTTCTCTCGTACCTATGCCAGCACAGACAGCAGGATCGAGAGGAGACGGGT 2843
QY 2040 CAGTTCCAGGAATCCCACTAAGGAATCGTACCTCTTCTCAGAGTCTTCGGTTTGGTCTC 2099
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QY 2100 AACAACTTCTAGACCTCTTGAAGATGCTGCTCTGGAGAGCCCAAGATACAGAGATG 2159
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QY 2210 CAGGCTTATGAAGATTTACTTCAGAGTGGTGTCTACTGAGTGTGCTTCTTCTTCTTAT 2269
DB 3024 GACCTGGAAGCTGATGAGGCTGACAGGCGCAGACAGGCGAGGTCAAGCTTTCCGCTGA 3083
QY 2270 CTCCTAAACACTCAGCTCAGGTTGCCTATGTCTTCA-----AGATTGCTGGCTTTCAT 2324
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QY 2385 AGAAGCTAGACTTAACCTGTAAGTAAATTAATCAGGTTTAAGTGTAGCTAGCTACCGTTTC 2444
DB 3204 CATGTCAACGGGACTCAGGACACACGAAAGTCCGGGTGAGCGTCTATGGAGCCCTGGG 3263
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DB 3264 CATTTCAAGGAGTGGCGGTGTTGGTACTCCATGGCGGTCTCATCGGGGGATCTT 3323
QY 2491 CTCCTTCAAACTTTCACAAACAAATGTTGAGTCAATTTCAAGCTTCCGGTATTATT 2550
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QY 2551 CTTTGTAGAAATCAATAGGAAGAAATTTAAATGTTCTTCAAGACATTTGCTGACACAGT 2610
DB 3384 CTTTGAAGGAGCCCTGAGTGGAACTGTTGAACCGCTTCTCCAGGAGCTGGACACAGT 3443
QY 2611 GGATGATTGCTGCGCTGACCTTTTATGATTTTCCAGACATTTGCTACAAGTGGTTGG 2670
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DB 3504 TGCCTGCATCTGTTCTGCTGCGCCACGCCCATGCCCATCATCCCGCCCTTTGG 3563
QY 2731 AATCATTTTCAATTTTCTCGCGATATTTTGGAAAGCTCAAGAGATGTAAGCGCT 2790
DB 3564 CCTCATCTACTTCTGCTCCAGAGGTTCTAGTGGCTTCTCCCGGCGAGCTGAAGCGCT 3623
QY 2791 GGAATCTACAACCTGGAAGTCCAGTCTTTTCCACCTTTGCTCTCCAGGGCTCTG 2850
DB 3624 CGAGTCGCTGACCGCTCCCGGCTCTATCCCATTTCAACAGAGCTTGTCTGGGGGTGAG 3683
QY 2851 GACCATCCGGGATACAAAGAGAGAGAGGTGTGAGAACTGTTGATGACACACAGGA 2910
DB 3684 CGTCAATCGAGCTTCGAGGAGCAGGAGCGCTTCAATCCACAGAGTGAACGTGGA 3743
QY 2911 TTTACATTCAGAGCTTGGTCTTGTGTTTTCACACAGTCCCGTGTGGCTGCGCTGCT 2970
DB 3744 CGAAGACAGAAAGGCTTATACCCAGCATCTGTGCGCAACAGGTGGCTGGCGCTGCGCT 3803
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DB 3804 GGAGTGTGCGCAACTGCATCTGTTGCTGCTGCTGTTGGGTGATCTCCAGGCA 3863
QY 3031 AACTCTGGATCCGGGAGGTTGGTGGCACTGTCTTATCCCTCAGCTCATGGGGAT 3090
DB 3864 CAGCTCAGTCTGCTGCTGGTGGCGCTCTCAGTGTCTTACTCATTTGCAAGTCAACAGTA 3923
QY 3091 GTTTTCACTGGTGTGTCGACAAAGTGTGAGTTGAGATATGATGATCTCAGTAGAAG 3150
DB 3924 CTTGAATGGCTGTTGGATGTCTCATCTGAAATGAAACCAACATCTGTCGCGGTGGAGAG 3983
QY 3151 GGTCAATTAATACAGACCTTTGAAAGAGACCTTTGGGAA--TATCAGAAACGCC 3207
DB 3984 GCTCAAGAGATTTACAGAGCTGAGAGGAGCGCCCTGGCAATTCAGGAGACACGTC 4043
QY 3208 ACCACAGCCTGCCCCATGAAGAGTGTATTAATCTTTGACAATGTGAATTTATGATACAG 3267
DB 4044 CCCCAGCAGTGGCCCCAGTGGCGGAGTGAATTCGGAACACTGCTGCTGCGCTACCG 4103
QY 3268 TCCAGTGGGCTCTGTTACTGAGAGTCTGACAGCATCTATTAAATCACAAGAAAGGT 3327
DB 4104 AGAGGACCTGGACTTCTGCTCAGGACATCAATGTCAAGTCAATGGGGAGAGAAAGT 4163
QY 3328 TGGCATTTGGGAAGAACCGAGCTGGAAGAGTTCCCTCATCTCAGCCCTTTTATGATTT 3387
DB 4164 CGGCATCTGGGGCGGAGGAGCTGGGAAGTCTGCTCCTGACCCCTGGGCTTATTTCCGAT 4223

QY 3388 GTCAGA---ACCGAAGGTAAAAATTTGGATTGATAAGATCTTGACAACTGAAATTTGACT 3444
DB 4224 CAACGAGTCTGCCGAGGAGAGATCATCATGATGGCATCAACATCCCAAGATCGGCCT 4283
QY 3445 TCAGGATTTAAGGAAGAAATGCAATCATACCTCAGGAACCTGTTTGTTCATCTGGAAC 3504
DB 4284 GCAGGACCTCCGCTTCAAGATCACCATCATCCCCCAGGACCTGTTTGTTCGGGTTC 4343
QY 3505 AATTGAGAAAAACCTGATCCCTTTAAGGAGCACACCGATCAGGAATCTGGATGCGCTT 3564
DB 4344 CTCCGAAATGAACTGGACCCATTGAGCCAGTACTCGGATGAAGAAGTCTGGACGCTCC 4403
QY 3565 ACAAGAGGTACAACTTTAAAGAAAACCATTTGAAGATCTTCCCTGGTAAATGATGATGAAT 3624
DB 4404 GGAGCTGGCCCACTCAAGGACTTCGTGTCAGCCCTTCCCTGACAAAGTACACCATGAATG 4463
QY 3625 AGCAGATCAGGATCCAAATTTTGTGTTGACAAAGACAACTGTTGCTGCTGCGAGGGC 3684
DB 4464 TGCAGAAAGCGGGGAGAACCTCAGTGTGGGCGAGCGGACGCTTGTGTGCTAGCCGGC 4523
QY 3685 AATTCTCAGAAAAATCAGATATTGATTTGATGAGCGACGCAAAATGTGGATCCAAG 3744
DB 4524 CTGCTGAGGAAGACGAGATCTTGTGTTGATGAGGCGACCGACGCGTGGACCTGGA 4583
QY 3745 AACTGATGATTTAAATACAAAAAATCCGGGAGAAATTTGCCACTGACCGCTGCTAAC 3804
DB 4584 AAGGAGGACCTCATCCAGTCCACCATCGGACACAGATTCGAGGACTGACCGCTCTCAC 4643
QY 3805 CATTCACACAGATTGAACACCATTTATGACAGCGACAAAGATAATGTTTATGATTCAGG 3864
DB 4644 CATCGCCCAAGGCTCAACACCATCATGACTACACAAGGCTGATGCTTTGGACAAAG 4703
QY 3865 AAGACTGAAGATATGATGAGCCGTATGTTTGTCTGCAAAATAAAGAGAGCTATTATTA 3924
DB 4704 AGAATCCAGGAGTACGGCGCCCATCGGACCTCTCTGACGACAGAG---GTCTTTCTA 4760
QY 3925 CAAGATGTGCAACAACTGGCAAGGCAAGCGCGCTGCGCT 3966
DB 4761 CAGCATGGCAAGAGCGCGGCTTGTGTGACGCCCGCAGACT 4802

RESULT 11
US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893

Query Match	9.2%; Score 390.4; DB 2; Length 5011;
Best Local Similarity	47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative	0; Mismatches 1786; Indels 77; Gaps 12;
QY	518 TACGCCATGCCACGGTCTCACITTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTA 577
Db	
Db	1285 TACTTCTACACCGTGTCTGCTTTGTCACTGCCCTGCAGACCGCTGTGCTGCACAG 1344
QY	578 TATTTTATCACGTTTCAGTGTCTGGGATGAGGTTACGAGTAGGCATGTGCCATATGATT 637
Db	
Db	1345 TACTTCCACATCTCTGCTCGTCAGTGGCATGAGGATCAAGACCGTGTCATTGGGCGTGC 1404
QY	638 TATCGGAAGGCACCTTCGCTCTTAGTAAATGCCATGGGGAAGACAACACAGGCCAGATA 697
Db	
Db	1405 TATCGGAAGCCCTGGTGATCAACAAATTCAGCAGAGAAATCTCTCACGGTCGGGAGATT 1464
QY	698 GTCAATCTGCTGTCCAATGATGTCAACAAGTTTCATCAGGTGCAGAGTCTTCTTACACTTC 757
Db	
Db	1465 GTCAACCTCATGTCTGGACGCTCAGAGGTTTCATGAGCTTGGCCACGTCATTAAACATG 1524
QY	758 CTGTGGCAGGACACCTGCAGCGCATGCAGTGACTGCCCTACTCTGGATGGAGATAGGA 817
Db	
Db	1525 ATCTGGTGCAGCCGCCCTGCAAGTCATCTTCTCTACCTCTCTGGCTGAATCTGGGC 1584
QY	818 ATATCTGTCCTTGGTGGGATGGAGTTCTTAATCAATCTCTGCGCCCTTGCAAGCTGTTTT 877
Db	
Db	1585 CTTTCCGCTCTGGCTGGAGTGGCGTGATGGTCTCATGTGTGCCCGCAATGCTGTGATG 1644
QY	878 GGGAAAGTGTCTCATCACTGAGGAGTAAAACTCGAACTTTCACGGATGCCAGATCAGG 937
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Db	1645 GCGATGAAGACCAAGCGTATCAGTGGCCCAATGAAGAGCAAAAGACAATCGGATCAAG 1704
QY	938 ACCATGAATGAAGTTATACTTGGTATTAAGGATATAAAAATGTACGGCTGGGAAAAGTCA 997
Db	
Db	1705 CTGATGAACAAATTCATCAATGGGATCAAAAGTGCTAAAGCTTTATGCTGGGACCTGGCA 1764
QY	998 TTTTCAATCTTATTACCAATTTGAGAAAGAGAGATTTCCAAAGATCTTGAGAAAGTTCC 1057
Db	
Db	1765 TTCAAGACAAGGTGCTTGGCCATCAGGCAGGAGGAGCTGAAGGTGCTGAAGAACTCTGCC 1824
QY	1058 TGCTCAGGGGGATGAATTTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTG 1117
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QY	1118 ACCTTCAACCACTACGTGCTCTCGGCAGTGTGATCACAGCCAGCCGGTGTTCGTGGCA 1177
Db	
Db	1885 ACATTGCCGCTACGTGACCATTTGAGAGAACACATCTCGGATGCCAGACAGCCTTC 1944
QY	1178 GTGACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCT---CTTCTTCCCTCAGCCATT 1234
Db	
Db	1945 GTGTCTTTGGCCCTGTGTCAACATCTCTCCGGTTCTCCCTGGACATCTCTCCCATCGTTCATC 2004

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE: 08/141,893
FILING DATE: 26-OCT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-460-907B-1

Query Match 9.2%; Score 390.4; DB 2; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

QY 518 TAGCCCTATGCCCGGTCGACTTTTGGCAGCTCATTTTGGCTATACGTCACCTTA 577
DB 1285 TACTTCTACACCGTGGTGTGTTGTCACGCTGCTGCGCTGAGACCCCTGCTGCACAG 1344
QY 578 TATTTTATCACGTTACGTCGTGGGATGAGGTTACGAGTACGATGTCATATGATT 637
DB 1345 TACTTCCACATCTGCTTCGTCAGTGGCATGAGATCAAGACCGTGTCAATGGGGCTC 1404
QY 638 TATCGAAGGACATTCGCTTTAGTAACATGGCCATGGGGAAGAACACACAGGCCAGATA 697
DB 1405 TATCGAAGGCCCTGGTGATCACCAATTACGCCAGAAATCTCCACGGTCCGGGAGATT 1464
QY 698 GTCAATCTGCTCCATGATGTAACAGTTTGTATGATGATGATGATGATGATGATGATG 757
DB 1465 GTCAACCTCATGCTGTGGACGCTCAGAGGTTTATGAGCTTGGCCAGGTACATTAACATG 1524
QY 758 CTGTGGCAGGACCACTGCAGGCGATCGCAGTGAATGCTGCTGATGGAGATAGGA 817
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QY 878 GGAAGTTGTTCTTCATGATGAGGATGAACCTGCACTTTCAGGATGCGGATGAGTACAGG 937
DB 1645 GCATGAAGACCAAGAGCTATCAGGTGGCCCATCAATGAAGACCAAGCAATTCGGATCAAG 1704
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DB 1825 TACCTGTACGCGGTGGGCAACCTTACCTGGGTCTCAGGCCCTTTCTGGTGGCTTGTGC 1884
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DB 1885 ACATTTGCGGTCTAGTGAACATTCACGAGAACACATCTCTGGATGCCAGACGCTTC 1944
QY 1178 GTGACGCTGTATGGGCTGTGCGGTGACGTTTACCTT---CTTCTTCCCTCAGCAAT 1234
DB 1945 GTGCTTTTGGCTTGTTCACATCTCCGCTTCCCTTGAACATCTCTCCCATGTCTATC 2004
QY 1235 GAGAGGTGTGAGAGGCAATGTGATGATCCGAGAAATCCAGACCTTTTGTACTTGTAT 1294
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DB 2065 GAGTGGAACTGACAGCATCGAGC-GACGGCTGTCAAGACGCGGGGCGACGAACAG 2123
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Db 3924 CTTGAAGTGTGTTGCTGAGTCTCATCTGNAATGGAACCAACATGTCGCTGGAG 3983
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RESULT 13

US-08-463-179A-1

; Sequence 1, Application US/08463179A

; Patent No. 6001563

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deeley, Roger G.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,179A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-463-179A-1

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Query Match          9.2%; Score 390.4; DB 3; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

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QY 3328 TGGCATTTGGGAAGAACCGGAGCTGGAAGTTCCTCATCTCAGCCCTTTTAGATT 3387
Db 4164 CGCATCTGGGCGGAGCGGAGCTGGAAGTCTGCTGCTGACCTGGCTTATTTCCGAT 4223
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Db 4404 GGAGCTGGCCCACTGAAGGACTTCGTGTCAGCCCTTCTGACAAAGTAGACCATGAAT 4463
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QY 3685 AATCTCAGAAAATCAGATTTTGAATTTGATGAAGCAGCGCAATGTGATCCAAG 3744
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QY 3805 CATTCACACAGATTTGAACACCATTTATGACAGCAGCAAGATAATGTTTATGATTCAG 3864
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QY 3865 AAGACTGAAAGATATGATGAGCGTATGTTTGTCTCAAAATTAAGAGAGCTTATTTA 3924
Db 4704 AGAAATCCAGGAGTACGGCGCCCATCGGACCTCTCTGACAGAGAG---GTCTTTCTA 4760
QY 3925 CAAGATGTCACAACTGGCAAGGAGCAAGCGCTGCTCCT 3966
Db 4761 CAGCATGGCCAAAGACCGCGCTGTTGTGTGAGCCCCAGAGCT 4802

RESULT 14

US-08-461-384B-1

; Sequence 1, Application US/08461384B

; Patent No. 6025473

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deeley, Roger G.

; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

; STREET: Queen's University at Kingston

; CITY: Kingston

; STATE: Ontario

; COUNTRY: CANADA

; ZIP: K7L 3N6

; COMPUTER READABLE FORM:

QY 2100 AACAACTTCTAGACCTCTCTCAAGATGGTCTCTGGAGAGCGAAGATACAGAGAAATG 2159
Db 2904 GGACATGAGGAAGAACTGCAGAGACAGCTCAGCAGCTCTCTCTATAGTGGGA 2963
QY 2160 TCCAG-----TTACACTATCAGAGGAGAACCGTTCTGA-----AGGAAATGGTGT 2209
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Db 3024 GACCTGGAAGCTGATGAGGCTGACAGGCGCAGACAGGCGATCAAGCTTTCCGCTGTA 3083
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RESULT 15

US-08-407-207A-1

; Sequence 1, Application US/08407207A
; Patent No. 6063621

; GENERAL INFORMATION:

; APPLICANT: Deeley, Roger G.

; APPLICANT: Cole, Susan P.C.

; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

; STREET: Queen's University at Kingston

; CITY: Kingston

; STATE: Ontario

; COUNTRY: CANADA

; ZIP: K7L 3N6

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1512
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-407-207A-1

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Query Match          9.2%; Score 390.4; DB 3; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

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 Job time : 181.375 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:49:35 ; Search time 102.455 Seconds
(without alignments)
16388.716 Million cell updates/sec

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Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4211	99.5	6082	10	US-09-822-827-535
5	3910.2	92.4	6140	9	US-10-012-896-536
6	3910.2	92.4	6140	10	US-09-759-143-536
7	3910.2	92.4	6140	10	US-09-780-669-536
8	3910.2	92.4	6140	10	US-09-822-827-536
9	3739.2	88.4	4395	9	US-10-012-896-1007
10	3738.6	88.4	3786	9	US-10-012-896-1006
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13	1045.4	24.7	1074	10	US-09-759-143-824
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21	351.8	8.3	4869	9	US-09-938-842A-1392	Sequence 1392, Ap
22	292.6	6.9	5728	10	US-09-917-800A-479	Sequence 479, App
23	274.6	6.5	3069	10	US-09-756-095-105	Sequence 105, App
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25	216.8	5.1	291	9	US-10-012-896-823	Sequence 823, App
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34	184.4	4.4	1977	10	US-09-954-456-804	Sequence 804, App
35	184.4	4.4	1977	10	US-09-880-107-3407	Sequence 3407, Ap
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37	181.4	4.3	1448	10	US-09-925-299-157	Sequence 157, App
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44	101.6	2.4	1980	10	US-09-841-132-462	Sequence 462, App
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ALIGNMENTS

RESULT 1
US-10-012-896-535
; Sequence 535, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-535

Query Match 99.5%; Score 4211; DB 9; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy 3601 T C C T G G T A A A T G G A T A C T G A A T T A G C A A A T C A G A T C C A A T T T T A G T C T T G G A C A A A G 3660
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Qy 3841 C A A G A T A A T G G T T T A G A T T C A G A A G A C T G A A A G A A A T A T G A T G A G C C G T A T G T T T G C T 3900
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RESULT 3

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US-09-780-669-535
; Sequence 535, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-535

Query Match          99.5%; Score 4211; DB 10; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      1  GGACAGCGGTGGCGGCGGAGCCCCAGCATCCCTGCTTGAGGTCCAGGAGCGGAGCCGCG 60
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QY 1141 CGGAGTGTGATACAGCCAGCCGCTGTCTGTCAGTGTGCTGTATGGGCTGTGG 1200
 DB 1211 CGGAGTGTGATACAGCCAGCCGCTGTCTGTCAGTGTGCTGTATGGGCTGTGG 1270
 QY 1201 GGTAGCGTTACCTTCTTCCCTCAGCCATTCAGAGGGTGTGAGAGCAATGCTCAG 1260
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RESULT 4

US-09-822-827-535
; Sequence 535, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-535

Query Match 99.5%; Score 4211; DB 10; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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DB	1091	GAGAAAGNAGAGATTTCCAAGATCTCAGAAAGTTCCCTGCCTCAGGGGATCAAAATTGGC	1150
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; Sequence 536, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Megaher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4535
; OTHER INFORMATION: n = A,T,C or G
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Query Match 92.4%; Score 3910.2; DB 9; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(6140)
; OTHER INFORMATION: n-A,T,C or G
; US-09-759-143-536

Query Match      92.48; Score 3910.2; DB 10; Length 6140;
Best Local Similarity 97.18; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

QY 189 GGTGCTCAATCCCTGTTTAAATGGCCATAAAGCGAGATTAGAGAAATGATATGT 248
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Db 3413 TCTCAGCCCTTTTGTAGTGTCTCAGAACCCCAAGSTAAAATTTGGATTTGATAAGATCTTGA 3472
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Db 3473 CAACTGAAATTTGACATTCAGATTTTAAAGGAAGAAATGTCAATCATACCTCAGGAACCTG 3532
QY 3489 TTTTGTCTACTGGAACAATGAGGAAACCTGGATCCCTTTTAAAGGAGCACACGATGAGG 3548
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QY 3549 AACTGTGGAATGCTTACAGAGGTACAACCTTAAAGAAACCATTTGAAGATCTTCTCTGGTA 3608
Db 3593 AACTGTGGAATGCTTACAGAGGTACAACCTTAAAGAAACCATTTGAAGATCTTCTCTGGTA 3652
QY 3609 AATGATGATCTGAATTAGCAGATCAGGATCCCAATTTTGTAGTGTGGNCAAGCAACTGG 3668
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Db 3773 CAAATGTGATCCAGAACTGATGAGTTTAAACAAAATAATCCGGGAGAAATTTGCCCC 3832
QY 3789 ACTGCACCCGTGTAACTTGCACACAGATTTGAACACCATTTATTGACAGGACAAAGATAA 3848
Db 3833 ACTGCACCCGTGTAACTTGCACACAGATTTGAACACCATTTATTGACAGGACAAAGATAA 3892
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QY 3909 AAGAGAGCCTATTTTACAAAGTGGTCCAACTGGGCAAGGACGAGCGCTGCCCTCA 3968
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Db 4013 CTGAACACGACAAACAGATGGGTTTTCCACATGTTGGCCAGGCTGTTCTCAAACTCCT 4072
QY 3986 ----- 3985
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QY 3986 -----GTATACTTCAAAAGAAATTTATCCACATATTTCCACACTGACCAAC 4030
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Db 4373 GTTCATTTGAATATTTCTCCC 4393

RESULT 7
US-09-780-669-536
; Sequence 536, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-536

Query Match 92.4%; Score 3910.2; DB 10; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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QY 249 ATTCAAGTCTGCCAAGAACCGCTCACAGCACCTTTGGAGAGAGTTGCCAAGGTTCTGGG 308
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QY 309 ATAAAGAGTTTAAAGAGCTGAGATGAGCAGACAGCCTTTCTTTAACAAGAGCAATCA 368
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QY 369 TAAAGTGTACTGGAAATCTATTAGTTTGGGAATTTTACGTTAATTGAGGAAGTG 428
Db 413 TAAAGTGTACTGGAAATCTATTAGTTTGGGAATTTTACGTTAATTGAGGAAGTG 472

QY 429 CCAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTTGAATAATTATGATC 488
Db 473 CCAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTTGAATAATTATGATC 532

QY 489 CCATGGATTCGTGGCTTTGAACACAGCGTACGCGTATGCCACGCTGCTGACTTTTCCA 548
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Db 713 CCATGGGAAGACAAACACAGGCGAGATAGTCAATCTGCTGTCCAAATGATGTGAACAGT 772
QY 729 TTGATCAGGTGACAGTGTCTTACATCTCTGCGGAGGACCACTCCAGCGGATCCGAG 788
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Db 833 TGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTCTGATGACAGTTCTAA 892
QY 849 TCATTTCTCTGCCCTTGCAGAAAGCTGTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAA 908
Db 893 TCATTTCTCTGCCCTTGCAGAAAGCTGTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAA 952
QY 909 CTGCAACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTATTAACATGATTAAGGA 968
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QY 1389 CCCCAACTCTAAGGCCCTTTTCTTACTGTCTGAGACTGCGGAAATGTTAGCTGTGGTCG 1448
Db 1433 CCCCAACTCTAAGGCCCTTTTCTTACTGTCTGAGACTGCGGAAATGTTAGCTGTGGTCG 1492
QY 1449 GCCCGTGGGAGCAGGAAGTCACTACTGTTAAGTCCCGTCTCGGGGAATTTGCCCCCAA 1508
Db 1493 GCCCGTGGGAGCAGGAAGTCACTACTGTTAAGTCCCGTCTCGGGGAATTTGCCCCCAA 1552
QY 1509 GTCAGGGCTGTGTCAGCTGTCATGGAAGATTTGCCCTATGTCTCTCAGACCCCTGGGTGT 1568
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QY 1569 TCTCGGAACTCTGAGGAGTAAATATTTTATTGGGAAATAATGAAAGGAACGATATG 1628
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QY 1689 TGACTGTGATAGGAGATCGGGGAACACCGCTGAGTGGAGGACAGAAACACGGGTAAACC 1748
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QY 1809 TAGATCGGAGTGTAGACAGACATTTGTTGCACTGTGATTTGTCACAAATTTTGGCAGAGA 1868
DB 1853 TAGATCGGAGTGTAGACAGACATTTGTTGCACTGTGATTTGTCACAAATTTTGGCAGAGA 1912
QY 1869 AGATCACAAATTTTACTGACTCATCAGTTGTCAGTACCTCAAGCTGCAAGTCAGATCTGA 1928
DB 1913 AGATCACAAATTTTACTGACTCATCAGTTGTCAGTACCTCAAGCTGCAAGTCAGATCTGA 1972
QY 1929 TATTGAAAGATGGTAAATGGTGCAGAAAGGGACTTACACTGAGTTCCTTAAATCTGGTA 1988
DB 1973 TATTGAAAGATGGTAAATGGTGCAGAAAGGGACTTACACTGAGTTCCTTAAATCTGGTA 2032
QY 1989 TAGATTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAACTCCAGTTCAG 2048
DB 2033 TAGATTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAACTCCAGTTCAG 2092
QY 2049 GAATCCACACTTAGGAATCGTACCTTCTCAGAGCTTCGCTGTTGGTCTCAACAACTCT 2108
DB 2093 GAATCCACACTTAGGAATCGTACCTTCTCAGAGCTTCGCTGTTGGTCTCAACAACTCT 2152
QY 2109 CTAGACCTCTCTGAAAGATGGTGTCTGAGAGCCAAAGATACAGAGATGTCCAGTTA 2168
DB 2153 CTAGACCTCTCTGAAAGATGGTGTCTGAGAGCCAAAGATACAGAGATGTCCAGTTA 2212
QY 2169 CACTATCAGAGAGAACCGTTCTGAAGGAAAGTGGTTTTCAGGCCATTAAGAAATTA 2228
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QY 2709 CAATACCCCTTGGTTCCTTCCCTTGGAAATCATTTTCAATTTTCTTGGCGCATATTTTGGAAA 2768
DB 2753 CAATACCCCTTGGTTCCTTCCCTTGGAAATCATTTTCAATTTTCTTGGCGCATATTTTGGAAA 2812
QY 2769 CGTCAAGAGATGTGAAGCGCCTTGGATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGT 2828
DB 2813 CGTCAAGAGATGTGAAGCGCCTTGGATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGT 2872
QY 2829 CATCTTCTCTCAGAGGCTCTTGACCATCCGGCATACAAAGCAGAGAGAGTGTTCAGG 2888
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QY 3009 TTGGTCTCTGATTTCTGCAAAACCTCTGATGCGGCGGAGGTTGGTTGGCACTGCTCT 3068
DB 3053 TTGGTCTCTGATTTCTGCAAAACCTCTGATGCGGCGGAGGTTGGTTGGCACTGCTCT 3112
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QY 3189 GGAATATCAGAAACCGCCACCACAGCTGCGCCCATGAAGAGTGAATCTTTGAGA 3248
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QY 3489 TTTTCTTCACTGGACATGAGGAAACCTGGATCCCTTTAAGGAGACACGGATGAGG 3548
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QY 3609 AATGGATGACTGAATTTAGCAGAAATCAGATGATTTAGTGTGTCGACAAAGACACTGG 3668
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QY 3729 CAATGTGATCCAAAGAACTGATGATTAATAACAAAAAATCCGGGAGAAATTTGCC 3788
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Db 3833 ACTGCACCGTGTAAACATTCACACAGATGAACACCATATTATGACAGCGACAAGATAA 3892
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QY CTGAACACAGCAAAACAG----- 3985
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Db 4253 TGAATCCAAACCAAAATGTCAGTCCGTTCCGAGGCAATTTGGCCACTAGTTTGGACTAT 4312
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QY GTTCATTTGAATATTTCTCCC 4231
Db 4373 GTTCATTTGAATATTTCTCCC 4393

RESULT 8

US-09-822-827-536
; Sequence 536, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-822-827-536

Query Match 92.4%; Score 3910.2; DB 10; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

QY 189 GTGGCTCAATCCCTGTGTTTAAATTTGGCCATAAAGCGAGATTAGAGGAAGATGATATGT 248
Db 233 GTGGGCTCAATCCCTGTGTTTAAATTTGGCCATAAAGCGAGATTAGAGGAAGATGATATGT 292
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Db 533 CCATGATTTCTGTCCTTTGAACACAGCGTACGCCATATGCCAGGTTGCTGACTTTTGGCA 592
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Db 713 CCATGGGAGACAAACACAGCGCAGATAGTCAATCTGCTGCTCAATGATGTGAACAGT 772
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QY TGACTGCCCTTACTCTGGATGGAGATAGGAATATCGTCCCTTGCCTGGGATGSCAGTTCTAA 848
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QY	1389	CCCCAACTCTACAAGGCGCTTTCCTTTACTGTACAGACTGCGGAATTCGTTAGCTGTGGTCG	1444
DB	1433	CCCCAACTCTACAAGGCGCTTTCCTTTACTGTACAGACTGCGGAATTCGTTAGCTGTGGTCG	1492
QY	1449	GCCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTGCCTGTCTCGGGGAATTCGCCCCAA	1508
DB	1493	GCCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTGCCTGTCTCGGGGAATTCGCCCCAA	1552
QY	1509	GTCAACGGCTGTCACGCTGCATGGAAGAAATTCCTTATGTCTCAGCAGCCCTGGGTGT	1568
DB	1553	GTCAACGGCTGTCACGCTGCATGGAAGAAATTCCTTATGTCTCAGCAGCCCTGGGTGT	1612
QY	1569	TCTCGGAACTCTGAGGAGTAATATTTTATTTCGGAAGAAATGAAAAGACGATATG	1628
DB	1613	TCTCGGAACTCTGAGGAGTAATATTTTATTTCGGAAGAAATGAAAAGACGATATG	1672
QY	1629	AAAAAGTCATAAAGGCTTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGTTGATC	1688
DB	1673	AAAAAGTCATAAAGGCTTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGTTGATC	1732
QY	1689	TCAGCTGTATAGAGATCGGGGAACCAACGCTGAGTGGAGGGCAGAAAGCACGGTAAAC	1748
DB	1733	TCAGCTGTATAGAGATCGGGGAACCAACGCTGAGTGGAGGGCAGAAAGCACGGTAAAC	1792
QY	1749	TTGCAAGACAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGATCTCTCAGTGCAG	1808
DB	1793	TTGCAAGACAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGATCTCTCAGTGCAG	1852
QY	1809	TAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAAATTTTGCATGAGA	1868
DB	1853	TAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAAATTTTGCATGAGA	1912
QY	1869	AGATCACAAATTTAGTGACTCATCAGTTCCAGTCTCAAGCTGCAAGTTCGATCTCA	1928
DB	1913	AGATCACAAATTTAGTGACTCATCAGTTCCAGTCTCAAGCTGCAAGTTCGATCTCA	1972
QY	1929	TATTCAAAGATGTTAAATGTTGCAGAGGGGACATTACACTCAGTTCCTAAATCTGGTA	1988
DB	1973	TATTCAAAGATGTTAAATGTTGCAGAGGGGACATTACACTCAGTTCCTAAATCTGGTA	2032
QY	1989	TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACTCCAGTTCAG	2048
DB	2033	TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACTCCAGTTCAG	2092
QY	2049	GAATCCACACACTAAGGAATCGTACTTCTCAGAGCTCTCGGTTGGTCTCAACAACTCT	2108
DB	2093	GAATCCACACACTAAGGAATCGTACTTCTCAGAGCTCTCGGTTGGTCTCAACAACTCT	2152
QY	2109	CTAGACCTCTCTTGAAGATGGTGTCTGAGAGCCAGATACAGAAATGTCACAGTTA	2168
DB	2153	CTAGACCTCTCTTGAAGATGGTGTCTGAGAGCCAGATACAGAAATGTCACAGTTA	2212
QY	2169	CACATATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCCTATAGAATTA	2228
DB	2213	CACATATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCCTATAGAATTA	2272
QY	2229	TCAGAGCTGGTCTCAGTGGATTGCTTCATTTTCCTTATTCCTCTCAAACTGCAGTCT	2288
DB	2273	TCAGAGCTGGTCTCAGTGGATTGCTTCATTTTCCTTATTCCTCTCAAACTGCAGTCT	2332
QY	2289	AGGTTGCCATGTGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAAAGTATGC	2348
DB	2333	AGGTTGCCATGTGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAAAGTATGC	2392
QY	2349	TAAATGTCACGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACCTGGTACT	2408
DB	2393	TAAATGTCACGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACCTGGTACT	2452
QY	2409	TAGGAATTTATCAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAGATCTCTAT	2468
DB	2453	TAGGAATTTATCAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAGATCTCTAT	2512

QY	2469	TGGTATTCTACGTCCTTGTGTTAACTCTTTCACAAACTTTTGCAACAACAAATGTTTGAGTCAA	2520
DB	2513	TGGTATTCTACGTCCTTGTGTTAACTCTTTCACAAACTTTTGCAACAACAAATGTTTGAGTCAA	2572
QY	2529	TTCTGAAAGCTCCGGTATTATTCTTTTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTT	2588
DB	2573	TTCTGAAAGCTCCGGTATTATTCTTTTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTT	2632
QY	2589	TTCTCCAAAGACATTGGACACTTGGATGATTGCTGCGCGTGACGTTTTPTAGATTTTCATCC	2648
DB	2633	TTCTCCAAAGACATTGGACACTTGGATGATTGCTGCGCGTGACGTTTTPTAGATTTTCATCC	2692
QY	2649	AGACATTTGCTACAAAGTGGTGGTGCTGCTGTGGCTGTGGCCGTGATTCCTTTGGATCG	2708
DB	2693	AGACATTTGCTACAAAGTGGTGGTGCTGCTGTGGCTGTGGCCGTGATTCCTTTGGATCG	2752
QY	2709	CAATACCCCTTGGTTCCCTTTGGAAATCATTTTTCATTTTTTCTTCGGCGATATTTTTTGGA	2768
DB	2753	CAATACCCCTTGGTTCCCTTTGGAAATCATTTTTCATTTTTTCTTCGGCGATATTTTTTGGA	2812
QY	2769	CGTCAAGAGATGTGAAGCGCTCGGAATCTACAACCTCGAGTCCAGTGTGTTTCCCACTGCT	2828
DB	2813	CGTCAAGAGATGTGAAGCGCTCGGAATCTACAACCTCGAGTCCAGTGTGTTTCCCACTGCT	2872
QY	2829	CATCTTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGGTGTCAAG	2888
DB	2873	CATCTTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGGTGTCAAG	2932
QY	2889	AACTGTTTATGCACACCAAGGATTACATTCAGAGCCTTGGTTCTTGTGTTTGGACAACGT	2948
DB	2933	AACTGTTTATGCACACCAAGGATTACATTCAGAGCCTTGGTTCTTGTGTTTGGACAACGT	2992
QY	2949	CCGCTTGGTTCCGCGTCCTCTGGATGCCATCTGTGCCATGTTTGTGCATCATCGTTGCCCT	3008
DB	2993	CCGCTTGGTTCCGCGTCCTCTGGATGCCATCTGTGCCATGTTTGTGCATCATCGTTGCCCT	3052
QY	3009	TTGGGTCCTTGATTCGCGAAAACCTCTGGATCGCGGCGAGTGTGTTTGGCACTGTCT	3068
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QY	3069	ATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTTCGACAAAGTGTGAAGTTGAGA	3128
DB	3113	ATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTTCGACAAAGTGTGAAGTTGAGA	3172
QY	3129	ATATGATGATCTCAGTAGAAAAGGTCATTGAATACACAGACCTTGAAAAGAAAGACACCTT	3188
DB	3173	ATATGATGATCTCAGTAGAAAAGGTCATTGAATACACAGACCTTGAAAAGAAAGACACCTT	3232
QY	3189	GGGAATATCAGAAAGCCCAACAGAGCCTGCCCCATGAAGGAGTGATTAATCTTTTGACA	3248
DB	3233	GGGAATATCAGAAAGCCCAACAGAGCCTGCCCCATGAAGGAGTGATTAATCTTTTGACA	3292
QY	3249	ATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGGTACTGAAGCATCTGCACAGCACTCA	3308
DB	3293	ATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGGTACTGAAGCATCTGCACAGCACTCA	3352
QY	3309	TTAAATCACAAGAAAAGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCA	3368
DB	3353	TTAAATCACAAGAAAAGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCA	3412
QY	3369	TCTCAGCCCTTTTATGATTTGCAGAACCCGAGGTAAAATTTGGATTTGATTAAGATCTTGA	3428
DB	3413	TCTCAGCCCTTTTATGATTTGCAGAACCCGAGGTAAAATTTGGATTTGATTAAGATCTTGA	3472
QY	3429	CAACTGAAATGGACTTCCAGGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTG	3488
DB	3473	CAACTGAAATGGACTTCCAGGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTG	3532
QY	3489	TTTTGTTTCACTGGAAACATGAGGAAAAACCTTGGATCCCTTTAAGGAGCACACGGATGAGG	3548
DB	3533	TTTTGTTTCACTGGAAACATGAGGAAAAACCTTGGATCCCTTTAAGGAGCACACGGATGAGG	3592
QY	3549	AACTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTTTGAAGATCTTCTCTGTA	3608


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Db 3593 AACGTGGAAATGCGCTTACAGAGAGTCAACAACCTAAAGAAACCACTGAAGATCTTCGTGTA 3652
Qy 3609 AAATGGATACGTAATAGCAGAAATCAGATCCAAATTTAGTGTGGACAAAGACAACATGG 3668
Db 3653 AAATGGATACGTAATAGCAGAAATCAGATCCAAATTTAGTGTGGACAAAGACAACATGG 3712
Qy 3669 TGTGCTTGGCAGGCAATCTCAGGAAATATCAGATATTCATTTGATGAAGCGACGG 3728
Db 3713 TGTGCTTGGCAGGCAATCTCAGGAAATATCAGATATTCATTTGATGAAGCGACGG 3772
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Db 3773 CAATGTGGATCCAAAGCACTGATGATTAACAAAAAATCCGGAGAAATTTGCC 3832
Qy 3789 ACTGCACGGTGTAAACATTCACACAGATTTGAACACCAATTTTCACAGCCACAAGATAA 3848
Db 3833 ACTGCACGGTGTAAACATTCACACAGATTTGAACACCAATTTTCACAGCCACAAGATAA 3892
Qy 3849 TGGTTTATGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTGTGCAAAATA 3908
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Qy 3909 AAGAGAGCTATTTTACAAGATGTTGCAACAACTGGGCAAGCGCAGAGCCGCTGCCCTCA 3968
Db 3953 AAGAGAGCTATTTTACAAGATGTTGCAACAACTGGGCAAGCGCAGAGCCGCTGCCCTCA 4012
Qy 3969 CTGAAACAGCAAAACAG----- 3985
Db 4013 CTGAAACAGCAAAACAGAGATGGGGTTTTCACCATGTTGGCCAGGCTGTCTCAAACTCCT 4072
Qy 3986 ----- 3985
Db 4073 GACCTCAAGTGATCCACCTGCGCTTGGCCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCA 4132
Qy 3986 -----GTACTTCAAAAGAAATATTCACATATTTGGTGCACACTGACAC 4030
Db 4133 CCACGCCAGCGCTGAGTATCTTCAAAAGAAATATTCACATATTTGGTGCACACTGACAC 4192
Qy 4031 ATGTTTACAACACTTCCAATGGACAGCCCTCGACCTTAACATATTTTCGAGACACACTG 4090
Db 4193 ATGTTTACAACACTTCCAATGGACAGCCCTCGACCTTAACATATTTTCGAGACACACTG 4252
Qy 4091 TGAATCAACCAAAATGCAAGTCCGTTCCGAAGCAATTTCCACTAGTATTTTGGACTAT 4150
Db 4253 TGAATCAACCAAAATGCAAGTCCGTTCCGAAGCAATTTCCACTAGTATTTTGGACTAT 4312
Qy 4151 GTAAACCAATTTGACTTTTTTTTACTTTGGCAACAAATATTTATACATAAAGATGCTA 4210
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Qy 4211 GTTCATTTGAATATTTCTCCC 4231
Db 4373 GTTCATTTGAATATTTCTCCC 4393
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RESULT 9

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US-10-012-896-1007
; Sequence 1007, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
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; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Repler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Megher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1007
; LENGTH: 4395
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-1007

Query Match 88.4%; Score 3739.2; DB 9; Length 4395;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3744; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 238 AGATGATATGTTTATGATGCTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTGCA 297
Db 603 AGAATTATGTTTATGATGCTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTGCA 662
Qy 298 AGGGTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGCAGACAGCCCTCTTTTAAAC 357
Db 663 AGGGTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGCAGACAGCCCTCTTTTAAAC 722
Qy 358 AAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAAT 417
Db 723 AAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAAT 782
Qy 418 TGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAATTTTAAATTTTGA 477
Db 783 TGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAATTTTAAATTTTGA 842
Qy 478 AAATTTATGATCCATGCTGCTGCTTGAACACAGCGTAGCCCTATGCCACGGTGCT 537
Db 843 AAATTTATGATCCATGCTGCTTGAACACAGCGTAGCCCTATGCCACGGTGCT 902
Qy 538 GACTTTTTCACGCTCATTTTGGCTATCTGATCATCTATATTTTATCATCAGTTCAAGT 597
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Qy 598 TGCTGGGATGAGTTTACGAGTAGCCCATGTGCCATATGATTTATCGGAAGCACTTCGCT 657
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Db 1083 TGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGGAGGACACTGCA 1142
Qy 778 GCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTTCCTGCTGGAT 837
Db 1143 GCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTTCCTGCTGGAT 1202
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QY 958 TGGTATAAGGATAATAAATAATACGCTCGGAAAGTCATTTTCAAAATCTTATTACCAA 1017
DB 1323 TGGTATAAGGATAATAAATAATACGCTCGGAAAGTCATTTTCAAAATCTTATTACCAA 1382
QY 1018 TTTGAGAAAGAGAGATTTCCAAAGATCTGAGAAGTTCCGCTCAGGGGGATGAATTT 1077
DB 1383 TTTGAGAAAGAGAGATTTCCAAAGATCTGAGAAGTTCCGCTCAGGGGGATGAATTT 1442
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QY 1738 ACGGGTAAACCTTGAAGAGCAGTGATCAAGATGCTGACACTATCTCCTGGACCATCC 1797
DB 2103 ACGGGTAAACCTTGAAGAGCAGTGATCAAGATGCTGACACTATCTCCTGGACCATCC 2162
QY 1798 TCTCAGTGCAGTAGATCGGGAAGTTAGCAGACACTTGTTCGAAGTGTGATTTGTCAAAAT 1857
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QY 1978 AAAATCTGATATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACACC 2037

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DB 2403 TCCAGTTCCAGGAACCTCCACACTAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGGTC 2462
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DB 2463 TCAACAATCTTCTAGACCTCCTTTGAAAGATGGTCTCTGGAGAGCCCAAGATACAGAGAA 2522
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DB 2763 TAAGTGTACTTAGGAAATTTATTCAGGTTTAACTGTAGTACCTGTTCTTTTGGCATAGC 2822
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QY 2638 AGATTTCAATCCAGACATTTGCTACAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGCTGAT 2697
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DB 3183 TTCCCACTTGTCTATCTCTCTCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGA 3242
QY 2878 GAGGTGTGAGGAATGTTTGTATGCACACAGGATTTTACATTCAGAGGCTTTGGTCTTGT 2937
DB 3243 GAGGTGTGAGGAATGTTTGTATGCACACAGGATTTTACATTCAGAGGCTTTGGTCTTGT 3302
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DB 3363 CATCGTTGCTTTGGTTCCTGATTTGGCAAAACCTCTGGATGCCGGCAGGTGGTTTT 3422
QY 3058 GGCACCTGCTATGCCCTCAGGCTCATGGGATTTTTCAGTGGTGTGTTTCGACAAAGTGC 3117

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Qy	3118	TGAAGTTTGAAGAATATGATGATCTCAGTGAAGAAGGTCAATTGAATACACAGACCTTTGAAAA	3177
Db	3483	TGAAGTTGAGAATATGATGATCTCAGTGAAGAAGGTCAATTGAATACACAGACCTTTGAAAA	3542
Qy	3178	AGAAGCACCTTTGGGAATATCAGAAACGCCACCCAGCGCTGGCCCCATGAAGGAGTGAT	3237
Db	3543	AGAAGCACCTTTGGGAATATCAGAAACGCCACCCAGCGCTGGCCCCATGAAGGAGTGAT	3602
Qy	3238	AATCTTTGCAATGTGAACTTCATGTACAGTCCAGGTGGGGCTCTGGTACTGAAGCATCT	3297
Db	3603	AATCTTTGCAATGTGAACTTCATGTACAGTCCAGGTGGGGCTCTGGTACTGAAGCATCT	3662
Qy	3298	GACAGCACTCATTAATAATCAAGAAAGGTTGGCATTTGTGGGAAGAACCCGGAGCTGGAAA	3357
Db	3663	GACAGCACTCATTAATAATCAAGAAAGGTTGGCATTTGTGGGAAGAACCCGGAGCTGGAAA	3722
Qy	3358	AAGTTCCCTCATCTCAGCCCTTTTTAGATGTCTCAGAACCCGGAAGTAAAAATTTGGATTGA	3417
Db	3723	AAGTTCCCTCATCTCAGCCCTTTTTAGATGTCTCAGAACCCGGAAGTAAAAATTTGGATTGA	3782
Qy	3418	TAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAAATGCAATCATACC	3477
Db	3783	TAAGATCTTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAAATGCAATCATACC	3842
Qy	3478	TCAGGAACCTGTTTGTTCACGTGGAACAAATGAGGAAAAACCTGCATCCCTTTAAGGAGCA	3537
Db	3843	TCAGGAACCTGTTTGTTCACGTGGAACAAATGAGGAAAAACCTGCATCCCTTTAAGGAGCA	3902
Qy	3538	CACGGATGAGGAACCTGTGGAATGCCTTACAAGAGGTCAACCTTAAGAAAAACCATTTGAAGA	3597
Db	3903	CACGGATGAGGAACCTGTGGAATGCCTTACAAGAGGTCAACCTTAAGAAAAACCATTTGAAGA	3962
Qy	3598	TCCTTCTGTGTAATTTGGATCTGAATTTAGCAGATCAGGATCCCAATTTTAGTTGGACA	3657
Db	3963	TCCTTCTGTGTAATTTGGATCTGAATTTAGCAGATCAGGATCCCAATTTTAGTTGGACA	4022
Qy	3658	AAGACAACTGGTGTGCTTTGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATTGA	3717
Db	4023	AAGACAACTGGTGTGCTTTGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATTGA	4082
Qy	3718	TGAAGCGACGGCAATTTGGATCCAAGAACTCATGAGTTAATACAAAAAATCCGGGA	3777
Db	4083	TGAAGCGACGGCAATTTGGATCCAAGAACTCATGAGTTAATACAAAAAATCCGGGA	4142
Qy	3778	GAATTTGCCCACTGCACCGTGTCAACATTTGCACACAGATTGAACACCATTTATGCAG	3837
Db	4143	GAATTTGCCCACTGCACCGTGTCAACATTTGCACACAGATTGAACACCATTTATGCAG	4202
Qy	3838	CGACAGATAAATGGTTTTAGATTGAGGAAGACTCAAGAATATCATGAGCCGTATGTTTT	3897
Db	4203	CGACAGATAAATGGTTTTAGATTGAGGAAGACTCAAGAATATCATGAGCCGTATGTTTT	4262
Qy	3898	GCTGCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGCGCAAGCGAAGC	3957
Db	4263	GCTGCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGCGCAAGCGAAGC	4322
Qy	3958	CGCTGCCCTCACTGAACAGCAAAACAGGTAT	3989
Db	4323	CGCTGCCCTCACTGAACAGCAAAACAGAT	4354

RESULT 10

RESULT TO
US-10-012-896-1006

US-10-012-898-1006
: Sequence 1006, Application US/10012896

; sequence 1006, Application US/1
; Publication No. US20020183251A1; PUBLICATION NO: US20
; GENERAL INFORMATION:
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

;; APPLICANT: AU, JIANGCHUN
;; APPLICANT: DILLON, DAVIN C.

APPLICANT: MITCHEM; MITCHAM; JENNIFER L

APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

? APPLICANT: Kalos, Michael D.
 ? APPLICANT: Retter, John W.
 ? APPLICANT: Stolk, John A.
 ? APPLICANT: Day, Craig H.
 ? APPLICANT: Vedvick, Thomas S.
 ? APPLICANT: Carter, Darrick
 ? APPLICANT: Li, Samuel X.
 ? APPLICANT: Wang, Aijun
 ? APPLICANT: Skeiky, Yasir A.W.
 ? APPLICANT: Hepler, William T.
 ? APPLICANT: Henderson, Robert A.
 ? APPLICANT: Hural, John
 ? APPLICANT: McNeill, Patricia D.
 ? APPLICANT: Houghton, Raymond L.
 ? APPLICANT: Vinals de Bassols, Carlota
 ? APPLICANT: Foy, Teresa
 ? APPLICANT: Fanger, Gary R.
 ? APPLICANT: Wantanabe, Yoshihiro
 ? APPLICANT: Meagher, Madeleine Joy
 ? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ? TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ? FILE REFERENCE: 210121.427C27
 ? CURRENT APPLICATION NUMBER: US/10/012.896
 ? CURRENT FILING DATE: 2001-12-10
 ? NUMBER OF SEQ ID NOS: 1011
 ? SOFTWARE: FastSeq for Windows Version 3.0
 ? SEQ ID NO 1006
 ? LENGTH: 3786
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 ? US-10-012-896-1006

Query Match	88.4%	Score 3738.6	DB 9	Length 3786
Best Local Similarity	99.9%	Pred. No. 0		
Matches 3741	Conservative	0	Mismatches	4
			Indels	0
Gaps				
QY	245	ATGTATTTCAGTGCCTGCCAAGAAGACCGCTCACAGCACCCTGGAGAGGAGTTGGCAAGGTTCC	304	
Db	1	ATGTATTTCAGTGCCTGCCAAGAAGACCGCTCACAGCACCCTGGAGAGGAGTTGGCAAGGTTCC	60	
QY	305	TGGGATAAAGAAGTTTTAAAGAGCTGGAATGAGCACAGCAAGGCTTCTTTTAACAAGAGCA	364	
Db	61	TGGGATAAAGAAGTTTTAAAGAGCTGGAATGAGCACAGCAAGGCTTCTTTTAACAAGAGCA	120	
QY	365	ATCATAAAGTTTGACTCGGAATCTTATTTAGTTTGGGAATTTTTACGTTAATGAGGAA	424	
Db	121	ATCATAAAGTTTGACTCGGAATCTTATTTAGTTTGGGAATTTTTACGTTAATGAGGAA	180	
QY	425	AGTSCCAAAGTAATCCAGGCCATATTTTCGSGAAAAATTAATTAATTTTTGAAAATTAT	484	
Db	181	AGTGCCAAGTAATCCAGGCCATATTTTCGSGAAAAATTAATTAATTTTTGAAAATTAT	240	
QY	485	GATCCCATGGATTCTGTGGCTTTGAACACACGCTACGCCCTATGCCACGGTGTGACTTTT	544	
Db	241	GATCCCATGGATTCTGTGGCTTTGAACACACGCTACGCCCTATGCCACGGTGTGACTTTT	300	
QY	545	TGCACGCTCAATTTGGCTATCTGTCATCACTTATTTTTTATCACGTTTCAGTGTGCTGGG	604	
Db	301	TGCACGCTCAATTTGGCTATCTGTCATCACTTATTTTTTATCACGTTTCAGTGTGCTGGG	360	
QY	605	ATGAGGTTACGAGTAGCCATGTGCCATATGATTTTATCGGAAGGCACCTTCGTCTTTAGTAAC	664	
Db	361	ATGAGGTTACGAGTAGCCATGTGCCATATGATTTTATCGGAAGGCACCTTCGTCTTTAGTAAC	420	
QY	665	ATGGCCATGGGAAGAACCAACAGGCCAGATAGTCAATCTGCTGCCAATGATGTGAAC	724	
Db	421	ATGGCCATGGGAAGAACCAACAGGCCAGATAGTCAATCTGCTGCCAATGATGTGAAC	480	
QY	725	AAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGCGCAGGACCACTGCAGGGCGATC	784	
Db	481	AAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGCGCAGGACCACTGCAGGGCGATC	540	
QY	785	GCAGTGACTGCCCTACTCTCGATGGAGATAGGAATATCGTGCCTTGTCTGGGATGCGCAGTT	844	

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Db 541 GCAGTACTGCCCTACTCTGGATGAGATAGAAATATCGTGCCTTCCTGGGATGCACTT 600
Qy 845 CTAATCATCTCTCCCTGCAAGCTGTTTGGGAAGTTGTTCTCATCATCAGGAGT 904
Db 601 CTAATCATCTCTCCCTGCAAGCTGTTTGGGAAGTTGTTCTCATCATCAGGAGT 660
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Db 661 AAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATACCTGGTATA 720
Qy 965 AGGATAATAAAATGTACGCTGGGAAAGTCATTTTCAAAATCTTATTACCAATTTGAGA 1024
Db 721 AGGATAATAAAATGTACGCTGGGAAAGTCATTTTCAAAATCTTATTACCAATTTGAGA 780
Qy 1025 AAGAGGAGATTTCCAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAATTTGGCTTCG 1084
Db 781 AAGAGGAGATTTCCAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAATTTGGCTTCG 840
Qy 1085 TTTTTCAGTGAAGCAAAATCATCTGTTGTTGAGCTTTCACCACTAGCTGCTCTCGGC 1144
Db 841 TTTTTCAGTGAAGCAAAATCATCTGTTGTTGAGCTTTCACCACTAGCTGCTCTCGGC 900
Qy 1145 AGTGTATCACAGCAGCCGCTGTTCTGTGGCAGTGAGCTGTATGGGCTGTGGCGTG 1204
Db 901 AGTGTATCACAGCAGCCGCTGTTCTGTGGCAGTGAGCTGTATGGGCTGTGGCGTG 960
Qy 1205 ACGTTTACCCCTTCTTCCCTCAGCCATTTGAGAGGTGTGAGAGGCAATCGTCAGCATC 1264
Db 961 ACGTTTACCCCTTCTTCCCTCAGCCATTTGAGAGGTGTGAGAGGCAATCGTCAGCATC 1020
Qy 1265 CGAAGATCCAGACTTTTCTACTTGTATGAGATATACAGCGCAACCGTCAGCTGCGG 1324
Db 1021 CGAAGATCCAGACTTTTCTACTTGTATGAGATATACAGCGCAACCGTCAGCTGCGG 1080
Qy 1325 TCAGATGGTAAAGAGTGGTCATGTGCAAGATTTTACTGCTTTTGGGATAAGGCATCA 1384
Db 1081 TCAGATGGTAAAGAGTGGTCATGTGCAAGATTTTACTGCTTTTGGGATAAGGCATCA 1140
Qy 1385 GAGACCCCACTCTACAGGCTTTCCTTTACTCTCAGACTGCGCAATTTTACCTGTG 1444
Db 1141 GAGACCCCACTCTACAGGCTTTCCTTTACTCTCAGACTGCGCAATTTTACCTGTG 1200
Qy 1445 GTCGGCCCGTGGGAGCAGGAAGTCATCTGTTAAGTCCGCTGCTCGGGGAATTTGGCC 1504
Db 1201 GTCGGCCCGTGGGAGCAGGAAGTCATCTGTTAAGTCCGCTGCTCGGGGAATTTGGCC 1260
Qy 1505 CCAAGTCACGGCTGGTCAGGTCATGGAAGATTTGCTATGTGCTCAGCAGCCCTGG 1564
Db 1261 CCAAGTCACGGCTGGTCAGGTCATGGAAGATTTGCTATGTGCTCAGCAGCCCTGG 1320
Qy 1565 GTGTTCTGGGAACCTCTGAGAGTAATTTTATTTGGGAAGAAATATGAAAGGAACGA 1624
Db 1321 GTGTTCTGGGAACCTCTGAGAGTAATTTTATTTGGGAAGAAATACGAAAGGAACGA 1380
Qy 1625 TATCAAAAGTCATAAAGCTGTGCTCTGAAAAGATTTACAGCTTTTGGAGATGGT 1684
Db 1381 TATCAAAAGTCATAAAGCTGTGCTCTGAAAAGATTTTACAGCTTTTGGAGATGGT 1440
Qy 1685 GATCTGACTGTATAGGATTCGGGGAACACCGTGTAGTGGAGGCAAGAACGCGGTA 1744
Db 1441 GATCTGACTGTATAGGATTCGGGGAACACCGTGTAGTGGAGGCAAGAACGCGGTA 1500
Qy 1745 AACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCATCTCTCAGT 1804
Db 1501 AACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCATCTCTCAGT 1560
Qy 1805 GCAGTAGATCGGGAAGTTAGCAGACATTTGCGAAGTGTATTTGTCAAAATTTTGCAT 1864
Db 1561 GCAGTAGATCGGGAAGTTAGCAGACATTTGCGAAGTGTATTTGTCAAAATTTTGCAT 1620
Qy 1865 GAGAGATCACAATTTTACTGACTCATCATGTTGCAGTACCTCAAGCTGCAAGTCAGATT 1924
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Db 1621 GAGAGATCACAATTTTACTGACTCATCATAGTTGCAAGTACCTCAAAAGTCAAGTCAGATT 1680
Qy 1925 CTGATATTTGAAAGATCGTAAATGGTGCAGAAGGGGACTTTACACTGAGTTTCTTAAATCT 1984
Db 1681 CTGATATTTGAAAGATCGTAAATGGTGCAGAAGGGGACTTTACACTGAGTTTCTTAAATCT 1740
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Db 1741 GGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGAGAAAGTGAACAACCTCCAGTT 1800
Qy 2045 CCAGGAATCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAA 2104
Db 1801 CCAGGAATCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAA 1860
Qy 2105 TCTTCTAGACCCCTCCTTGAAGATGGTCTCTGGAGAGCAAGATACAGAGAAATGTCCCA 2164
Db 1861 TCTTCTAGACCCCTCCTTGAAGATGGTCTCTGGAGAGCAAGATACAGAGAAATGTCCCA 1920
Qy 2165 GTTACACTATCAGAGAGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCCCTATAAGAA 2224
Db 1921 GTTACACTATCAGAGAGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCCCTATAAGAA 1980
Qy 2225 TACTTACAGAGCTGGTCTCAGTGGATTTGCTTTCATTTTCCCTTATCTCTTAACACTGCA 2284
Db 1981 TACTTACAGAGCTGGTCTCAGTGGATTTGCTTTCATTTTCCCTTATCTCTTAACACTGCA 2040
Qy 2285 GCTCAGGTTGCCATGTCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAACT 2344
Db 2041 GCTCAGGTTGCCATGTCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAACT 2100
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Qy 2645 ATCCAGACATTTGCTACAAAGTGGTGGTGGTCTCTGCTGGCTGCTGCGCTGATTCCTTGG 2704
Db 2401 ATCCAGACATTTGCTACAAAGTGGTGGTGGTCTCTGCTGGCTGCTGCGCTGATTCCTTGG 2460
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Db 2461 ATCCGAATACCTTGGTTCCTTGGAAATCATTTTCATTTTCTTCGGCGATATTTTGG 2520
Qy 2765 GAAACGTCAGAGATGTGAAGCGCTGGAATCTCAAACTCCGAGTCCAGTGTTCCTCCAC 2824
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Db 2821 TCCTATGCCCTCAGCTCATGGGATGTTTCAGTGGTGTGTCGACAAGTCTGAAGTT 2880
Qy 3125 GAGATATGATGATCTCAGTAAAGGTCATTTGAATACACAGACTTTGAAAAAGACA 3184
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Db 3601 ATATATGTTTATGATTCAGGAAGTCTGAAAGAAATATGATGAGCCGTATGTTTGTGCAA 3660
Qy 3905 AATAAGAGAGCCCTATTTTACAAGATGTTGCAACAACTGGGCAAGGCGAGAGCCCTGCC 3964
Db 3661 AATAAGAGAGCCCTATTTTACAAGATGTTGCAACAACTGGGCAAGGCGAGAGCCCTGCC 3720
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Db 3721 CTCACCTGAAACAGCAAAACAGAGAT 3745
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RESULT 11
US-09-925-300-613
; Sequence 613, Application US/09925300

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; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 613
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (297)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-613
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Query Match 28.8%; Score 1218; DB 10; Length 1427;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1221; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

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Qy 1490 CTCGGGGGAATTCGCCCAAGTCACGGGCTGTCAGCGTCATCGAGGAATGTCCTATGTG 1549
Db 62 CTCGGGGGAATTCGCCCAAGTCACGGGCTGTCAGCGTCATCGAGGAATGTCCTATGTG 121
Qy 1550 TCTCAGCAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAAGAAA 1609
Db 122 TCTCAGCAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAAGAAA 181
Qy 1610 TATGAAAGGAACGATATGAAAAAGTCATAAAGCTTGCTCTGAAAAAGGATTTTACAG 1669
Db 182 TMCGAAAAAGGACGATATGAAAAAGTCATAAAGCTTGCTCTGAAAAAGGATTTTACAG 241
Qy 1670 CTGTTGGAGGATGGTGAATCTGACTGTGATAGGAGATCGGGGAACCACTGAGTGGAGGG 1729
Db 242 CTGTTGGAGGATGGTGAATCTGACTGTGATAGGAGATCGGGGAACCACTGAGTGGAGGG 301
Qy 1730 CAGAAAGCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTG 1789
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Qy 1790 GAGGATCTCTCAGTGCAGTAGATCGGGAAGTTAGCAGACACTTGTTCGAACTGTGTATT 1849
Db 362 GAGGATCTCTCAGTGCAGTAGATCGGGAAGTTAGCAGACACTTGTTCGAACTGTGTATT 421
Qy 1850 TCTCAAAATTTTCATCAGAGAAGATCAAAATTTTAGTCACATCATCAGTTGCACTACCAAA 1909
Db 422 TCTCAAAATTTTCATCAGAGAAGATCAAAATTTTAGTCACATCATCAGTTGCACTACCAAA 481
Qy 1910 GCTGCAAGTCAGATTTCTGATATTTGAAAGATGTTAAATGTTGCAAGAGGAGCTTACACT 1969
Db 482 GCTGCAAGTCAGATTTCTGATATTTGAAAGATGTTAAATGTTGCAAGAGGAGCTTACACT 541
Qy 1970 GAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAAGT 2029
Db 542 GAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAAGT 601
Qy 2030 GAACAACCTCCAGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCG 2089
Db 602 GAACAACCTCCAGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCG 661
Qy 2090 GTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGAGTGGTCTCTGGAGAGCCCAAGAT 2149
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Db 662 GTTGGTCTCAACAATCTCTAGACCCCTCTGAAGATGGTCTCTGAGAGCAAGAT 721
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Db 722 ACAGAGAAATGTCAGTACACTATCAGAGGAGAACCGTCTGAAAGAAAGTTGGTTTT 781
Qy 2210 CAGGCTATAGAAATCTTACAGAGCTGGTCTACTGGATGGTCTTCAATTTCTTAT 2269
Db 782 CAGGCTATAGAAATCTTACAGAGCTGGTCTACTGGATGGTCTTCAATTTCTTAT 841
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Db 842 CTCCTAAACACTGACGCTCAGTCTCCCTATGCTTCAAGATGGTCTTCACTACG 901
Qy 2330 GCAACAAACAAAGATGCTAAATGTCTACTGTAATGAGGAGGAAATGTAACCGAGAAG 2389
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Db 1082 AACAAATGTTTGGTCAATCTGAAAGCTCCGCTATTTCTTTGATAGAAATCCAAATA 1141
Qy 2570 GGAAGAAATTTAAATCGTTTCTCAAGACATTTGACACTTTGGATTTGCTCCGCGTG 2629
Db 1142 GGAAGAAATTTAAATCGTTTCTCAAGACATTTGACACTTTGGATTTGCTCCGCGTG 1201
Qy 2630 ACGTTTTAGATTTTATCAGACATTTGCTACAAGT 2664
Db 1202 ACGTTTTAGATTTTATCAGACATTTGCTACAAGT 1236
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RESULT 12

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US-10-012-896-824
; Sequence 824, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012, 896
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; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-824
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Query Match 24.7%; Score 1045.4; DB 9; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 4 TCAGCCATTGAGAGGTGTTCAGAGGCAATCGTCAGCATCCGGAAGATCCAGACCTTTTGG 63
Qy 1286 CTACTTGATGAGATATTCACAGCGCAACCGTCAGCTGCCGTGAGTGGTAAAAAGATGGTG 1345
Db 64 CTACTTGATGAGATATTCACAGCGCAACCGTCAGCTGCCGTGAGTGGTAAAAAGATGGTG 123
Qy 1346 CATGTGCAAGATTTTACTGCTTTTGGGATAAGGCATCAGACCCCAACTCTACAAAGC 1405
Db 124 CATGTGCAAGATTTTACTGCTTTTGGGATAAGGCATCAGACCCCAACTCTACAAAGC 183
Qy 1406 CTTTCTTTTACTGTGTCAGACCTGGCGAATTTGTTAGCTGTGGTCCGCCCTGGAGCAGGG 1465
Db 184 CTTTCTTTTACTGTGTCAGACCTGGCGAATTTGTTAGCTGTGGTCCGCCCTGGAGCAGGG 243
Qy 1466 AAGTCATCAGCTTTAAGTGCCGTGCTCGGGGAAATTTGGCCCCAAGTCACGGGCTGGTCAGC 1525
Db 244 AAGTCATCAGCTTTAAGTGCCGTGCTCGGGGAAATTTGGCCCCAAGTCACGGGCTGGTCAGC 303
Qy 1526 GTGCATGGAAGAAATTCCTATGCTGTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGG 1585
Db 304 GTGCATGGAAGAAATTCCTATGCTGTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGG 363
Qy 1586 AGTAATATTTTATTTGGGAAGAAATATGAAAGGAACATATGAAAAAGTCAATAAGGCT 1645
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Qy 1646 TGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGTCTGACTGTGATAGAGAT 1705
Db 424 TGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGTCTGACTGTGATAGAGAT 483
Qy 1706 CGGGGAACACGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAGAGCAGCTGTAT 1765
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Qy 1826 AGACACTTGTTCGAACTGTGATTTGTCAAATTTTGGCAGAGAAAGTCAATAATTTTAGTG 1885
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Db 904 GATGGTCTCTGGAGAGCCCAAGATACAGAGAAATGTCCTCCAGTTACATATACAGAGAGAAC 963
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QY 2186 CGTTCTCAAGGAAAAGTTGCTTTTTCAGGCGCTATAGAATTACTTTCAGAGCTGGTGTCTCAC 2245
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Db 964 CGTTCTCAAGGAAAAGTTGCTTTTTCAGGCGCTATAGAATTACTTTCAGAGCTGGTGTCTCAC 1023
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QY 2246 TGGATTGCTCTTCATTTTCCCTATTCTC 2272
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Db 1024 TGGATTGCTCTTCATTTTCCCTATTCTC 1050
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RESULT 13
US-09-759-143-824
; Sequence 824, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Repler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-824
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Query Match 24.7%; Score 1045.4; DB 10; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1226 TCAGCCATTGAGAGGTGTGTCAGAGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTGG 1285
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Db 424 TGTCTCTGTAAGAAAGAGTTTACAGCTGTTGGAGAGTGTGATCTGACTGTGTATAGAGAT 483
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QY 1706 CGGGGAACCCAGCTGAGTGGAGGCGAGAAAGCAGGGTAAACCTTGCAGAGCAGTGTAT 1765
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Db 484 CGGGGAACCCAGCTGAGTGGAGGCGAGAAAGCAGGGTAAACCTTGCAGAGCAGTGTAT 543
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Db 544 CAAGATGCTGACATCTATCTCTCGGAGCATCTCTCAGTCAGTAGATGCCGAAGTTAGC 603
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QY 1826 AGACACTTGTTCGAACCTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAAATTTAGTG 1885
      |||
Db 604 AGACACTTGTTCGAACCTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAAATTTAGTG 663
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QY 1886 ACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCAGATTCGTATTTGAAAGATGGTAAA 1945
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Db 664 ACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCAGATTCGTATTTGAAAGATGGTAAA 723
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QY 1946 ATGGTGCAGAGGGGACTTACACTGAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTT 2005
      |||
Db 724 ATGGTGCAGAGGGGACTTACACTGAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTT 783
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QY 2006 TTAAGGAAGGATAATGAGGAAGTGAACACCTCCAGTTCAGGAACCTCCACACTAAGG 2065
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Db 784 TTAAGGAAGGATAATGAGGAAGTGAACACCTCCAGTTCAGGAACCTCCACACTAAGG 843
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QY 2066 AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCCTTGA 2125
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Db 844 AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCCTTGA 903
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QY 2126 GATGGTCTCTGGAGAGCCCAAGATACAGAGAAATGTCCTCCAGTTACACTATCAGAGAGAAC 2185
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Db 904 GATGGTCTCTGGAGAGCCCAAGATACAGAGAAATGTCCTCCAGTTACACTATCAGAGAGAAC 963
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QY 2186 CGTTCTCAAGGAAAAGTTGCTTTTTCAGGCGCTATAGAATTACTTTCAGAGCTGGTGTCTCAC 2245
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RESULT 14
US-09-780-669-824
; Sequence 824, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
```


; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-780-669-824

Query Match 24.7%; Score 1045.4; DB 10; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1226 TCAGCCATTGAGAGGCTGTCAGAGGCAATCGTCAGCATCCGAAGAAATCCAGACCTTTTGG 1285
DB 4 TCAGCCATTGAGAGGCTGTCAGAGGCAATCGTCAGCATCCGAAGAAATCCAGACCTTTTGG 63
QY 1286 CTACTTGATGAGATATACAGCGCAACCGTCAGCTGCCGTGATGATGTTAAAGATGGTG 1345
DB 64 CTACTTGATGAGATATACAGCGCAACCGTCAGCTGCCGTGATGATGTTAAAGATGGTG 123
QY 1346 CATGTGCAGGATTTTACTGCTTTTGGGATAGGATAGGATAGGATAGGATAGGATAGG 1405
DB 124 CATGTGCAGGATTTTACTGCTTTTGGGATAGGATAGGATAGGATAGGATAGGATAGG 183
QY 1406 CTTTCCCTTACTGTCAGACCTGGCGAAATGTTAGTGTGGTGGCGCCGTCGGGACAGG 1465
DB 184 CTTTCCCTTACTGTCAGACCTGGCGAAATGTTAGTGTGGTGGCGCCGTCGGGACAGG 243
QY 1466 AAGTCATCAGTGTAAAGTGGCGAAATGTTAGTGTGGTGGCGCCGTCGGGACAGG 1525
DB 244 AAGTCATCAGTGTAAAGTGGCGAAATGTTAGTGTGGTGGCGCCGTCGGGACAGG 303
QY 1526 GTGATGGAAGAAATGCTATGCTGTCAGAGCCCTGGGTTTCTCGGGAATCTGAGG 1585
DB 304 GTGATGGAAGAAATGCTATGCTGTCAGAGCCCTGGGTTTCTCGGGAATCTGAGG 363
QY 1586 AGTAATATTTTATTTGGGAAGAAATACGAAAGGAAACGATATGAAAGGCT 1645
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DB 424 TGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGTTGATCTGCTGATAGGAT 483
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QY 1766 CAAGATGCTGACATCTATCTCTCGACGATCCTCTCAGTCAGTAGATGCGGAAGTTAGC 1825
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QY 1826 AGACATGTTGCGAAGTGTGTATTTGTCATGTTGCAATTTTGCATGAGAAGATCAACAATTTAGT 1885
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QY 1886 ACTCATGTTGCGAAGTGTGTATTTGTCATGTTGCAATTTTGCATGAGAAGATCAACAATTTAGT 1945
DB 664 ACTCATGTTGCGAAGTGTGTATTTGTCATGTTGCAATTTTGCATGAGAAGATCAACAATTTAGT 723
QY 1946 ATGTCGAGAAAGGAGCTTACATGAGTGTCTTAAATCTGATATAGATTTTGGCTCCCTT 2005
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QY 2006 TTAAGAAGGATAATGAGGAAAGTGAACAACTCCAGTTCAGGAACTCCACACTAAGG 2065
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DB 904 GATGTCCTCTGAGAGCCCAAGATACAGAGAATGTCAGTTCACACTATCAGAGGAAAC 963
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US-09-822-827-824
; Sequence 824, Application US/09822827
; Patent No. US20020081680A1

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-824

Query Match 24.7%; Score 1045.4; DB 10; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1226 TCAGCCATTGAGAGGCTGTCAGAGGCAATCGTCAGCATCCGAAGAAATCCAGACCTTTTGG 1285
DB 4 TCAGCCATTGAGAGGCTGTCAGAGGCAATCGTCAGCATCCGAAGAAATCCAGACCTTTTGG 63
QY 1286 CTACTTGATGAGATATACAGCGCAACCGTCAGCTGCCGTGATGATGTTAAAGATGGTG 1345
DB 64 CTACTTGATGAGATATACAGCGCAACCGTCAGCTGCCGTGATGATGTTAAAGATGGTG 123
QY 1346 CATGTGCAGGATTTTACTGCTTTTGGGATAGGATAGGATAGGATAGGATAGGATAGG 1405
DB 124 CATGTGCAGGATTTTACTGCTTTTGGGATAGGATAGGATAGGATAGGATAGGATAGG 183
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QY 1826 AGACACTTGTGCACTGTATTTGTCATAAATTTTCATGAGAGATCACAATTTTAGTG 1885
Db 604 AGACACTTGTGCACTGTATTTGTCATAAATTTTCATGAGAGATCACAATTTTAGTG 663
QY 1886 ACTCATCAGTTGCAGTACCTCAAGCTCAAGTCAAGTCAAGTCTGATATTGAAAGATGTTAA 1945
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QY 1946 ATGGTSCAGAAGGGGACTTACACTGAGTTCCTAAATCTGGTATAGATTTTGGCTCCCTT 2005
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QY 2006 TTAAGAGAGGATAATGAGGAAAGTGAACAACTCCAGTTCAGGAACTCCACACTAAGG 2065
Db 784 TTAAGAGAGGATAATGAGGAAAGTGAACAACTCCAGTTCAGGAACTCCACACTAAGG 843
QY 2066 AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTCTAGACCCCTCTTGAA 2125
Db 844 AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTCTAGACCCCTCTTGAA 903
QY 2126 GATGGTGTCTCTGAGAGGCCCAAGATACAGAGAAATGTCCAGTTACACTATCAGAGGAGAAC 2185
Db 904 GATGGTGTCTCTGAGAGGCCCAAGATACAGAGAAATGTCCAGTTACACTATCAGAGGAGAAC 963
QY 2186 CGTTCGAAGGAAAGTTGGTTTTTCAGGCCTATAGAATTTACTTCAGAGCTGGTGTCTAC 2245
Db 964 CGTTCGAAGGAAAGTTGGTTTTTCAGGCCTATAGAATTTACTTCAGAGCTGGTGTCTAC 1023
QY 2246 TGGATTGTCTTCATTTTCCTTTATCTC 2272
Db 1024 TGGATTGTCTTCATTTTCCTTTATCTC 1050

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BQ225211.1
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13215 row: e column: 24
High quality sequence stop: 622.

BQ225211
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/lab_host="DH10B (phage-resistant)"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;  
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."  
BASE COUNT 184 a 201 c 198 g 278 t  
ORIGIN
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Query Match 13.8%; Score 805.2; DB 14; Length 861;  
Best Local Similarity 98.8%; Pred. No. 6e-116;  
Matches 832; Conservative 0; Mismatches 8; Indels 2; Gaps 2;  
  
QY 4285 GCCTGCACACGGTCTAGGCTCCGATAGATTATGGTCTGCGCCACGAGGAGTGGTGG 4344  
DB 1 GCCTGCACACGGTCTAGGCTCCGATAGATTATGGTCTGCGCCACGAGGAGTGGTGG 60  
  
QY 4345 AGTTTGACACCCATCGCTCTCTGTGCCAACGAGTTCGCCGATTCATGCCATGTTTG 4404  
DB 61 AGTTTGACACCCATCGCTCTCTGTGCCAACGAGTTCGCCGATTCATGCCATGTTTG 120  
  
QY 4405 CTGCTGCAGACAAAGTCTGCTCAAGGCTGACTCTCCCTGTTGACGAAGTCTCTT 4464  
DB 121 CTGCTGCAGACAAAGTCTGCTCAAGGCTGACTCTCCCTGTTGACGAAGTCTCTT 180  
  
QY 4465 TTCTTTAGAGCATTCGCCATTCCTGCTGGGGGGGCGCCCTCATCGGCTCTCTACCGA 4524  
DB 181 TTCTTTAGAGCATTCGCCATTCCTGCTGGGGGGGCGCCCTCATCGGCTCTCTACCGA 240  
  
QY 4525 AACCTTGCTTCTCGATTTATCTTTCGCACACAGTTCGCGATTCGCTGTTGTTTC 4584  
DB 241 AACCTTGCTTCTCGATTTATCTTTCGCACACAGTTCGCGATTCGCTGTTGTTTC 300  
  
QY 4585 ACTTTTAGGAGAGCATATTTTCATTTATGTTATTTATTCATATTCATGTAACAAAT 4644  
DB 301 ACTTTTAGGAGAGCATATTTTCATTTATGTTATTTATTCATATTCATGTAACAAAT 360  
  
QY 4645 TTAGTTTTTGTCTTAATTCGACCTCTAAAGTTTCAGGAGCCGCTTATATAATTGATC 4704  
DB 361 TTAGTTTTTGTCTTAATTCGACCTCTAAAGTTTCAGGAGCCGCTTATATAATTGATC 420  
  
QY 4705 AGAGGCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCGTACATAGC 4764  
DB 421 AGAGGCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCGTACATAGC 480  
  
QY 4765 CTATATTCAGTGAATAATGAAGCTTTATATTTATATTTATATTTATATTTATATTTAT 4824  
DB 481 CTATATTCAGTGAATAATGAAGCTTTATATTTATATTTATATTTATATTTATATTTAT 540  
  
QY 4825 AACAGTGCATATTCCTTCTATCATTTTGTACAGTTTGTCTACTAGACATCTGGTTTT 4884  
DB 541 AACAGTGCATATTCCTTCTATCATTTTGTACAGTTTGTCTACTAGACATCTGGTTTT 600  
  
QY 4885 GCTATTAGACTGTAGGAAGAGTAGCATTTCTTCTAGCTGTGGTGTTCACGGTGC 4944  
DB 601 GCTATTAGACTGTAGGAAGAGTAGCATTTCTTCTAGCTGTGGTGTTCACGGTGC 660  
  
QY 4945 CAGTTTCTTGGGTGTCACAAAGGAGACGTGTGGCAATAGTGGGCCCTCCGACAGCCCC 5004  
DB 661 CAGTTTCTTGGGTGTCACAAAGGAGACGTGTGGCAATAGTGGGCCCTCCGACAGCCCC 720  
  
QY 5005 TCTGCCCTCCACACAGCGCTCCAGGGGTGGCTGGAGAGGGTGGGGGCTGGAGACC 5064  
DB 721 TCTGCCCTCCACACAGCGCTCCAGGGGTGGCTGGAGAGGGTGGGGGCTGGAGACC 780  
  
QY 5065 ATGCAGAGCGCCCTGAGTTCTCAGGGCTCCTG-CCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 5122  
DB 781 ATGCAGAGCGCGGAGTTCTCAGGGCTCCTGAGGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 840
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QY 5123 TT 5124  
DB 841 TT 842
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RESULT 2

BG697157

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG697157 880 bp mRNA linear EST 07-MAY-2001
602660381F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803357 5',
mRNA sequence.

BG697157
BG697157.1 GI:13963059
EST.
human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 880)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM10699 row: a column: 22
High quality sequence stop: 820.

FEATURES

Source

1. 880
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4803357"
/clone_lib="NCI_CGAP_Skn3"

/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 153 a 244 c 226 g 257 t
ORIGIN

Query Match 13.7%; Score 802.2; DB 12; Length 880;
Best Local Similarity 98.0%; Pred. No. 1.8e-115;
Matches 854; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

QY 4829 GTGCATATTCCTTTCTATCATTTTGTACACTTTGCTGCTACTAGAGATCTGGTTTGCTA 4888
DB 1 GTGCATATTCCTTTCTATCA-TTTTGTACAGTTTGTGCTACTAGAGATCTGG-TTTGCTA 58

QY 4889 TTAGACTGTAGGAAGAGTAGCATTTTCATTTCTCTAGCTGGTGGTTCACGGTGCCAGG 4948
DB 59 TTAGACTGTAGGAAGAGTAGCATTTTCATTTCTCTAGCTGGTGGTTCACGGTGCCAGG 118

QY 4949 TTTTCTGGGTGTCACAAAGGAGAGCGTGTGGCAATAGTGGGCCCTCCGACAGCCCCCTGTG 5008
DB 119 TTTTCTGGGTGTCACAAAGGAGAGCGTGTGGCAATAGTGGGCCCTCCGACAGCCCCCTGTG 178

QY 5009 CCGGCTCCCGACAGCCGCTCCAGGGGTGGCTGGAGAGGGTGGGGCTGGAGACCATGC 5068
DB 179 CCGGCTCCCGACAGCCGCTCCA-GGGTGGCTGGAGAGGGTGGGGCTGGAGACCATGC 237

QY 5069 AGAGCGCGGTGAGTCTCTAGGGCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5128
DB 238 AGAGCGCGGTGAGTCTCTAGGGCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297

QY 5129 CAGGAGAGCGGGGGGGAAGCCCGAGCCCTTTTTCATCTCCCTCCATCAAGAATGGGAT 5188
DB 298 CAGGAGAGCGGGGGGGAAGCCCGAGCCCTTTTTCATCTCCCTCCATCAAGAATGGGAT 357

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QY 5189 CACAGAGACATCTCCGAGCGGGAGTTCCTTCTCGCTTCTCTCTTTTCTGCTGTGT 5248
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Db 358 CACAGAGACATCTCCGAGCGGGAGTTCCTTCTCGCTTCTCTCTTTTCTGCTGTGT 417
|||||
QY 5249 TTCTAAACAAGATCAGTCTATCCACAGAGAGTCCCACTGCCTCAGGTTCTCTATGGCTGG 5308
|||||
Db 418 TTCTAAACAAGATCAGTCTATCCACAGAGAGTCCCACTGCCTCAGGTTCTCTATGGCTGG 477
|||||
QY 5309 CCACTGCACAGAGCTCTCCAGCTCCAAAGAGCTGTGGTCCCAAGCCCTGAGGCAACTGC 5368
|||||
Db 478 CCACTGCACAGAGCTCTCCAGCTCCAAAGAGCTGTGGTCCCAAGCCCTGAGGCAACTGC 537
|||||
QY 5369 TGCCTTTTTCAGGTGGGACATTTTTCATTTGCTATTCCACAGCTCCACAGCTTCAGTGGCA 5428
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Db 538 TGCCTTTTTCAGGTGGGACATTTTTCATTTGCTATTCCACAGCTCCACAGCTTCAGTGGCA 597
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QY 5429 GGGCTCAGGATTTCTGGGTCTGTTTTCTCTCCCGCAGTCTGCTGCGCACAGTCTCTCT 5488
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Db 598 GGGCTCAGGATTTCTGGGTCTGTTTTCTCTCCCGCAGTCTGCTGCGCACAGTCTCTCT 657
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QY 5489 CTCTCTCTCCCTCAAGCTGCAACTTTAAGCAGCTCTGCTAACTCAGTCTCTCAGACT 5548
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Db 658 CTCTCTCTCCCTCAAGCTGCAACTTTAAGCAGCTCTGCTAACTCAGTCTCTCAGACT 717
|||||
QY 5549 GCGGTAGAAGTTTCTTACTGT- AAAGAGACCTTACCTCAGGTTGCTGTTGCTGTGGT 5607
|||||
Db 718 GCGGTAGAAGTTTCTTACTGTAAAGAGACCTTACCTCAGGTTGCTGTTGCTGTGGT 777
|||||
QY 5608 TTGGTGTGTTCCGCAAAACCCCTTTTGTGCTGTGGGCTGGTAGCTCAGGTGGGCGTGGT 5667
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Db 778 TTGGTGTGTTCCGCAAAACCCCTTTTGTGCTGTGGGCTGGTAGCTCAGGTGGGCGTGGT 837
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QY 5668 CACTGCTGCATCAGTTGAATGCTCAGGTT 5698
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Db 838 CACTGCTGCATCAGTTGAATGCTCAGGTT 868
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RESULT 3

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LOCUS AUI32064 NT2RP3 Homo sapiens cDNA clone NT2RP3003721 5', mRNA
DEFINITION AUI32064 862 bp mRNA linear EST 01-AUG-2002
sequence.
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```
ACCESSION AUI32064
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```
VERSION AUI32064.1 GI:10992418
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KEYWORDS EST.
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SOURCE human.
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```
ORGANISM Homo sapiens
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
1 (bases 1 to 862)
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```
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
```

```
Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
```

```
Isogai.T.
```

```
TITLE HRI human cDNA project
```

```
JOURNAL Unpublished (2000)
```

```
COMMENT Contact: Takao Isogai
```

```
Genomics Laboratory
```

```
Helix Research Institute
```

```
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
```

```
Tel: 81-438-52-3975
```

```
Fax: 81-438-52-3986
```

```
Email: genomics@hri.co.jp
```

```
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
```

```
Research Institute; cDNA library construction: Department of
```

```
Virology, Institute of Medical Science, University of Tokyo, and
```

```
Helix Research Institute.
```

```
FEATURES Location/Qualifiers
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1..862
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone="NT2RP3003721"
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/clone_lib="NT2RP3"
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```
/cell_type="teratocarcinoma"
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/cell_line="NT2"
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/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor  
cells after 2-weeks retinoic acid (RA) induction"
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BASE COUNT 188 a 230 c 227 g 4 others
ORIGIN
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Query Match 13.7%; Score 798.8; DB 9; Length 862;
Best Local Similarity 95.2%; Pred. No. 6e-115;
Matches 821; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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QY 3018 ACGACCCCCACAGGAGGATTTCTCAACAGGTTTTCCAAAGACATGATGAAGTTGACGTG 3077
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```
Db 1 ACGACCCCCACAGGAGGACTCTCAACAGGTTTTCCAAAGACATGATGAAGTTGACGTG 60
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```

```
QY 3078 CGGCTGCCGTTCCAGGCCGAGATGTTTCATCCAGAACGTTATCTCTGGTGTCTTCTGTGTG 3137
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Db 61 CGGCTGCCGTTCCAGGCCGAGATGTTTCATCCAGAACGTTATCTCTGGTGTCTTCTGTGTG 120
|||||
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QY 3138 GGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGGCAGTGGGCCCTTGTTCATCCTC 3197
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Db 121 GGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGGCAGTGGGCCCTTGTTCATCCTC 180
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QY 3198 TTTTCACTCTCGACATTTGTCTCCAGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAAT 3257
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Db 181 TTTTCACTCTCGACATTTGTCTCCAGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAAT 240
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QY 3258 ATCAGCAGTCACTTTCTCTCCACATCAGTCCAGCATACAGGGCTTGGCCACCATC 3317
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Db 241 ATCAGCAGTCACTTTCTCTCCACATCAGTCCAGCATACAGGGCTTGGCCACCATC 300
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QY 3318 CAGCCCTACAAATAAGGGCAGGAGTTTCTGCACAGATACACAGGAGCTCTCGTGATGACAA 3377
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Db 301 CAGCCCTACAAATAAGGGCAGGAGTTTCTGCACAGATACACAGGAGCTCTCGTGATGACAA 360
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QY 3378 CAAGCTCCTTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGGCTGGCTGGCTGGCTG 3437
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Db 361 CAAGCTCCTTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGGCTGGCTGGCTGGCTG 420
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QY 3438 ATCAGCATCGCCCTCATCACACACGGGGCTGATGATCGTTCTATGACGGGCGAGATT 3497
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Db 421 ATCAGCATCGCCCTCATCACACACGGGGCTGATGATCGTTCTATGACGGGCGAGATT 480
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QY 3498 CCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAAACGGGGCTGTTCAG 3557
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Db 481 CCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAAACGGGGCTGTTCAG 540
|||||
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QY 3558 TTTACGCTCAGACTGGCATCTGACACAGAGCTCGATTCACCTCGGTGGAGAGGATCAAT 3617
|||||
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Db 541 TTTACGCTCAGACTGGCATCTGACACAGAGCTCGATTCACCTCGGTGGAGAGGATCAAT 600
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QY 3618 CACTACATTAAGACTCTGCTTGGAGAGCCTCCAGAGCCTCCAGAAATTAAGAACGGCTCCCTCC 3677
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Db 601 CACTACATTAAGACTCTGCTTGGAGAGCCTCCAGAGCCTCCAGAAATTAAGAACGGCTCCCTCC 660
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QY 3678 CCTGACTGGCCCCCAGGAGGAGGTGACCTTTGAGAACGCGAGAGATGAGGTACCGAGAA 3737
|||||
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Db 661 CCTGACTGGCCCCCAGGAGGAGGTGACCTTTGAGAACGCGAGAGATGAGGTACCGAGAA 720
|||||
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QY 3738 AACCTCCTCTTGTCTTAAAGAAAGTATCTTTCAGATCAAAACCTTAAAGAGAGATTGGC 3797
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Db 721 AACCTTCTCTCTCTTAAAGAAAGTATCTTTCAGATCAAAACCTTAAAGAGAGATTGGC 780
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QY 3798 ATTGTGGGGCGGACAGATCAGGAAAGTCTCTCGCTGGGGATGGCCCTCTTCGGTCTGGTG 3857
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Db 781 ATTGTGGGGCGGACAGATCAGGAAAGTCTCTTCCTTGGGGATGGCCCTCTTCGGTCTGGTG 840
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QY 3858 GAGTTATCTGGAGGCTGCATCA 3879
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Db 841 GTTATCTGGAGGCTTGCATCA 862
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RESULT 4

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BQ898022      935 bp      mRNA      linear      EST 16-AUG-2002
LOCUS      AGENCOURT_8122242_Lupski_dorsal_root_ganglion_Homo_sapiens_cdna
DEFINITION      clone IMAGE:6179508 5', mRNA sequence.
ACCESSION      BQ898022
VERSION      BQ898022.1 GI:22290036
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13560 row: m column: 13
High quality sequence stop: 701.
FEATURES             source
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   /db_xref="taxon:9606"
   /clone="IMAGE:6179508"
   /clone_lib="Lupski_dorsal_root_ganglion"
   /sex="male"
   /tissue_type="dorsal root ganglia"
   /dev_stage="adult, 36 yr"
   /lab_host="DH10B"
   /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGGCTCG-3' and
5'-GACTAGTTAGATCGGAGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT      220 a      230 g      264 t      1 others
ORIGIN
Query Match      13.5%; Score 787.2; DB 14; Length 935;
Best Local Similarity 95.9%; Pred. No. 3.7e-113;
Matches 842; Conservative 0; Mismatches 28; Indels 8; Gaps 3;

Qy 3789 AAGATTGGCATTGTGGGCGGACAGATCAGGAAGTCTCTCGCTGGGATGCCCTCTTC 3848
Db      |||||||
Db 1 AAGATTGGCATTGTGGGCGGACAGATCAGGAAGTCTCTCGCTGGGATGCCCTCTTC 60
Qy 3849 GCTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAATCAGTGATATT 3908
Db      |||||||
Db 61 GCTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAATCAGTGATATT 120
Qy 3909 GGCCTTGGCGACCTCCGAGCAACTCTCTATCTTCCTCAAGACCGGCTGTTCAGT 3968
Db      |||||||
Db 121 GGCCTTGGCGACCTCCGAGCAACTCTCTATCTTCCTCAAGACCGGCTGTTCAGT 180
Qy 3969 GGCCTGTGCAGATCAAAATTTGGACCCCTTCAACAGTACACTGAAGACACAGATTGGGAT 4028
Db      |||||||
Db 181 GGCCTGTGCAGATCAAAATTTGGACCCCTTCAACAGTACACTGAAGACACAGATTGGGAT 240
Qy 4029 GCCCTGGAGAGACACATGAAGAATGTATTGCTCAGCTACCTCTGAACCTTGAATCT 4088
Db      |||||||
Db 241 GCCCTGGAGAGACACATGAAGAATGTATTGCTCAGCTACCTCTGAACCTTGAATCT 300
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Qy 4089 GAAGTGATGAGAAATGGGGATAAATTCTCTAGTGGGGAACGGCAGCTCTTGTGATAGCT 4148
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Db 301 GAAGTGATGAGAAATGGGGATAAATTCTCTAGTGGGGAACGGCAGCTCTTGTGATAGCT 360
Qy 4149 AGAGCCCTGCTCGCCCACTGTAAAGATTCTGATTTAGATGAAGCCAGCTGCCATGGAC 4208
Db      |||||||
Db 361 AGAGCCCTGCTCGCCCACTGTAAAGATTCTGATTTAGATGAAGCCAGCTGCCATGGAC 420
Qy 4209 ACAGAGACAGACTATTGATTCAAGAGACCATCCGAGAAGCATTTCAGAGCTGACCATG 4268
Db      |||||||
Db 421 ACAGAGACAGACTATTGATTCAAGAGACCATCCGAGAAGCATTTCAGAGCTGACCATG 480
Qy 4269 CTGACCAATGCCCATCGCCCTGCACACGGTTCTTAGGCTCCGATAGGATTATGGTCTGCC 4328
Db      |||||||
Db 481 CTGACCAATGCCCATCGCCCTGCACACGGTTCTTAGGCTCCGATAGGATTATGGTCTGCC 540
Qy 4329 CAGGGACAGGTGGTGGAGTTTGACACCCCATCGCTCTCTGTCACACGACAGTTCGCCGA 4388
Db      |||||||
Db 541 CAGGGACAGGTGGTGGAGTTTGACACCCCATCGCTCTCTGTCACACGACAGTTCGCCGA 600
Qy 4389 TTCTATGCCATGTTTGTGCTGCAGAGAACAGTCTGCTCAAGGGCTGACTCTCCCT 4448
Db      |||||||
Db 601 TTCTATGCCATGTTTGTGCTGCAGAGAACAGTCTGCTCAAGGGCTGACTCTCCCT 660
Qy 4449 GTTGACGAAGTCTCTTTTCTTTTAGAGCATTCGCCATTCCTT-GCCTGGGGGGGGCCCTCA 4507
Db      |||||||
Db 661 GTTGACGAAGTCTCTTTTCTTTTAGAGCATTCGCCATTCCTTGGGGGGGGCCCTCA 720
Qy 4508 TCGCTGCTCTCTACCGAAGACCTTGCCTTCTCGATTTATCTTTCGACAGAGATTCCCG 4567
Db      |||||||
Db 721 TCGCTGCTCTCTACCGAAGACCTTGCCTTCTCGATTTATCTTTCGACAGCAATTCGG 780
Qy 4568 -ATTGGCTTGTGTTTCACTTTTAGGAGAGTCATATTTTATT-----ATTGATT 4620
Db      |||||||
Db 781 AATTGCTTGTGTTTCACTTTTAGGAGAGTCATATTTTATTGATTAAATTTGATT 840
Qy 4621 ATTCCATATTCATGTAACAAAATTTAGTTTGTCT 4658
Db      |||||||
Db 841 TTTCATATTCATGTAACAAAATTTAGTTTGTCT 878

RESULT 5
BI770993      851 bp      mRNA      linear      EST 25-SEP-2001
LOCUS      603055332F1 NIH_MGC_122 Homo sapiens cdna clone IMAGE:5204983 5',
DEFINITION      mRNA sequence.
ACCESSION      BI770993
VERSION      BI770993.1 GI:15762571
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11513 row: p column: 08
High quality sequence stop: 784.
FEATURES             source
   1..851
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:5204983"
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/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/Note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed, and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 197 a 198 c 184 g 272 t
ORIGIN
Query Match 13.2%; Score 769.2; DB 13; Length 851;
Best Local Similarity 98.6%; Pred. No. 2.5e-110;
Matches 818; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
QY 4176 CTGATTTTGTAGTGAAGCCACAGCTGCGATGGACACAGACAGACACTTATTGATTCAAGAG 4235
DB 1 CTGATTTTGTAGTGAAGCCACAGCTGCGATGGACACAGACAGACACTTATTGATTCAAGAG 60
QY 4236 ACCATCCGAGAACATTTGCAGACTGTACATGCTGACCAATGCCCATCGCCCTGCACAG 4295
DB 61 ACCATCCGAGAACATTTGCAGACTGTACATGCTGACCAATGCCCATCGCCCTGCACAG 120
QY 4296 GTTCTAGGCTCCGATAGGATTATGGTGTGCTGGCCAGGACAGGTGGAGTTGACACC 4355
DB 121 GTTCTAGGCTCCGATAGGATTATGGTGTGCTGGCCCA-GGACAGGTGGAGTTGACACC 179
QY 4356 CCATCGGTCTCTGTCACACAGACAGTCCCGATTTCTATGCCATGTTGCTGCTGCAGAG 4415
DB 180 CCATCGGTCTCTGTCACACAGACAGTCCCGATTTCTATGCCATGTTGCTGCTGCAGAG 239
QY 4416 AACAGGTGCTGTCAGGGCTGACCTCCCTGTTGTGACGAAGTCTCTTTCTTTTAGAGC 4475
DB 240 AACAGGTGCTGTCAGGGCTGACCTCCCTGTTGTGACGAAGTCTCTTTCTTTTAGAGC 299
QY 4476 ATGCGCATTCCTGCTGGGGGGGGCCCTCATCGCTGCTCTCTACCGAACCTTGCGCTT 4535
DB 300 ATGCGCATTCCTGCTGGGGGGGGGGCCCTCATCGCTGCTCTCTACCGAACCTTGCGCTT 359
QY 4536 TCTCGATTTTATCTTCGACACAGACAGTTCGCGATTTGGCTTGTGTTTACACTTTTAGGGA 4595
DB 360 TCTCGATTTTATCTTCGACACAGACAGTTCGCGATTTGGCTTGTGTTTACACTTTTAGGGA 419
QY 4596 GAGTCATATTTTGAATTTGATTTATTTATTCATATTCATGTAACAAATTTAGTTTTGT 4655
DB 420 GAGTCATATTTTGAATTTGATTTATTTATTCATATTCATGTAACAAATTTAGTTTTGT 479
QY 4656 TCTTAATTCACCTCTAAAGGTTTCAGGACCCCTTATTAATTTGATGAGGCCCTATA 4715
DB 480 TCTTAATTCACCTCTAAAGGTTTCAGGACCCCTTATTAATTCGATACAGGCCCTATA 539
QY 4716 ATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCGTACATAGCCCTATATTACA 4775
DB 540 ATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCGTACATAGCCCTATATTACA 599
QY 4776 GTGAAATGTAGCTGTTTATTTTATATAATAAGCACTGTGCTAATAACAGTGCATA 4835
DB 600 GTGAAATGTAGCTGTTTATTTTATATAATAAGCACTGTGCTAATAACAGTGCATA 659
QY 4836 TTCTTTCTATCAATTTTGTACAGTTTGTGTTACTAGAGATCTGGTTTTCCTATTAGACT 4895
DB 660 TTCTTTCTATCAATTTTGTACAGTTTGTGTTACTAGAGATCTGG-TTTCTCTATTAGACT 718
QY 4896 GTAG-GAAGAGTAGCATTTTCATTTCTCTAGCTGGTGTTCACGCTGCCAGGTTTTCT 4954
DB 719 GTAGCGAAGAGTAGCATTTTCATTTCTCTAGCTGGTGTTCACGCTGCCAGGTTTTCT 778
QY 4955 GGGTGT-CCAAAGGAAGACGTGTGGCAATAGTGGGGCCCTCCGACAGCCCC 5003
||||| ||||||| ||||||| || ||||||| |||

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Db 779 GGGTGTCCAAAGGACGACGCTGTGGCAACTGCTGGGGCTCCGACAGCCCC 828
RESULT 6
BM541578 1083 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6448278 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531707
5', mRNA sequence.
ACCESSION BM541578
VERSION BM541578.1 GI:187770340
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1083)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaops-f@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12213 row: m column: 20
High quality sequence stop: 643.
FEATURES
source
1..1083
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5531707"
/lab_host="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT 229 a 318 c 270 g 265 t 1 others
ORIGIN
Query Match 13.0%; Score 761.6; DB 13; Length 1083;
Best Local Similarity 98.2%; Pred. No. 3.4e-109;
Matches 812; Conservative 0; Mismatches 10; Indels 5; Gaps 4;
QY 2968 ATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGGACAGACCCCCA 3027
DB 2 ATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGGACAGACCCCCA 61
QY 3028 CAGGAGGATTTCAACAGGTTTTTCCAAAGACATGGATGAAGTTGACGTGGCGTGCCT 3087
DB 62 CAGGAGGATTTCTCAACAGGTTTTTCCAAAGACATGGATGAAGTTGACGTGGCGTGCCT 121
QY 3088 TCAGGCGGAGATGTTTCATCCAGAACGTTATCCTGTTGGTCTTCTGTTGGGAATGATCG 3147
DB 122 TCAGGCGGAGATGTTTCATCCAGAACGTTATCCTGTTGGTCTTCTGTTGGGAATGATCG 181
QY 3148 CAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTGTCTATCCTCTTTTCAGTCC 3207
DB 182 CAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTGTCTATCCTCTTTTCAGTCC 241
QY 3208 TGCACATTTGCTCCAGGGTCTGATTCGGGAGCTGAAGCGTCTGGACAATATCAGCAGT 3267
DB 242 TGCACATTTGCTCCAGGGTCTGATTCGGGAGCTGAAGCGTCTGGACAATATCAGCAGT 301
QY 3268 CACCTTTCTCTCCACATCAGTCCAGCATACAGGGCTTGGCCACCATCCAGCCTACA 3327
DB 302 CACCTTTCTCTCCACATCAGTCCAGCATACAGGGCTTGGCCACCATCCAGCCTACA 361
QY 3328 ATAAAGGGCAGGAGTTTTTCTGCACAGATACAGGAGCTCTCGATGACAAACAGCTCCTT 3387

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Db 362 ATAAAGGGCAGAGTTCTGCACAGATACCAGAGGCTGCTGGATGACAAACAGCTCCTT 421
QY 3388 TTTTTFGTGTTTACGTGCGATCGCGTGGCTGGCTGTGCGGTGGACCTCATCAGCATCG 3447
Db 422 TTTTTFGTGTTTACGTGCGATCGCGTGGCTGGCTGTGCGGTGGACCTCATCAGCATCG 481
QY 3448 CCTCATCACACACCGGGGCTGATGCTGTTATGACACGGGAGATTCCTCCCGAGCT 3507
Db 482 CCTCATCACACACCGGGGCTGATGCTGTTATGACACGGGAGATTCCTCCCGAGCT 541
QY 3508 ATGCGGGTCTGCCATCTCTTATGCTGCTCCAGTTAACGGGGCTGTTCACAGTTTACGGTCA 3567
Db 542 ATGCGGGTCTGCCATCTCTTATGCTGCTCCAGTTAACGGGGCTGTTCACAGTTTACGGTCA 601
QY 3568 GACTGGCATCTGAGACAGAAGCTCGATTACCTCGGTGGAGAGGATCAATCACTACATTA 3627
Db 602 GACTGGCATCTGAGACAGAAGCTCGATTACCTCGGTGGAGAGGATCAATCACTACATTA 661
QY 3628 AGACTCTGCTTGAAGCACCCTGCAGAAATTAAGAACAGGCTCCTCCCTGACTGGC 3687
Db 662 AGACTCTGCTTGAAGCACCCTGCAGAAATTAAGAACAGGCTCCTCCCTGACTGGC 721
QY 3688 CCCA--CGAGGGAGAGGTGACCTTTG-AGAAGCGAGAGATGAGTA-CGAGAGAAACCTC 3743
Db 722 CCCAAGNAGGAGAGGTGACCTTTGAGAGCCGAGAGATGAGGTACCCGAGAAACCTC 781
QY 3744 CCTCTGTCTTAAAGAAAGTAT-CCTTCACGATCAAACTTAAAGAGA 3789
Db 782 CCTCTGTCTTAAAGAAAGTATCCTTCCCGATCAAAACCTTAAAGAGA 828

RESULT 7
LOCUS BG678114
DEFINITION 602625870P1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750984 5',
mRNA sequence.
ACCESSION BG678114
VERSION BG678114.1 GI:13909511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 887)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10606 row: k column: 17
High quality sequence start: 3
High quality sequence stop: 786.
Location/Qualifiers
1..887
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4750984"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
193 a 223 c 204 g 267 t

FEATURES
source
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ORIGIN

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Query Match 13.0%; Score 757.4; DB 12; Length 887;
Best Local Similarity 95.6%; Pred. No. 1.7e-108;
Matches 854; Conservative 0; Mismatches 31; Indels 8; Gaps 7;

QY 4687 CGTTATTATAATTTGATATACAGAGCCCTATAATGAAGCTTTTATACGTGTAGCTATATCTATA 4746
Db 1 CGTTATTATAATTTGATATACAGAGCCCTATAATGAAGCTTTTATACGTGTAGCTATATCTATA 60
QY 4747 TATAATTTCTGTACATACCTATATTTTACAGTGAAAATGTAAGCTGTTTA-TTTATATTAA 4806
Db 61 TATAATTTCTGTACATACCTATATTTTACAGTGAAAATGTAAGCTGTTTA-TTTATATTAA 119
QY 4807 AATAAGCACTGTCTCTAATAACAGTGCATATTCCTTTCTATCATATTTTGTACACTTTTGCTG 4866
Db 120 AATAAGCACTGTCTCTAATAACAGTGCATATTCCTTTCTATCA-TTTGTACAGTTTGCTG 178
QY 4867 TACTAGATATCTGTTTCTCTATTTAGACTGTAGAAAGAGTAGCATTTCAATTTCTCTCTAG 4926
Db 179 TACTAGATATCTGTTTCTCTATTTAGACTGTAGAAAGAGTAGCATTTCAATTTCTCTCTAG 238
QY 4927 CTGGTGGTTTCACGGTGCAGGTTTCTGGGTGTCCTAAAGGAAGAGCTGTGGCAATAGTG 4986
Db 239 CTGGTGGTTTCACGGTGCAGGTTTCTGGGTGTCCTAAAGGAAGAGCTGTGGCAATAGTG 298
QY 4987 GGCCCTCCGACAGCCCTCTGCGGCTCCCCACAGCCGCTCCAGGGGTGGCTGGAGACG 5046
Db 299 GGCCCTCCGACAGCCCTCTGCGGCTCCCCACAGCCGCTCCAGGGGTGGCTGGAGACG 358
QY 5047 GTGGGGCGCTGGAGACCATGACAGCGCCGTGAGTTCTCAGGGCTCTGCCCTTCTGTCC 5106
Db 359 GTGGGGCGCTGGAGACCATGACAGCGCCGTGAGTTCTCAGGGCTCTGCCCTTCTGTCC 418
QY 5107 TCGTGTCACTTACTCTTCTGTCTCAGAGAGCAGCGGGGCGAAGCCCGAGCCCTTTTTCAC 5166
Db 419 TCGTGTCACTTACTCTTCTGTCTCAGAGAGCAGCGGGGCGAAGCCCGAGCCCTTTTTCAC 478
QY 5167 TCCTCCATCAAGAATGGGGATCACAGACATTCCTCCGAGCGGGGAGTTTCTTTTCT 5226
Db 479 TCCTCCATCAAGAATGGGGATCACAGACATTCCTCCGAGCGGGGAGTTTCTTTTCT 538
QY 5227 GCCTTCTCTTTTGTGTGTGTTTCTTAAACAAGATCACTCTATCCACAGAGAGTCCAC 5286
Db 539 GCCTTCTCTTCTTTGTGTGTGTTTCTTAAACAAGATCACTCTATCCACAGAGAGTCCAC 597
QY 5287 TCCTTCAGTTTCTATGCTGGCCACTGCACAGAGCTCTCCAGCTCCACAGACTGTGGT 5346
Db 598 TCCTTCAGTTTCTATGCTGGCCACTGCACAGAGCTCTCCAGCTCCACAGACTGTGGT 657
QY 5347 TCCTTCAGTTTCTATGCTGGCCACTGCCTGCTTTTGTGGTGGCACTTTTTCATTTGCTTATCC 5406
Db 658 TCCTTCAGTTTCTATGCTGGCCACTGCCTGCTTTTGTGGTGGCACTTTTTCATTTGCTTATCC 717
QY 5407 ACCTTCACAGTTTCAGTGGGAGGCTCAGGATTCGTGGGTGCTGTTTCTCTCTTCTCAC 5466
Db 718 ACCTTCACAGTTTCAGTGGGAGGCTCAGGATTCGTGGGTGCTGTTTCTCTCTTCTCAC 776
QY 5467 GCAGTCTGCACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5525
Db 777 GCAGTCTGCACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 836
QY 5526 CTGTGTAATCATAGTCTCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5578
Db 837 CTGTGTAATCATAGTCTCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886
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RESULT 8
BG676445
LOCUS 602622898F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748039 5',
mRNA sequence.
ACCESSION BG676445

841 bp mRNA linear EST 01-MAY-2001
DEFINITION 602622898F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748039 5',
mRNA sequence.
ACCESSION BG676445

BASE COUNT 193 a 223 c 204 g 267 t


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|||||
Db 450 GCTTTTGGAGTGGCACTTTTTCATTGGCTATTGCCATATCCACACCTCCACAGTTCAGTGGCAG 391
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QY 5430 GGCCTCAGGATTTTGGTGTGTTTTCCTTTCACCGCAGTGTGTCGACAGTCTCTCTC 5489
|||||
Db 390 GGCCTCAGGATTTTGGTGTGTTTTCCTTTCACCGCAGTGTGTCGACAGTCTCTCTC 331
|||||
QY 5490 TCTCTCTCCCTCAAAAGTCTGCAACTTTAAGCAGCTCTTCTAATCAGTGTCTCACACTG 5549
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Db 330 TCTCTCTCCCTCAAAAGTCTGCAACTTTAAGCAGCTCTTCTAATCAGTGTCTCACACTG 271
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QY 5550 GCGTAGAAGTTTGTGCTGTAAGAGACCTACCTCAGGTTGCTGTTGCTGTGTTT 5609
|||||
Db 270 GCGTAGAAGTTTGTGCTGTAAGAGACCTACCTCAGGTTGCTGTTGCTGTGTTT 211
|||||
QY 5610 GGTGTGTTCCGCAAAACCCCTTGTGCTGGGCTGTGCTGAGTGTGCTGAGTGGGCTGTCA 5669
|||||
Db 210 GGTGTGTTCCGCAAAACCCCTTGTGCTGGGCTGTGCTGAGTGTGCTGAGTGGGCTGTCA 151
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QY 5670 CTGCTGTCTCAGTGTGAATGCTCAGGCTGTGCTGACCACTAGACATTTCTGTGCG 5729
|||||
Db 150 CTGCTGTCTCAGTGTGAATGCTCAGGCTGTGCTGACCACTAGACATTTCTGTGCG 91
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QY 5730 CTTAGCATGTTTCTGTAACACCTTTGTGGAAGCAAAATCTGAAATGTGAATTAATAT 5789
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Db 90 CTTAGCATGTTTCTGTAACACCTTTGTGGAAGCAAAATCTGAAATGTGAATTAATAT 31
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QY 5790 TTTGGATTTGTAAAAAATAAAAAA 5819
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Db 30 TTTGGATTTGTAAAAAATAAAAAA 1

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RESULT 11
AUI37090 761 bp mRNA linear EST 02-AUG-2002
LOCUS AUI37090 PLACE1 Homo sapiens cDNA clone PLACE1005753 5', mRNA
DEFINITION sequence.
ACCESSION AUI37090
VERSION AUI37090.1 GI:10597629
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isozaki.T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isozaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .761
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="PLACE1"
/tissue_type="placenta"
/notes="Vector: pME18SPL3"
BASE COUNT 200 a 185 c 204 g 165 t 7 others
ORIGIN
Query Match 11.7%; Score 685; DB 9; Length 761;

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Best Local Similarity 96.3%; Pred. No. 3.3e-97;
Matches 720; Conservative 0; Mismatches 25; Indels 3; Gaps 2;
QY 3660 AAGAACAGGCTCCCTCCCTGACTGGCCAGGAGGAGGAGTCCACCTTTGAGAACCA 3719
|||||
Db 1 AAGAACAGGCTCCCTCCCTGACTGGCCAGGAGGAGGAGTCCACCTTTGAGAACCA 60
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QY 3720 GAGATGAGGTACCGAGAAACCTCCCTCTTCTCTAAAGAAAGATCTCTCAGCATCAA 3779
|||||
Db 61 GAGATGAGGTACCGAGAAACCTCCCTCTTCTCTAAAGAAAGATCTCTCAGCATCAA 120
|||||
QY 3780 CCTAAAGAGAGATGTCATTTGGGGGAGAGATCAGGAAAGTCTCTCGCTGGGAGT 3839
|||||
Db 121 CCTAAAGAGAGATGTCATTTGGGGGAGAGATCAGGAAAGTCTCTCGCTGGGAGT 180
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QY 3840 GCCTCTCTCGCTGCTGGGAGTTATCTGGAGGCTGCATCAAGATTTGAGGAGTCAATC 3899
|||||
Db 181 GCCTCTCTCGCTGCTGGGAGTTATCTGGAGGCTGCATCAAGATTTGAGGAGTCAATC 240
|||||
QY 3900 AGTGATATTGGCCCTTGGCCAGCTCCGAAAGCAAACTCTCTATCTCTCAAGAGCCGGT 3959
|||||
Db 241 AGTGATATTGGCCCTTGGCCAGCTCCGAAAGCAAACTCTCTATCTCTCAAGAGCCGGT 300
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QY 3960 CTGTTAGTGGCAGTGTGATCAAAATTTGGACCCCTTCAACCACTGACCTGAGAAC 4019
|||||
Db 301 CTGTTAGTGGCAGTGTGATCAAAATTTGGACCCCTTCAACCACTGACCTGAGAAC 360
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QY 4020 ATTTGGGATGCCCTGGAGAGACACATGAAAGAAATGTTGTCAGCTACCTCTGAAA 4079
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Db 361 ATTTGGGATGCCCTGGAGAGACACATGAAAGAAATGTTGTCAGCTACCTCTGAAA 420
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QY 4080 CTTGAATCTGAAGTGTGGGAGTGGGATAAATCTTCAGTGGGGAACGCGAGCTCTTG 4139
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Db 421 CTTGAATCTGAAGTGTGGGAGTGGGATAAATCTTCAGTGGGGAACGCGAGCTCTTG 480
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QY 4140 TGCATAGCTAGAGCCCTGCTCCGCACTGTAAAGATTTCTAGATTAAGAGCCACAGCT 4199
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Db 481 TGCATAGCTAGAGCCCTGCTCCGCACTGTAAAGATTTCTAGATTAAGAGCCACAGCT 540
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QY 4200 GCATGACACAGACAGACAGACTTATGATTCAGAGACCATCCGAGAGACATTTGCGAC 4259
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Db 541 GCATGACACAGACAGACAGACTTATGATTCAGAGACCATCCGAGAGACATTTGCGAAC 600
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QY 4260 TGTACCATGCTGACCATTTGCCATCGCTGCACAGCTGTAGGCTCCGATA-GGATTAT 4318
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Db 601 TGTACCATGCTGACCATTTGCCATCGCTGCACAGCTGTAGGCTCCGATAGGATAT 660
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QY 4319 GGTGCTGGCCAGGACAGGTTGGAGTTTGCACACCCCATCGG--TCCTTCTGTCCAAC 4376
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Db 661 GGTGCTGGCCAGGACAGGTTGGAGTTTGCACACCCCATCGGCTCTCCNGTCCAAC 720
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QY 4377 GACAGTTCCCGATTTCTATGCCATGTTG 4404
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Db 721 GACAGTTCCCGATTTCCNATGCAAGTTG 748

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RESULT 12
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LOCUS BM665074 UI-E-CQ1-aew-h-01-0-UI.s1 UI-E-CQ1 Homo sapiens cDNA clone
DEFINITION UI-E-CQ1-aew-h-01-0-UI 3', mRNA sequence.
ACCESSION BM665074
VERSION BM665074.1 GI:18971693
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 716)
Bonaldo.M.F., Lennon.G. and Soares.M.B.
Normalizaton and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)

```

MEDLINE
COMMENT
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-41, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1. 716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-aew-h-01-0-UI"
/clone_lib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site:1: EcoR I; Site:2: Not I;
UI-E-CQ1 is a normalized cDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dfr)18 tail. The sequence tag for this library is
CCATTAAAGT. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
TAG_LIB=UI-E-CQ1
TAG_TISSUE=human optic nerve
TAG_SEQ=CCATTAAAGT"
BASE COUNT 212 a 165 c 185 g 154 t

Query Match 11.78; Score 683.4; DB 13; Length 716;
Best Local Similarity 99.7%; Pred. No. 6.1e-97;
Matches 695; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 5123 TTCGTGTCAGGAGACGAGCGGGCGAAGCCAGGCCCTTTTCACTCCCTCCATCAAGAA 5182
DB TTTCTTCTGAGGAGACGAGCGGGCGAAGCCAGGCCCTTTTCACTCCCTCCATCAAGAA 637
QY 5183 GGGGATCACAGAGACATTCCTCCGAGCGGGGAGTTCTTCTCCCTCTCTTTTTCG 5242
DB GGGGATCACAGAGACATTCCTCCGAGCGGGGAG-TTCTTCTCCCTCTCTTTTTCG 578
QY 5243 TGTGTTTCTTAAACAAGATCAGTCTATCCACAGAGAGTCCCACTGCTCAGGTTCCAT 5302
DB TGTGTTTCTTAAACAAGATCAGTCTATCCACAGAGAGTCCCACTGCTCAGGTTCCAT 518
QY 5303 GGCCTGGCCACTGCACAGAGCTCCAGCTCCAGACCTGTTGGTTCCAGCCCTGGAGCC 5362
DB GGCTGGCCACTGCACAGAGCTCTCCAGCTCCAGACCTGTTGGTTCCAGCCCTGGAGCC 458
QY 5363 AACTGCTGCTTTTGTAGGTGGCACTTTTTCATTGTCCTATTCCACACACTCCACAGTTCA 5422
DB AACTGCTGCTTTTGTAGGTGGCACTTTTTCATTGTCCTATTCCACACACTCCACAGTTCA 398

QY 5423 GTGGCAGGCTCAGGATTTGTTGGGTCTGTTTCTCTTCTCACCAGTGTGTCACAGT 5482
DB GTGGCAGGCTCAGGATTTGTTGGGTCTGTTTCTCTTCTCACCAGTGTGTCACAGT 338
QY 5483 CTTCTCTCTCTCTCCCTCAAGTCTGCAACTTTAAGCAGCTCTTCTAATCAGTGTCT 5542
DB CTTCTCTCTCTCTCCCTCAAGTCTGCAACTTTAAGCAGCTCTTCTAATCAGTGTCT 278
QY 5543 CACACTGGCGTGAAGCTTTTGTACTGTAAGAGACCTACCTCAGTGTGCTGTGCTGT 5602
DB CACACTGGCGTGAAGCTTTTGTACTGTAAGAGACCTACCTCAGTGTGCTGTGCTGT 218
QY 5603 GTGGTTGTGTGTTTCCCGCAACCCCTTTGTGTGTGGGCTGTAGCTCAGGTGGGC 5662
DB GTGGTTGTGTGTTTCCCGCAACCCCTTTGTGTGTGGGCTGTAGCTCAGGTGGGC 158
QY 5663 GTGGTCACCTGCTCATCAGTTGAATGGTCAGGTTGCATGTCGTACCAACTAGACAT 5722
DB GTGGTCACCTGCTCATCAGTTGAATGGTCAGGTTGCATGTCGTACCAACTAGACAT 98
QY 5723 CTGTCGCCCTTAGCATGTTTGTCTGAACACCTTGTGGAAGCAAAAATCTGAAAATGTGAATA 5782
DB CTGTCGCCCTTAGCATGTTTGTCTGAACACCTTGTGGAAGCAAAAATCTGAAAATGTGAATA 38
QY 5783 AAATTATTTTGGATTTGTAAAAAATAAAAAAAAAAAAAA 5819
DB AAATTATTTTGGATTTGTAAAAAATAAAAAAAAAAAAAA 1
RESULT 13
AL543173 AL543173 889 bp mRNA linear EST 16-FEB-2001
LOCUS AL543173 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI002YC13 5
DEFINITION prime, mRNA sequence.
ACCESSION AL543173
VERSION AL543173.1 GI:12875651
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI002YC13"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
was primed with a NotI-oligo(drr) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 208 a 218 c 254 g 208 t 1 others

Query Match 11.6%; Score 677.8; DB 9; Length 889;

Best Local Similarity 99.0%; Pred. No. 4.1e-96;
Matches 682; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 680)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM10599 row: j column: 19
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Location/Qualifiers
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Db 121 TAGCTATATTTACAGTGAATCTAAGCTCTTTATTTATTTATTTAAATAAGCACTGTC 180
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Db 181 TAATAACAGTGCATATTCCTTTCTATCATTTTGTACAGTTTGTCTAGTACAGATCTGG 240
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Qy 5001 CCCCTCTGCGCCCTCCCCACAGCGCTCCAGGGGTGGCTGGAGACGGGTGGCGGCTGGA 5060
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:49:35 ; Search time 141.369 Seconds
(without alignments)
16388.716 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	442	7.6	442	10	US-09-954-456-1684
2	435.8	7.5	3786	9	US-10-012-896-1006
3	435.8	7.5	4395	9	US-10-012-896-1007
4	435.8	7.5	6140	9	US-10-012-896-536
5	435.8	7.5	6140	10	US-09-759-143-536
6	435.8	7.5	6140	10	US-09-780-669-536
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21	275.6	4.7	418	10	US-09-960-352-4836	Sequence 4836, Ap
22	248.2	4.3	1936	10	US-09-880-107-3832	Sequence 3832, Ap
23	245.8	4.2	1977	10	US-09-954-456-804	Sequence 804, App
24	245.8	4.2	1977	10	US-09-880-107-3407	Sequence 3407, Ap
25	245.8	4.2	1977	10	US-09-967-768A-190	Sequence 190, App
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ALIGNMENTS

RESULT 1
US-09-954-456-1684/c
; Sequence 1684, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1684
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Best Local Similarity 100.0%; Pred. No. 3.3e-91;
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US-10-012-896-1007

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US/10-012-896-1007
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: Publication No. US2002018325A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skelky, Isair A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Wantanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS
: TITLE OF INVENTION: COMPOSITIONS OF PROSTAT
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/012,896
: CURRENT FILING DATE: 2001-12-10
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1007
: LENGTH: 4395
: TYPE: DNA

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ORGANISM: Homo sapiens
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; OTHER INFORMATION: n=A,T,C or G									
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QY	2334	GTCTGTGTTGTTACCCACAGTACAGTACCTGTTGATGATGATGATGATGATGATG	2393						
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QY	2394	AAAGAGGCTGTATTACGAAAGAGGACCCATCAGGAAGTATGATGATGATGATGATG	2453						
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QY	2694	TTGCAATTCCTGTTATTTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2753						
DB	2278	GCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2337						
QY	2754	ACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2813						
DB	2338	CCCTATGCTTCAAGATTTGGTGGCTTTCATCTGGGCAACCAACAAAGATGCTAAT	2397						
QY	2814	AACGAGACCTCGGTGAGTGACAGCATGAAGGACAAATCTCTATATGCTACTATGCCAGC	2873						

DB	2398	GTCACTGTAATGGAGGAGAAATGTAAACGAGAGCTAGATCTTAACCTGGTACTTAGA	2457						
QY	2874	ATCTAGCGCCTCTCCATGCGAGCTATGCTGATGCTCTGAAAGCCATTCGAGGAGTGTCTTT	2933						
DB	2458	ATTTATTACAGGTTTAACTAGTACCTACCGTTCTTTTGGCATACGAGATCTCTATTGGTA	2517						
QY	2934	GTCAAGGACGCTCGGAGCTCTCCCGGCTGATGAGAGCTTTTTCGAGAGGATCTTT	2993						
DB	2518	TTCTACGCTCTTGTAACTCTTCAAACTTTCACAACTTTCGCAACAAATGTTGAGTCAATCTG	2577						
QY	2994	CGAAGCCCTATGAAGTTTTCACACAGCCGCCACAGGAGGATCTCAACAGGTTTTC	3053						
DB	2578	AAAGCTCGGATTAATTCCTTGTATGAATAATCAATAGGAAGAAATTTTAAATCGTTCTCC	2637						
QY	3054	AAAGACATGGATGAAGTTGACGCTGGGCTGCGGCTCCAGCGGAGATGTTTCAATCCAGAAC	3113						
DB	2638	AAAGACATTTGACACTTGGATGATTTGCTGCGCTGACCTTTTAGATTTTCATCCAGACA	2697						
QY	3114	GTTATCTGGTGTCTTCTGTGTGGAAATGATCGCAGGAGTCTTCCCGTGGTTCCTTTG	3173						
DB	2698	TTGCTACAAGTGGTGGTGTCTGTGGCTGTGGCTGATTCCTTTGGATCGCAATA	2757						
QY	3174	GCAGTGGGCGCTTGTCTATCTCTTTTTCAGTCTCTGCAATTTCTCCAGGCTCTGAT	3233						
DB	2758	CCCTTGGTTCCTTGGAAATCAATTTTCTTCTCGCGATATTTTGGAAACGTCA	2817						
QY	3234	CGGAGCTGAAGCTGTGGACAATATCAGCAGTACCTTTCTCTCCACATCAGCTCC	3293						
DB	2818	AGAGATGGAAGCGCTGGAATCTACAATCGAGTCCAGTGTTCCTCCACTTGTCTATCT	2877						
QY	3294	AGCATACAGGCGCTTCCACCATCCAGCTTACAATAAAGGCGAGGATTTCTTCACAGA	3353						
DB	2878	TCTCTCCAGGCGCTCTGGACCATCGGCAATACAAAGCAGAGAGGTTCTCAGGAATG	2937						
QY	3354	TACAGGAGCTCTGGATGACAACCAAGTCTCTTTTGTGTACGTGTGGATGGG	3413						
DB	2938	TTTGATGACACAGGATTTACATTCAGAGGCTGGTCTTGTGTGTGTGTGTGTGTGTGT	2997						
QY	3414	TGGCTGGCTGTGGCTGACCTCATCAGCATCGCCCTCATACACACAGGCGCTGATG	3473						
DB	2998	TGGTTGCGGCTCGTCTGGATGCCATCTGTGCTGCTGTGTGTGTGTGTGTGTGTGTGT	3057						
QY	3474	ATCGTCTTATGACGCGGAGATTTCCCGAGCTATCGCGGCTCTCGCCATCTCTTATGCT	3533						
DB	3058	TCCCTGATCTCGCAAAACTCTGGATCGCGGAGGTTGGTTGGCACTGTCTCTATGCC	3117						
QY	3534	GTCCAGTTAACGGGCTGTTCAGTTTACGGTTCAGACTGGCATCTCAGACAGAGCTCGA	3593						
DB	3118	CTCAGCTCATGGGATGTTTTCAGTGTGTGTGCAAAAGTGTGAGTGTGAATAATG	3177						
QY	3594	TTCACTCGGTGGAGGATCAATCACTACATTAAGACTCTGTCTTGGAGGACCTGCC	3653						
DB	3178	ATGATCTCAGTAGAAGGCTGATTAATACACAGACTT-----GAAAGAGGACCT	3231						
QY	3654	AGAATTAAGAACAGCTCTCCCTGCTGATGCTGCGCCAGAGGAGGAGTGTGAGTGTGAG	3713						
DB	3232	TGGGAATATCAGAAACGCCCAACACAGCTGGCCCATCATGAAGGATGATAATCTTTGAC	3291						
QY	3714	ACGAGAGATGAGTACCGAGAAACCTCTCTTGTCTTAAAGAAAGTATCTTCAAG	3773						
DB	3292	ATTTGAACTTCTATGTACAGTCCAGTGGGCTCTGCTTCTGTAAGGATCTGACAGACTC	3351						
QY	3774	ATCAAACTTAAAGAGAGATTTGGCATTGTGGGCGGACAGGATCAGGAGTCTCTGCTG	3833						
DB	3352	ATTAATCACAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAGAAAGTCTCCCTC	3411						
QY	3834	GGGATGGCCCTCTCTGCTGTGGATTTATCTGGAGGCTGCTCAAGATTTGATGAGTG	3893						
DB	3412	ATCTCAGCCCTTTTAGATTGTGACA--ACCCGAAGTAAATTTGGATTGATAAGATC	3468						
QY	3894	AGAATCAGTATTTGGCCCTTGGCCAGCTCCGAGCAAACTCTCTATCATCTCAGAG	3953						

Db 3469 TTGACAACTGAAATGGACTTCACGATTTAAGGAAGAAAAATGTCATCATACCTACAGGNA 3528
Qy 3954 CCGGTGCTGTTTCAGTGGGACACTGTCAGATCAAAATTTGGACCCCTTCAACACAGTACACTGAA 4013
Db 3529 CTTGTTGTTTCTACCTGGAACAAATGAGGAACAACTGGATCCCTTTAATGAGCACACGGAT 3588
Qy 4014 GACCAGATTTGGGATGCCCTGGAGAGGACACATGAAAGAAATGTTATGCTCAGCTACCT 4073
Db 3589 GAGGAACCTGTGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCCCT 3648
Qy 4074 CTGAACCTTGAATCTGAAGTATGAGAGAAATGGGATAACTTCTCAGTGGGGGAACGGCAG 4133
Db 3649 GGTAAATGGTACTGAAATAGCAGAAATCAGGATCCCAATTTTAGTGTGGACAAAGACAA 3708
Qy 4134 CTCCTGTCATAGCTAGAGCCCTGCTCGGCCACTGTAAGATTCGTATTTAGATGAAGCC 4193
Db 3709 CTGGTGTGCCCTTGGCAGGGCAATTTCTCAGGAAGAAATCAGATATTGATTTATGATGAAGCG 3768
Qy 4194 ACAGCTGCCATGGACACAGACAGACTTATTGATCAAGAGACCATCCGAGAAAGCATTT 4253
Db 3769 ACGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGGGAGAAATTT 3828
Qy 4254 GCAGACTGTACATGCTGACCAATGCCCATCGCCCTGCACACGGTTCTAGGCTCCGATAGG 4313
Db 3829 GCCCACTGCACCGTCTAAACCATTTGCACACAGATTGAACACCAATTATTGACAGCGACAAG 3888
Qy 4314 ATTATGCTGTCGCCAGGACAGCTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCPC 4373
Db 3889 ATAATGCTTTAGATTTCAGGAAGACTGAAGAATATGATGAGCGGTATGTTTTCGTCGAA 3948
Qy 4374 AACCAAGTTTCCCGATCTTATGCCATGTT 4402
Db 3949 AATAAGAGAGCCCTATTTTACAAGATGTT 3977

RESULT 6

US-09-780-669-536
; Sequence 536, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)....(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-536

Query Match 7.5%; Score 435.8; DB 10; Length 6140;
Best Local Similarity 48.8%; Pred. No. 3.4e-89;
Matches 1243; Conservative 0; Mismatches 1297; Indels 9; Gaps 2;

Qy 1854 ACATGTCACAGATCGATCTGGAGATCCAAAGAGGTAAATGGTTGGAATCTGCGGCAGT 1913
Db 1438 ACTCTACAAGGCTTTCCTTTACTGTGACACCTGCGGAATTTGTAGCTGTGTCGGCCCC 1497
Qy 1914 GTGGGAAGTGGAAAAACCTCTCTCATTTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAG 1973
Db 1498 GTGGGAGCAGGGAAGTCACTGTTAAGTGCCTGCTCGGGGAATTTGCCCCCAAGTCAC 1557
Qy 1974 GGCAGCATTTGCAATCAGTGGAACTTCGCTTATGTGGCCACGACGCTGGATCCTCAAT 2033
Db 1558 GGGCTGGTCAGCGTCCATGGAAAGATTCCTATGTCTCAGCAGCCCTGGGTGTTCTCG 1617
Qy 2034 GCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCT 2093
Db 1618 GGAATCTGAGAGTAATATTTATTTGGGAAGAAATACGAAAGGACGATATGAAAAA 1677
Qy 2094 GTGCTGAACAGCTGCTGCTGAGGCCCTGACCTGGCCATTTCTCCAGCAGCCAGCTGACG 2153
Db 1678 GTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGTGACT 1737
Qy 2154 GAGATTGAGAGCGAGGAGCCAACTGAGCGGTGGCGAGCCGAGAGGATCAGCCTTGCC 2213
Db 1738 GTGATAGGAGATCGGGGAACCCAGCTGAGTGGAGGAGGAGAAAGCAGCGTAAACCTTGA 1797
Qy 2214 CGGCTTTGTATAGTACAGAGGACATCTACATCTCTGGAGCAGCCCTCAGTCCCTTAGAT 2273
Db 1798 AGACAGTGTATCAAGATGCTGACATCTATCTCTGGAGGATCTCTCAGTGCAGTAGAT 1857
Qy 2274 GCCATGTGGCAACCACATCTTCAATAGTGTATCCGGAACACATCTCAAGTCCCAAGACA 2333
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Qy 2334 GTTCTGTTTGTACCCACAGTTACAGTACCTGGTGTGATGTGATGAAGTATCTTCATG 2393
Db 1918 ACAATTTAGTACTCATCATCTGAGTACCTCAAGCTGCAAGTCAAGTCTGATCTGATATG 1977
Qy 2394 AAAGAGGCTGTATTACGGAAGAGGCCACCCATGAGGAACATGATGAATTTAAATGGTGAC 2453
Db 1978 AAAGATGTTAAATGGTGCAGAGGGGACTTACACTGAGTTCTTAAATCTGGTATAGAT 2037
Qy 2454 TATGCTACCATTTTATAACCTGTTGCTGGAGAGACACCCGAGTTGAGATCAATTCAT 2513
Db 2038 TTTGGCTCCCTTTTAAAGAGGATAATGAGGAAAGTGAACAACCTCCAGTTCAGGAATC 2097
Qy 2514 AAAAAGAAACACAGTGTTCACAGAAGAGTCAACAGACAGGGTCTTAAACAGAGATCA 2573
Db 2098 CCCACATAGGAATCGTACCTCTCAGAGTCTTCGGTGTTCAGCAACATCTTCTAGA 2157
Qy 2574 GTAAAGAGGAAAAAGCAGTAAAGCCAGAGGAGGAGGAGCTTGTGACAGTGAAGAGAAA 2633
Db 2158 CCCTCCTTGAAGATGTTGCTCTGGAGAGCCAAAGATCAGAGAATGTCCAGTTACACTA 2217
Qy 2634 GGGCAGGTTCAAGTGCCTTGTGCTAGTATATGTTGTCTACATCCAGGCTGTGGGGGCCCC 2693
Db 2218 TCAGAGGAGAAACCGCTTCTGAAGGAAAAAGTTGGTTTTCAGGCTTATAAGAAATTTACTT 2277
Qy 2694 TTGTCATCTCTGTTTATTATGTCCTTTTTCATGCTGATGTAGGAGCAGCCGCTTACG 2753
Db 2278 GCTGGTCTCAGTGGATTTGCTTTCATTTTCTTCTTAAACACTGACGCTCAGGTT 2337
Qy 2754 ACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAGGAGGAGGAGTGTGCTGACTCGAGG 2813
Db 2338 GCCTATGCTTCAAGATTTGGTGGCTTTCATCTAGTGGCAACAAACAAAGTATGCTAAT 2397
Qy 2814 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCTACTATGCCAGC 2873

Db 2398 GTCACTGTAATGGAGGAAATGTAACCGAGAGCTAGATCTTAACCTGGTACTTAGGA 2457
Qy 2874 ATCTAGGCCCTCTCCATCGGAGTCACTGATCCTGGAAGCCATTCGAGGAGTTGCTTTT 2933
Db 2458 ATTTATTCAGGTTAACTGTAGTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGGTA 2517
Qy 2934 GTCAAGGCGCGCTCGAGCTTCCTCCCGGTGCATGACGAGCTTTTCCGAAGGATCCCT 2993
Db 2518 TTCTACGCTCTTTGTAATCTTCAACAATTTGCAACAATAATGTTGAGTCAATCTG 2577
Qy 2994 CGAAGCCCTATGAAGTTTTTACACGACGCCACACAGGAGGATTTCTCAACAGGTTTTCC 3053
Db 2578 AAAGCTCCGGTATTATCTTTGATAGAAATCCAAATAGGAAGAAATTTAAATCGTTCTCC 2637
Qy 3054 AAAGACATGGATGAAGTTGACGTGGCGCTGCGGTCCAGCCGAGATGTTCAATCCAGAAC 3113
Db 2638 AAAGACATTTGGACACTTGGATGATTGCTGCGCTGACGTTTTTATGATTTCAATCCAGACA 2697
Qy 3114 GTTATCCTGGTCTTCTGTGTGGAAATGATCGCAGGAGTCTTCCGCTGGTTCCCTTGTG 3173
Db 2698 TTGCTACAAAGTGGTGTGCTCTGTGGCTGTGGCGCTGATTCCTTGGATCGCAATA 2757
Qy 3174 GCAGTGGGCCCCCTTGTATCCTCTTTTCACTCCTGACATTTGTCTCCAGGCTCTGATT 3233
Db 2758 CCCTTGGTCCCTTGGAAATCATTTTCAATTTCTTCGGCGGATATTTTGGAAACGTCA 2817
Qy 3234 CGGAGCTGAAGCGCTGTGCAATATACCGAGTCACTTCTCTCCACATCAGTCC 3293
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Qy 3294 AGCATACAGGCGCTTGCACCATCACCGCTTACATAAAGGCGAGGATTTCTGACACAGA 3353
Db 2878 TCTCTCCAGGCGCTCGACCATCGGCGATACAAAGCAGAGAGGTTCTCAGGAATG 2937
Qy 3354 TACCAGGAGCTGCTGGATGACAAACAGCTCCTTTTTTTTGTACGTGCGATGCGG 3413
Db 2938 TTTGATGCACACAGGATTTACATTCAGAGGCTTGGTTCTTGTGTTGACAAAGTCCCGC 2997
Qy 3414 TGGCTGCTGCGGCTGGACCTCATCAGCATCGCCCTCATCACACACGCGGCTGATG 3473
Db 2998 TGGTTGCGCGCTCGCTGATGCCATCTGTGCGCATGTTTGTATCATCATGCTTCCCTTGGG 3057
Qy 3474 ATCGTCTTATACACGCGGAGATTCGCCAGCTATGCGGGTCTGCCATCTCTTATGCT 3533
Db 3058 TCCCTGATTCGGAAAAAATCTGATGATCGCGGAGGTTGGTTGGCACTGCTCTATGCC 3117
Qy 3534 GTCCAGTTAAACGGGCTGTTCCAGTTTACGGTCAAGTGGCATCTGAGACAGAAGTCA 3593
Db 3118 CTCACGCTCATGGGATGTTTCAGTGGTGTGTTGCAAAAGTCTGAAGTTGAGAATATG 3177
Qy 3594 TTCACCTCGGTGGAGGATCAATCACTACATTAAGACTCTGTCTTGAAGCACTGCC 3653
Db 3178 ATGATCTCAGTAAAGGCTATTGAATACACAGACCTT-----GAAAGAAAGCACCT 3231
Qy 3654 AGAATTAAGAAAGCTCCCTCCCTGACTGGCCCGGAGGAGGAGGCTGACCTTTGAG 3713
Db 3232 TGGGAATATCAGAAAGCCACCCAGCTGAGGCTGGCCCATGAGGAGTGATATCTTTGAC 3291
Qy 3714 AACGAGAGATGAGTACCGAGAAACCTCCCTCTTGTCTTAAAGAAAGTATCCTTACG 3773
Db 3292 AATGTGAATCTCATGTACAGTCCAGTGGGCTCTGTTGCAAAAGTCTGAAGCATCTGACAGCACTC 3351
Qy 3774 ATCAACCTTAAGAGAAGATTGGCATTTGGGCGGACAGGATCAGGAGTCCCTGCTG 3833
Db 3352 ATTAATAACAAAGAAAGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTC 3411
Qy 3834 GGGATGGCCCTCTCCGCTGCTGGAGTTATCTGAGGCTGCAATCAAGATTGATGAGTG 3893
Db 3412 ATCTCAGCCCTTTTATGATTTGTCAGA---ACCGAAGGTAATAATTTGGATTTGATAAGATC 3468
Qy 3894 AGAATCAGTGATATTGGCCCTTGGCCACCTCCGAAAGCAAACTCTCTATCATTTCTCAAGAG 3953

Db 3469 TTGCACAACTGAATTTGGACTTTCAGATTTTAAGGAAGAAAAATGTCAATCATACCTCAGGAA 3528
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Qy 4014 GACCAGATTTGGATGCCCTCGGAGGACACATCAAGAAATGATTTGCTCAGCTACCT 4073
Db 3589 GAGGAATCTGGAATGCCTTACAAGAGGTACAACCTTAAAGAAACCATTTGAAGATCTTCT 3648
Qy 4074 CTGAACCTTGAATCTCAAGTGTGGAGATGGGATTAACCTTCTCAGTGGGGGACGCGAG 4133
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Qy 4134 CTCTCTGTATAGTACGAGCCCTCGCCACTGTAAAGATTTCTGATTTTGTAGATGAAGCC 4193
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Qy 4194 ACAGCTGCCATGACACAGACAGACTTATGATTTCAAGAGACCATCCGAGAGCAATTT 4253
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Db 3829 GCCCACTGCACCGTGTAAACCATTTGCACACAGATTTGAACACCATTTATGACAGCGACA 3888
Qy 4314 ATTTGCTGTGCGCCAGGACAGGTGGTGGAGTTTGCACACCCCATCGGCTCTCTGTC 4373
Db 3889 ATATGTTTATGATTCAGGAAGACTGAAAGATATGATGATGATGATGATGATGATGATG 3948
Qy 4374 AACGACAGTTCCCGATTTCTATGCCATGTT 4402
Db 3949 AATAAAGAGAGCCCTATTTTACAAGATGTT 3977

RESULT 7
US-09-822-827-536
; Sequence 536, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-822-827-536

Query Match 7.5%; Score 435.8; DB 10; Length 6140;
Best Local Similarity 48.8%; Pred. No. 3.4e-89;
Matches 1243; Conservative 0; Mismatches 1297; Indels 9; Gaps 2;

Qy 1854 ACATCTCACAGCATCGATCTGGAGATCCAAAGAGGTAACCTGGTTGCAATCTCGGCAGT 1913
Db 1438 ACTCTACAGGCCCTTCTCTTACTGTGTCAGACCTGGCGAATTTAGTGTGTCGCCCC 1497
Qy 1914 GTGGAGTGGAAAAACCTCTCTCATTTAGCCCAATTTAGCCAGATGACGCTTCTAGAG 1973
Db 1498 GTGGAGGAGGAGTCACTACTGTTAAGTCCGCTGCTCGGGGATTTGGCCCCAAGTCAC 1557
Qy 1974 GGCAGCATTCATCAGTGAACCTTCGCTTATGTGCCCCAGCAGGCTTGATCCTCAAT 2033
Db 1558 GGGCTGTGTCAGCGTGCATGGAAGAAATTCCTATGTCTCAGACGCTTGGTCTTCG 1617

Qy	2034	GCTACTCTGAGACACACATCCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACCTCT	2093
Db	1618	GAACCTCTGAGGAGTAATAATTTTATTTTGGGAAGAATAACGAAAGAACGATATCAAAA	1677
Qy	2094	GTGCTGAACAGCTGTCGCCCTGAGGCCCTGACCTGGCCATTCCTTCCAGCAGCGACCTGACG	2153
Db	1678	GTCTAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACT	1737
Qy	2154	GAGATTGGAGCAGGAGAGCCACCTGAGCGGTGGGCGACGCCACAGAGATCAGCTTGCC	2213
Db	1738	GTGATAGAGATCGGGAAACCGCTGAGTGGAGGCGAGAAGCAGCGGTAAACCTTGCA	1797
Qy	2214	CGGCCCTTGATAGTGACAGGAGCATCTACATCTCTGGACGCCCTCAGTGCCTTAGAT	2273
Db	1798	AGACAGTGTATCAAGATGCTGACATCTATCTCTGGAGGATCCTCTCAGTGCAGTAGAT	1857
Qy	2274	GCCATGTGGGCACCAACCATCTTTCAATAGTGTATCTCCGGAACAATCTCAAGTCCAAGACA	2333
Db	1858	CGCGAAGTTAGCAGACACTGTTTCGAACCTGTGTATTTGTCAAATTTTGCATGAGAAGTC	1917
Qy	2334	GTCTGTTTCTTACCACACAGTACAGTACCTGGTTGACTGTGATGAGTCAATCTTCAATG	2393
Db	1918	ACAAATTTAGTGACTCATCAGTTGCGTACCTTCAAGCTGCAAGTCAAGTCTCGATATTG	1977
Qy	2394	AAAGAGGCTGTATTACGGAAGAGCGACCCATGAGGAACGTATGAATTTAAATGGTGAC	2453
Db	1978	AAAGATGTTAAATGTCAGRAGGGGACTTACACTGAGTTCTTAAATCTGGTATPAGAT	2037
Qy	2454	TATGCTACCAATTTTTAATACCTGTTGCTGGGAGAGACACCGCGAGTGTGAGATCAATPCA	2513
Db	2038	TTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAGTGAACAACCTCCAGTTCCTCAGGAAC	2097
Qy	2514	AAAAAGGAACACAGTGGTCTCAGRAGRAGTCAACRAGACRAGGCTCTTAAACAGGATCA	2573
Db	2098	CCCACTAAGGAATCGTACCTCTCAGAGCTTCGCGTTTGGTCTCAACAATCTTCTPAGA	2157
Qy	2574	GTAAGAAGGAAGAACAGCTAAAGCCAGAGGAAGGCGACGTTGTCCAGCTGGAAGAGAAA	2633
Db	2158	CCCTCTTTGAAGATGTTGCTCTGGAGAGCCAAAGATACAGAGATGTCCCAAGTTACACTA	2217
Qy	2634	GGGAGGTTTCACTGCCCTTGTCAGTATATGAGTGTCTACATCCAGGCTGCTGGGGGGCCC	2693
Db	2218	TCAGAGGAGAACCGGTTCTGAAGGAAAGTTGGTTTTCAGGCGCTATAAGAATTTACTTCAGA	2277
Qy	2694	TTGSCATTTCTGGTTATTATGCGCCTTTTTCATGCTGATGTAGCCAGCAGCGCCTTCAGC	2753
Db	2278	GCTGGTGCTACRGGATGTCTCAATTTTCCCTATTCTCCCTTAAACACTCGAGCTCAGGTT	2337
Qy	2754	ACCTGTGGTTGAGTTTACTTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGG	2813
Db	2338	GCCTATGTCTCAAGATTGGTGGCTTTCATCTGAGGCAACAAAGATATGCTTAAT	2397
Qy	2814	AACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGC	2873
Db	2398	GTCACTGTAAATGGAGGAGAAATCTAAACGAGAAGCTAGATCTTAACTGGTACTTAGGA	2457
Qy	2874	ATCTACGCCCTCTCCATGTCAGTCACTGCTGATCTCTGAAAGCCATTCAGGAGTGTGCTTT	2933
Db	2458	ATTTATTAGGTTTAACTGTACTACCGTCTCTTTTGGCATPAGCAAGATCTCTATTGGTA	2517
Qy	2934	GTCAAGGCGACGCTGGAGCTTCTCCCGGCTGCTACGAGCTTTTCCGAAAGATCCCT	2993
Db	2518	TTCTACGTCCTTGTAACTCTTCACAACTTTGACACACAAATGTTTGAGTCAATCTCG	2577
Qy	2994	CGAAGCCCTATGAAGTTTTTTCACACAGACCCGCCACAGGAGGATTTCTCAACAGGTTTCC	3053
Db	2578	AAAGCTCCGGTATTATCTTTGTATGAAATCCAAATAGGAAGAAATTTTAAATCGTTCTCC	2637
Qy	3054	AAAGACATGGATGAAGTTACGTGGCGCTGCGGTTCCAGCGCCGAGATGTTTCATCCAGAAC	3113
Db	2638	AAAGACATTGGACATTTGATGATTTGGCGCTGACGTTTTTTAGATTTTCATCCAGACA	2697

QY	3114	GTTATCCCTGGTCTTCTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCTCTTG	3117
DB	2698	TTGCTACAAGTGGTGTGGTGTCTGTGTGGTGTGGCGGTGATCTCTTGGATCGCAATA	2757
QY	3174	GCAGTCGGGCGCCTTCTGCATCCTCTTTTTCAGTCTCTGCACATGTCCTCCAGGAGTCC	3233
DB	2758	CCCTTGGTTCCTCTTGGAAATCATTTTTCATTTTCTTCGGCGATATTTTGTGGAAACGT	2817
QY	3234	CGGGAGCTGAAGCGTCTGGACAAATATACGCAGTCACTTTCCTCTCTCCACATCAGTCC	3293
DB	2818	AGAGATGTGAAGCGCTGGAATCTACAACCTCGGAGTCCAGTGTTCCTCCACTGTCTATCT	2877
QY	3294	AGATACAGGGCCTTGCCACCATCCAGCCTACAATAAAGCGCAGGAGTTCTTCACACAGA	3353
DB	2878	TCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAAGAACTG	2937
QY	3354	TACCAGGAGCTGCTGGATGACAAACCAAGTCTCTTTTTCATTTTGTTCGGCGATATTTT	3413
DB	2938	TTTGATGACACACAGGATTTACATTCAGAGGCTTGGTTCTTGTTCATCAATGTCGCGC	2997
QY	3414	TGCGTGGCTGTGGCGTGGACCTCATCAGCATCGCCCTCATCACCAACCGGGGCTGATG	3473
DB	2998	TGGTTCGGCGTGGCTGTGATGCCATCTGTGCCATGTTTGTTCATCAATGCTTGGCTTGGG	3057
QY	3474	ATCGTCTTTATGACGGGCGAGATTCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCT	3533
DB	3058	TCCTTGATTCGGCAAAACTCTGGATGCGGGCAGGTTGGTTTGGCACTGTCTATGCC	3117
QY	3534	GTCCAGTTAACGGGGCTGTTCAGTTTACGTCAGACTGGCATGGCATCTGAGACAGAAGCTCGA	3593
DB	3118	CTCAGCTCATGGGATGTTTCAGTGTGTGTTCGACAAAGTCTGAAGTTGAGAATATG	3177
QY	3594	TTCACTCGGTGTGGAGGATCAATCACTACATTAAGACTCTGTCTTGGAGCAACCTGCC	3653
DB	3178	ATGATCTCAGTAGAAGGTCATTGATACACAGACCTT-----GAAAGAAAGCACCT	3231
QY	3654	AGAAATTAAGAACAGGCTCCCTCCCTGACTGGCCCCAGGAGGAGAGGTGACCTTTGAG	3713
DB	3232	TGGGAATATCAGAAACGCCACACACCAGCTGTGGTCTGAGGAGTGATATCTTTGAC	3291
QY	3714	TAACGAGAGATCAGGTACCGAGAAACCTCCCTCTGTCTCTTAAGAAAGATTCCTTCAGC	3773
DB	3292	AATGTGAACCTCATGTACAGTCCAGGTGGCGCTCTGGTACTGAAGCATCTGCAGCACCTC	3351
QY	3774	ATCAAACTTAAGAGAAGATTTGGCATTTGTGGGGGACAGGATCAGGGAAGTCTCGCTG	3833
DB	3352	ATTAATACAGAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGGAAGAGTTCCCTC	3411
QY	3834	GGGATGGCCCTCTCCGTCTGTGTGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTG	3893
DB	3412	ATCTCAGCCCTTTTAGATTGTGAGA--ACCCGAAGGTAAAAATTTGGATTGATAAGATC	3468
QY	3894	AGAACTAGTGATTTGGCCTTGCCACCTCCAGCAAACTCTCTATCATCTCTCTCAAGAG	3953
DB	3469	TTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCATCTCTCAGGAA	3528
QY	3954	CCGTGCTGTTTCAGTGGCACTCTCAGATCAAAATTTGGACCCCTTCAACCAGTACACTGAA	4013
DB	3529	CCTGTTTGTCTCACTGGAAACATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGAT	3588
QY	4014	GACCAGATTTGGGATGCCCTGGGAGGACACATCAAGAAATGTATTGCTCAGCTACCT	4073
DB	3589	GAGGAACGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCT	3648
QY	4074	CTGAACCTTGATCTGAAGTGTAGAGAAATGGGGTAACCTTCTAGTGGGGGAACGGCAG	4133
DB	3649	GGTAAATTTGGTACTGAAATTAACAGAAATCAGATCAAGATCCCAATTTTAGTGTGGACA	3708
QY	4134	CTCTGTGCATAGCTAGAGCCCTGTCCGCCACTGTNAGATTCTCATTTTACATGAAGCC	4193
DB	3709	CTGTGTGCCCTTGCCAGGGCAATCTCAGGAAAAATTCAGATATTGATATTGATGAAGCG	3768
QY	4194	ACAGCTGCCATGGACACAGACAGACTTTATTGATTCAAGACACCATCCGAGAAGCATTT	4253

Db 3769 ACGCAAAATGGATCCAGAACTGATGAGTTAATACAAAAAATCCGGGAGAAATTT 3828
QY 4254 GCAGACTGTACCATGCTGACCATCCCATCGCTGCACACAGTTCTAGGCTCCGATAGG 4313
Db 3829 GCCCACTGCACCGCTCAACCATTCACACAGATTGAACACCATTTATGACAGCCACAG 3888
QY 4314 ATTATGTGCTGGCCCGACGAGCTGGTGGAGTTTGAACCCCATCGGTCCTCTGTGC 4373
Db 3889 ATAATGGTTTATGATTCAGGAAGACTGAAAGAAATATGATGAGCCCTATGTTTGTGCA 3948
QY 4374 AACGACAGTTCCTCCGATTTCTATGCCATGTT 4402
Db 3949 AATAAGAGAGCCCTATTTTACAAGATGGT 3977

RESULT 8

US-10-012-896-535
; Sequence 535, Application US/10012896
; Publication No. US20020183251A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-012-896-535
Query Match 7.3%; Score 425.4; DB 9; Length 6082;
Best Local Similarity 48.8%; Pred. No. 7.8e-87;
Matches 1243; Conservative 0; Mismatches 1296; Indels 10; Gaps 3;

QY 1854 ACATGTCACATCATGCTGGAGATCCAGAGGTAACCTGGTTGGAATCTCGGSCAGT 1913
Db 1464 ACTCTACAAAGCCCTTTCCTTTACTGTACACCTGGCGAATTTTACTGTGTCGCGCCCC 1523
QY 1914 GTGGAACTGGAAAACTCTCTCATTTTCAGCCATTTTAGGCGAGATGACGCTTCTAGAG 1973
Db 1524 GTGGAGAGGGAAGTCACTGTTAAGTGGCTGCTCGGGAATTTGCCCAAGTCAC 1583
QY 1974 GCGACATTTGCAATCAGTGAACCTTCGCTTATGTGGCCCGACGAGCCCTGGAATCCTCAAT 2033
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QY 2034 GCTACTCTGAGACACAACATCTCTGTTTGGAGAAATATGATGAAGAAAGATACAACTCT 2093
Db 1644 GGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAAAAGGAAACGATATGAAAA 1703
QY 2094 GTGCTGAACAGCTGCTGCTGAGCCCTGACCTGGCCATCTTCCAGCAGCAGCCTGACG 2153
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QY 2214 CGGGCTTCTATATAGTACAGAGGAGCATCTACATCTCGACGACCCCTCAGTGCCTTAGAT 2273
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QY 2274 GCCCATGTGGGCAACACACATCTTCAATAGTGTATTCGGGAAACATCTCAAGTCCAAGACA 2333
Db 1884 GCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTAATTTGTCAAAATTTTGCATGAGAAGATC 1943
QY 2334 GTTCTGTTTGTACCCACAGTTACAGTACCTGTTGACTGTGATGAAGTATCTTTCATG 2393
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QY 2394 AAAGAGGCTGTATTACGGAAGAGGACCCCATGAGGAACTGATGAATTTAAATTTGTTGAC 2453
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QY 2454 TATGCTACCATTTTAAATACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTC 2513
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QY 2634 GGGCAGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2693
Db 2244 TCAGAGAGGAAACCGTCTCTGAAGGAAAGTGGTTTTCAGGCCCTATAAGAAATTTACTTCA 2303
QY 2694 TTGGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2753
Db 2304 GCTG 2363
QY 2754 ACCTG 2813
Db 2364 GCCTATGCTTCAAGATTTGCTGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2423
QY 2814 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAACTCTCATATGCAAGTACTATGCGCAGC 2873
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QY 2994 CGAAGCCCTATGAAGTTTGTGACAGACCCCGAGGAGGATTTCTCAACAGGTTTCTC 3053
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 QY 2154 GAGATTGGAGGAGGAGGAGCAACCTGAGGGTGGGCGCCAGAGGATCAGCTTGGC 2213
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 Db 1824 AGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAGCATCTCTCAAGTGTGAGTAGAT 1883
 QY 2274 GCCCATGTGGCAACACATCTTCAATAGTGTATCCGGAAACATCTCAAGTCCCAAGACA 2333
 Db 1884 GCGGAAGTGTAGCAGACATGTTTGCAGACTGTGTATTTGTCAAAATTTTGCATGAGAAGATC 1943
 QY 2334 GTTCTGTGTTTACCACACAGTTCACAGTACCTGTGTGACTGTGATGAAGTGTCTTCATG 2393
 Db 1944 ACAATTTAGTACTCATCAGTTGCGAGTACTCAAGTCTCAAGTCTGATTCATGATTTG 2003
 QY 2394 AAGAGGGCTGTATTACGGAAGAGGACCCCATGAGGAATGATGAATTTAAATGTGTAC 2453
 Db 2004 AAGATGGTAAATGGTGCAAGAGGACTTACATGAGTTCCTAAATCTGGTATAGAT 2063
 QY 2454 TATGCTTACCAATTTTAAATACCTGTTCTGGGAGAGACCGCCAGTGTGATCAATTTCA 2513
 Db 2064 TTTGGCTCCCTTTTAAAGAGGATAATGAGGAAGTGAACAACCTCCAGTTCACGGAAC 2123
 QY 2514 AAAAAGGAACAGTGGTTCACAGAAGACTCAAGACAGAGGTCTCTAAACAGAGTCA 2573
 Db 2124 CCCACACTAAGGAATCGTACTCTCAGAGTCTTCGCTTGGTCTCAACAATCTTCTAGA 2183
 QY 2574 GTAAGAAGGAAGAAAGCAGTAAAGCCAGAGGAGGCGAGCTGTGACGTGGAGAGAAA 2633
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 Db 2304 GCTGGTCTCACTGGATGTCTTCATTTCTTCTTCTTAAACATGCTGAGCTCAGGTT 2363
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 Db 2364 GCCTATGTGCTTCAAGATTTGGTGGCTTTCATCTGAGGCAAGCAAGGATGCTAAAT 2423
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 Db 2724 TTGCTACAAGTGGTGTGGTGTCTGTGCTGTGGCGGTGATTCCTTGGATCGCAATA 2783
 QY 3174 GCAGTGGGGCCCTGTGTCATCTCTTTCAGTCTCTGACATGTTGCTCCAGGGTCTCTGAT 3233
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QY 3234 CGGAGCTGAAGCGCTGTGGCAATATCACGAGTACACCTTCTCTCCCATCATACGTC 3293
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 Db 3144 CTCAGCTCATGGGATGTTTTCAGTGGTGTGTGACAAAGTGTGAAGTTGAGAAATG 3203
 QY 3594 TTCACTCGGTGGAGAGATCAATCACTACATTAAGACTCTGTCTTGGAGACACTGCC 3653
 Db 3204 ATGATCTCAGTGAAGGGTCTATTGAATACAGACCTT-----GAAAGAGACACT 3257
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 QY 3774 ATCAAACTTAAGAGAGATTTGGCATTTGGGCGGAGAGGATCAGGAAAGTCTCTCGTG 3833
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 QY 3894 AGAATCAGTGTATTTGGCTTGGCGACCTCGCAACCACTCTCTATCATCTCTCAAGAG 3953
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DB 2964 TTTGATGCACACAGAGTTTACATTCAGAGGCTTGTGTTTGTGTTTGTGACAGCTCCCG 3023
QY 3414 TGGCTGGCTGTGGCTGGACCTCATCAGCATCGCCCTCATCACCAACCCAGGGGCTGATG 3473
DB 3024 TGGTGGCGCTGCTGTGATGCCATCTGTGCCATGTTTGTATCATCTGTTGCCCTTGG 3083
QY 3474 ATCGTTTATGACGGGAGATATCCCCAGCCTATGCGGGTCTGCCATCTTATGCT 3533
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QY 3534 GTCCAGTTAACGGGCTGTTCAGTTTACGTTAGCTGGCATCTGACACAGAAAGCTCGA 3593
DB 3144 CTCAGCTCATGGGATGTTTCAGTGGTGTGTCGACAAAGTCTGAAGTTGAGAAATG 3203
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DB 3204 ATGATCTAGTAGAAGGTCTATGATACAGACCTT-----GAAAAGAACACCT 3257
QY 3654 AGAATTAAGAACAGGCTCCCTCCCTGTACTGGCCCGAGGAGGAGGTGACCTTTGAG 3713
DB 3258 TGGGAATATCAGAAACGCCACACCCAGCCTGGCCCATGAAGGATGATATCTTTGAC 3317
QY 3714 AACGACAGATAGGTACCGAGAAACCTCCCTCTGTCTTAAAGAAATATCCTTCAGG 3773
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QY 3774 ATCAAACCTAAAGAGAAGATGGCATTTGGGCGGACAGGATCAGGGAAGTCTCGCTG 3833
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QY 3894 AGAATCAGTATATTGGCTTCCGACCTCCGAAGCAACTCTATCATTTCTCTCAAGAG 3953
DB 3495 TTGCAACTGAAATTTGGACTTCCACATTTAAGGAAGAAATGTCAATCATCTCAGGAA 3554
QY 3954 CCGGTGCTGTTCAGTGGCACTGTCAATCAAAATTTGGGCCCTTCAACCAGTACACTGAA 4013
DB 3555 CCGTTTGTCTGACGTGACATGAGAAACCTGGATCCCTTTAATGACACACGGAT 3614
QY 4014 GACCAATTTGGATGCCCCGTGGAGGACACACATGAAAGAAATGTATGCTCAGCTACCT 4073
DB 3615 GAGGAATCTGGAATGCCCCATAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCC 3674
QY 4074 CTGAACCTGATCTGAAGTATGAGATGGGATTAATCTCAGTGGGGAACGGCAG 4133
DB 3675 GGTAAATGGATGATGATTAACGAATCAGGATCCAAATTTTGTGTTGGCAAAAGACAA 3734
QY 4134 CTCTGTGTGATAGTACGCTGTCTCCGCCACTGTGAAGTTCTGATTTTATGATGAAGCC 4193
DB 3735 CTGTTGTGCTTCCAGGCAATTTCTCAGAAATATCAGATTTATGATGATGAAGCG 3794
QY 4194 ACAGCTGCCATGGACACAGACAGACTTATTTGATTCAGAGACCATCCGAGAAGCATTT 4253
DB 3795 ACCGAAATTTGGATCCCAAGAACTGATGATTAATACAA-AAAAATCCGGGAGAAATTT 3853
QY 4254 GCAGACTGTACCATGCTGACCATTTGCCATTCGCCCTGCACACAGGTTCTAGGCTCCGATGG 4313
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DB 3914 ATATGGTTTTAGATTCAGGAAGACTGAAGAATATGATGAGCCCGTATGTTTTGTGCAAA 3973

QY 4374 AACACAGTTCCCGAATCTATGCCATGTT 4402
DB 3974 AATAAAGAGAGCTATTTTACAAGATGTT 4002

RESULT 11

US-09-822-827-535
; Sequence 535, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-535

Query Match 7.3%; Score 425.4; DB 10; Length 6082;
Best Local Similarity 48.8%; Pred. No. 7.8e-87;
Matches 1243; Conservative 0; Mismatches 1296; Indels 10; Gaps 3;

QY 1854 ACACCTGCACAGCATCGATCGGAGATCCAGAGGGTAACTGTTGGAATCTTGGCGCAGT 1913
DB 1464 ACTCTACAAGCCCTTCTCTTACTGTCTAGACCTGGCGAATTTAGCTGTGGTGGCCCC 1523
QY 1914 GTGGGAAGTGGAAAACCTCTCTCATTTAGCCATTTTAGCCAGATGACGCTTCTAGAG 1973
DB 1524 GTGGGAGCAGGAGTCACTCACTGTTAAGTGGCGTGTCTCGGGGAATTTGGCCCCAAGTCAC 1583
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DB 1584 GGGCTGGTCAAGCTGATGGAAGAAATTTGCTCTCAGCAGCCCTGGGTCTCTCG 1643
QY 2034 GCTACTCTGAGACACATCCTGTTTGGGAAGAAATATGATGAGAAATACAACTCT 2093
DB 1644 GGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAAAGAACGATATGAAAA 1703
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DB 1824 AGAGCAGTGTATCAAGATGCTGATCTATCTCTGGACGATCTCTCAGCTGAGTATAGAT 1883
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DB 1884 GCGGAAGTTAGCAGACATCTGTTGCAACTGTATTTGTCAAAATTTTGCATGAGAAGATC 1943
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RESULT 12

US-09-917-800A-1578

; Sequence 1578, Application US/09917800A

; Patent No. US20020119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917.800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1578
; LENGTH: 4918
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462a1 NM_012833
US-09-917-800A-1578

Query Match 6.78; Score 392; DB 10; Length 4918;
Best Local Similarity 49.4%; Pred. No. 2.8e-79;
Matches 1308; Conservative 0; Mismatches 1235; Indels 105; Gaps 7;
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QY 1897 TTGGAATCTGGCGAGCTGGGAGTGGAAAAACCTCTCTCATTTACGCCATTTTAGGCC 1956
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QY 1957 AGATGACGCTTCTAGAGGCGAGCATGCAATCAGTGGAACTTGCCTTATCTGCGCCAGC 2016
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Db 4656 GAGGTTCC 4663

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RESULT 13

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US-09-880-107-3373
; Sequence 3373, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.

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; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3373
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U49248
; US-09-880-107-3373

Query Match          6.5%; Score 382.2; DB 10; Length 5300;
Best Local Similarity 48.8%; Pred. No. 5e-77;
Matches 1277; Conservative 0; Mismatches 1233; Indels 105; Gaps 5;

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Qy 1914 GTGGAGAGTGGAAAACCTCTCTCATTTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAG 1973
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RESULT 14

US-09-917-800A-479
; Sequence 479, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029

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; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 479
; LENGTH: 5728
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010466
US-09-917-800A-79

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; Sequence 1392, Application US/09938842A
; Patent No. US2002160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepis, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1392

; LENGTH: 4869

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1392

Query Match

Best Local Similarity 6.0%; Score 349.2; DB 9; Length 4869;

Matches 1237; Conservative 0; Mismatches 1233; Indels 78; Gaps 7;

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DB 1951 ACAGGAGAAGAAAAACCTCCCTGATATCTGCTATGCTTGGGGAATCTCTGCAAGATCT 2010

QY 1971 GAGGCGAGCATTTGCAATCAGTGGAACTTTCGCTTATGTGGCCAGCAGGCTGATCCTC 2030

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4724.2	80.9	4781	2	US-03-001-273-1 Sequence 1, Appli
3	4724.2	80.9	4781	4	US-08-843-459A-1 Sequence 1, Appli
4	510	8.7	5011	1	US-08-463-092B-3 Sequence 3, Appli
5	510	8.7	5011	2	US-08-462-109A-3 Sequence 3, Appli
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7	510	8.7	5011	3	US-08-463-179A-3 Sequence 3, Appli
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20	422	7.2	5889	1	US-08-463-092B-5 Sequence 5, Appli
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23	422	7.2	5889	3	US-08-463-179A-5 Sequence 5, Appli
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25	370	6.3	4931	4	US-08-726-320-2 Sequence 2, Appli
26	370	6.3	4931	4	US-09-208-716-2 Sequence 2, Appli
27	346.8	5.9	4877	2	US-08-404-531B-7 Sequence 7, Appli

28 346.8 5.9 4877 2 US-08-404-531B-8 Sequence 8, Appli
29 346.8 5.9 4877 3 US-08-476-900A-7 Sequence 7, Appli
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31 346.8 5.9 4877 3 US-08-488-546A-7 Sequence 7, Appli
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33 344.4 5.9 5175 4 US-08-972-927-4 Sequence 4, Appli
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40 339.2 5.8 463 2 US-09-001-273-3 Sequence 3, Appli
41 339.2 5.8 463 3 US-09-061-400-3 Sequence 3, Appli
42 339.2 5.8 463 4 US-08-843-459A-3 Sequence 3, Appli
43 337.8 5.8 5232 4 US-08-972-927-1 Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-061-400-1
; Sequence 1, Application US/09061400
; Patent No. 6077936
; GENERAL INFORMATION:
; APPLICANT: SHVJAM, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; NUMBER OF SEQUENCES: POLYPEPTIDE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,400
; FILING DATE: 16-APRIL-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-056CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4847 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..4426
US-09-061-400-1

Query Match 82.1%; Score 4792.6; DB 3; Length 4847;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
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DB 1 GGCTCATGCTCGGAGCGGTGTTGAGCGGCTGCGCGGTGTTCTCTGAGGAGGGCGCAG 60

QY 71 GAATTCGTGTAACAACTAAGTCTGTGAGCCCTGGAACTCCCGCTCAGAGAAGATGAA 130
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DB 481 CCACAAAGAGGGGAGCTCTCAATGGAAGAGCTGTGGTCTCTGTCCCAAGCAGAGTCTTC 540
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DB 1201 TACTTACATTAATTTATCAAAATGTATGCTGGGTCAAGACATTTTCTCAGAGTGTTC 1260
QY 1271 AAAAATCCCGAGGAGCGCTGGATATTTGAAAAGCCGGGTACTTCCAGGGTATCAC 1330
DB 1261 GAAAATCCCGAGGAGCGCTGGATATTTGAAAAGCCGGGTACTTCCAGAGCATCAC 1320
QY 1331 TGTGGGTGTGGCTCCCATTTGTGGTGTATGCTCCAGCTGTGGTGTCTCTCTTATAT 1390
DB 1321 TGTGGGTGTGGCTCCCATTTGTGGTGTATGCTCCAGCTGTGGTGTCTCTCTTATAT 1380
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DB 1381 GACCTGTGGCTTCGATCTGCACAGCAGCACAGGCTTTTACAGTGTGACAGTCTTCAATTC 1440
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QY 1511 GGCTGTGACAGATTAAGAGTTTGTCTTAATGGAAGAGTTTACATGATAAAGACAA 1570
DB 1501 GGCTGTGACAGATTAAGAGTTTGTCTTAATGGAAGAGTTTACATGATAAAGACAA 1560
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DB 1681 TTCCAGGGCAAGAAAGAGTGTAGGAGCTGTAGGAGCTGTAGGAGCTGTAGGAGCTGT 1740
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RESULT 2

US-09-001-273-1
; Sequence 1, Application US/09001273
; Patent No. 5954130
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,273
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PENTON, Gillian M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..4360
US-09-001-273-1

Query Match 80.9%; Score 4724.2; DB 2; Length 4781;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4737; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
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QY 1277 CCGGAGGAGAGCGTCCGATTTGGAAGAGCCGGTACTTCCAGGATACACTGTGGG 1336
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Db 2941 CAGCAGCCCGACAGGAGGATTTCTCAACAGGTTTTTCCAAAGACATCGATGAAGTTGACGT 3000
QY 3077 GCGGCTGCGCTTCCAGGCGGAGATGTTTCATCCAGAACGTTATCTCTGGTGTCTTCTGTGTGT 3136
Db 3001 GCGGCTGCGCTTCCAGGCGGAGATGTTTCATCCAGAACGTTATCTCTGGTGTCTTCTGTGTGT 3060
QY 3137 GGAATATGTCGAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTGTGTATCTCT 3196
Db 3061 GGAATATGTCGAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTGTGTATCTCT 3120
QY 3197 CTTTTTCAGTCTGACATGTTCTCCAGGCTCTGATTCGGGAGCTGAAGGCTTGACAAA 3256
Db 3121 CTTTTTCAGTCTGACATGTTCTCCAGGCTCTGATTCGGGAGCTGAAGGCTTGACAAA 3180
QY 3257 TATCAGGAGTCACTTCTCTCCACATCAGTCTCCAGCATACAGGCTTCCAGGCTTCCAGGCT 3316
Db 3181 TATCAGGAGTCACTTCTCTCCACATCAGTCTCCAGCATACAGGCTTCCAGGCTTCCAGGCT 3240

Qy	3317	CCAGCCTACAATAAAGGCGAGGATTTCTGCACAGATACACAGAGCTGCTGGATGACAA	3376
Db	3241	CCAGCCTACAATAAAGGCGAGGATTTCTGCACAGATACACAGAGCTGCTGGATGACAA	3300
Qy	3377	CCAAGCTCCCTTTTTTTTGTGTTACGTGTCGATGCGGTGGCTGGCTGTCGGCGCTGGACCT	3436
Db	3301	CCAAGCTCCCTTTTTTTTGTGTTACGTGTCGATGCGGTGGCTGGCTGTCGGCGCTGGACCT	3360
Qy	3437	CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCTTTATGCACGGGCAGAT	3496
Db	3361	CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCTTTATGCACGGGCAGAT	3420
Qy	3497	TCCCCAGCCTATGCGGGTCTGCCTATCTTTATCCTGCTCCAGTTAAGGGGCTGTTCCA	3556
Db	3421	TCCCCAGCCTATGCGGGTCTGCCTATCTTTATCCTGCTCCAGTTAAGGGGCTGTTCCA	3480
Qy	3557	GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTACCTCGGTGGAGAGGATCAA	3616
Db	3481	GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTACCTCGGTGGAGAGGATCAA	3540
Qy	3617	TCACTACATTAAGACTCTCTCCTTGAAGACCTGCCAGAATTAAAGAACAGGCTCCCTC	3676
Db	3541	TCACTACATTAAGACTCTCTCCTTGAAGACCTGCCAGAATTAAAGAACAGGCTCCCTC	3600
Qy	3677	CCCTGACTGCCCCAGGAGGAGAGGTGACCTTTGAGAACCCAGAGATGAGGTACCGAGA	3736
Db	3601	CCCTGACTGCCCCAGGAGGAGAGGTGACCTTTGAGAACCCAGAGATGAGGTACCGAGA	3660
Qy	3737	AAACCTCCCTTTGTCTTAAAGAAATGATCCCTTACGATCAAACTTAAAGAGAAGATTGG	3796
Db	3661	AAACCTCCCTTCTGCTCTTAAAGAAATGATCCCTTACGATCAAACTTAAAGAGAAGATTGG	3720
Qy	3797	CATTGGGGCGGACAGGATCAGGAAAGTCCCTCGCTGGGGATGCCCTCTTCCGCTGTGGT	3856
Db	3721	CATTGGGGCGGACAGGATCAGGAAAGTCCCTCGCTGGGGATGCCCTCTTCCGCTGTGGT	3780
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Qy	3917	CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGCTGCTTTCAGTGGCACTGT	3976
Db	3841	CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGCTGCTTTCAGTGGCACTGT	3900
Qy	3977	CAGATCAAAATTTGGACCCCTTCAACAGTACACTGAAGACCAGATTTGGGATGCCCTGGA	4036
Db	3901	CAGATCAAAATTTGGACCCCTTCAACAGTACACTGAAGACCAGATTTGGGATGCCCTGGA	3960
Qy	4037	GAGGACACATGAAGAATGTATTGCTCAGTCACTCTGAAACTTCAATCTGAAGTGAT	4096
Db	3961	GAGGACACATGAAGAATGTATTGCTCAGTCACTCTGAAACTTCAATCTGAAGTGAT	4020
Qy	4097	GGAGAATGGGATAACTTCTCAGTGGGGAAACGGCAGCTCTTGTGCATAGTAGCCCT	4156
Db	4021	GGAGAATGGGATAACTTCTCAGTGGGGAAACGGCAGCTCTTGTGCATAGTAGCCCT	4080
Qy	4157	GCCTCCGCCACTGTAGATTCTGATTTTATGATGAAGCCACAGCTGCCATGACACAGAGAC	4216
Db	4081	GCCTCCGCCACTGTAGATTCTGATTTTATGATGAAGCCACAGCTGCCATGACACAGAGAC	4140
Qy	4217	AGACTTTATTGATTCAGAGACCATCCGAGAAGCATTTGACAGCTGTACCATGCTGACCAT	4276
Db	4141	AGACTTTATTGATTCAGAGACCATCCGAGAAGCATTTGACAGCTGTACCATGCTGACCAT	4200
Qy	4277	TGCCCCATCGCCTGCACACCCCATCGGCTCTTCTGCTTCCAAACGACAGTTCCCGATTCTATGC	4336
Db	4201	TGCCCCATCGCCTGCACACCCCATCGGCTCTTCTGCTTCCAAACGACAGTTCCCGATTCTATGC	4260
Qy	4337	GGTGGTGGAGTTTGACACCCCATCGGCTCTTCTGCTTCCAAACGACAGTTCCCGATTCTATGC	4396
Db	4261	GGTGGTGGAGTTTGACACCCCATCGGCTCTTCTGCTTCCAAACGACAGTTCCCGATTCTATGC	4320

[illegible]

LOCATION: 2...4360
US-08-843-459A-1

Query Match 80.9%; Score 4724.2; DB 4; Length 4781;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4737; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 77 TGATGTGAACTACAGTCTGTGAGCCCTGGAACCTCCGCTCAGAGAGATGAAGGATAT 136
DB 1 TGATGTGAACTACAGTCTGTGAGCCCTGGAACCTCCGCTCAGAGAGATGAAGGATAT 60

QY 137 CGACATAGGAAAGAGATATATCATCCCGAGTCCCTGGGTATAGAGTGTGAGGAGAGAAC 196
DB 61 CGACATAGGAAAGAGATATATCATCCCGAGTCCCTGGGTATAGAGTGTGAGGAGAGAAC 120

QY 197 CAGCACTTCTGGGACGACAGAGACCGGTGAAGATTCCAAAGTTCAGGAGAACTCGACCCGT 256
DB 121 CAGCACTTCTGGGACGACAGAGACCGGTGAAGATTCCAAAGTTCAGGAGAACTCGACCCGT 180

QY 257 GGAATGCCAAGATGCTTGGAAACAGACGCCGAGGCCGAGGGCTCTCTTTGATGGCTC 316
DB 181 GGAATGCCAAGATGCTTGGAAACAGACGCCGAGGCCGAGGGCTCTCTTTGATGGCTC 240

QY 317 CATGATCTCAGCTCAGAACTCCGAGTGGATGAGGAGCATCCCAAGGAGAAAGTACCATATGG 376
DB 241 CATGATCTCAGCTCAGAACTCCGAGTGGATGAGGAGCATCCCAAGGAGAAAGTACCATATGG 300

QY 377 CTTGAGTGTCTGAAGCCCATCCGAGTACTTCCAAACACAGCAGCCAGTGGCAATGC 436
DB 301 CTTGAGTGTCTGAAGCCCATCCGAGTACTTCCAAACACAGCAGCCAGTGGCAATGC 360

QY 437 TGGCTTTTTCCTGTATGACTTTTTCGTGGCTTTCTCTGCGCCGTGTGGCCCAAA 496
DB 361 TGGCTTTTTCCTGTATGACTTTTTCGTGGCTTTCTCTGCGCCGTGTGGCCCAAA 420

QY 497 GAAGGGGAGCTCTCAATGGGAAGAGTGTGTCTCTGCTCCAAAGCAGAGTCTTCTGAGCT 556
DB 421 GAAGGGGAGCTCTCAATGGGAAGAGTGTGTCTCTGCTCCAAAGCAGAGTCTTCTGAGCT 480

QY 557 GAAGTGCAGAGACTAGAGAGACTGTGGCAAGAGAGCTGAATGAAGTGGGCCAGAGCC 616
DB 481 GAAGTGCAGAGACTAGAGAGACTGTGGCAAGAGAGCTGAATGAAGTGGGCCAGAGCC 540

QY 617 TGCCTTCCCTGCAAGGTTGTGGATCTTCTGCGGACAGAGCTCATCTGTCATGCT 676
DB 541 TGCCTTCCCTGCAAGGTTGTGGATCTTCTGCGGACAGAGCTCATCTGTCATGCT 600

QY 677 GTGCTGATGATCAGCAGCTGGCTGGCTTCAGTGGACAGCCTTTCATGGTGAACACCT 736
DB 601 GTGCTGATGATCAGCAGCTGGCTGGCTTCAGTGGACAGCCTTTCATGGTGAACACCT 660

QY 737 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTGTTAGTCTGGG 796
DB 661 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTGTTAGTCTGGG 720

QY 797 CTTCTCTGAGGAAATCGTGGGTCTTGTGCGTTCGACTGACTTGGGATGGAATTA 856
DB 721 CTTCTCTGAGGAAATCGTGGGTCTTGTGCGTTCGACTGACTTGGGATGGAATTA 780

QY 857 CCGAACCGGTCTGCGCTTGGCGGGGGCCATCCTAACCATGGCATTTAAGAGATGCTTAA 916
DB 781 CCGAACCGGTCTGCGCTTGGCGGGGGCCATCCTAACCATGGCATTTAAGAGATGCTTAA 840

QY 917 GTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAAAGATGG 976
DB 841 GTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAAAGATGG 900

QY 977 GCAGAGAAATTTGAGGACAGCCGTTGGAGCCCTGTGCTGGAGAGACCCGTTGTTGC 1036
DB 901 GCAGAGAAATTTGAGGACAGCCGTTGGAGCCCTGTGCTGGAGAGACCCGTTGTTGC 960

QY 1037 CATCTTAGCATGATTTATATGTAATTTATCTGGGACCAACAGGCTTCTGGGATCAGC 1096
DB 1037 CATCTTAGCATGATTTATATGTAATTTATCTGGGACCAACAGGCTTCTGGGATCAGC 2100

DB 961 CATCTTAGCATGATTTATATGTAATTTATCTGGGACCAACAGGCTTCTGGGATCAGC 1020

QY 1097 TGTCTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCAGGCTCACAGCATATTTTCAG 1156

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QY 1217 CATTTAAATTTATCAAAATGATGCTCCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAT 1276

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QY 1277 CCGCAGGAGGAGCGCTCGGATATTGAAAAAGCCGGGTACTTCCAGGGTATCACTGTGGG 1336

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QY 1397 GGGCTTCGATCTGACAGCAGCAGGCTTTTCACAGTGGTGACAGTCTTCAATTTCCATGAC 1456

DB 1321 GGGCTTCGATCTGACAGCAGCAGGCTTTTCACAGTGGTGACAGTCTTCAATTTCCATGAC 1380

QY 1457 TTTTGGCTTGAAGTAACACCGTTTTTCAGTAAAGTCCCTCTCAGAAAGCCCTCAGTGGCTGT 1516

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QY 1517 TCACAGATTTAGAGTGTGTTCTTAATGGAAGAGTTTACATGATTAAGAACAAACAGC 1576

DB 1441 TCACAGATTTAGAGTGTGTTCTTAATGGAAGAGTTTACATGATTAAGAACAAACAGC 1500

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DB 1561 CAGTATCCAGAACTCGCCCAAGCTGACCCCAAGTGAACCAAGTGAAGAGAGTGGCTTCCAG 1620

QY 1697 GGGCAGAAAGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1756

DB 1621 GGGCAGAAAGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1680

QY 1757 GCAGAAAGCCACCTCTCTGACAGTGCAGAGCGGCCAGTCCCGAAGAGAGAGAGAGAGAGAG 1816

DB 1681 GCAGAAAGCCACCTCTCTGACAGTGCAGAGCGGCCAGTCCCGAAGAGAGAGAGAGAGAGAG 1740

QY 1817 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1876

DB 1741 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1800

QY 1877 GATCCAGAGGTTAACTGGTTGGAATCTGCGGCACTGCGGAGTGGGAAAGTGGGAAAGTCTCT 1936

DB 1801 GATCCAGAGGTTAACTGGTTGGAATCTGCGGCACTGCGGAGTGGGAAAGTGGGAAAGTCTCT 1860

QY 1937 CATTTAGGCAATTTAGGCGCAGATGACCTTCTAGAGGGCAGCATTTGCAATCAGTGAAC 1996

DB 1861 CATTTAGGCAATTTAGGCGCAGATGACCTTCTAGAGGGCAGCATTTGCAATCAGTGAAC 1920

QY 1997 CTTTGGCTTATGGGCCACAGGCGCTGGATCCTCAATGCTACTCTGAGAGACAACTCTCT 2056

DB 1921 CTTTGGCTTATGGGCCACAGGCGCTGGATCCTCAATGCTACTCTGAGAGACAACTCTCT 1980

QY 2057 GTTTGGGAGGAAATATGATGAAGAAAGATACAACTCTGCTGCTGAACAGCTGCTGCTGAG 2116

DB 1981 GTTTGGGAGGAAATATGATGAAGAAAGATACAACTCTGCTGCTGAACAGCTGCTGCTGAG 2040

QY 2117 GCCTGACCTGGCCATCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2176

DB 2041 GCCTGACCTGGCCATCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2100

Qy	2177	CCTGAGCGGTGGCGACGGCCAGAGGATCAGCCTTGCCTCGGCGCCTTGATAGTGACACGAG	2236
Db	2101	CCTGAGCGGTGGCGACGGCCAGAGGATCAGCCTTGCCTCGGCGCCTTGATAGTGACACGAG	2160
Qy	2237	CATCTACATCCTGGACGACCCCTCAGTGCCTTAGATGCCATGTGGCAACCAACATCTT	2296
Db	2161	CATCTACATCCTGGACGACCCCTCAGTGCCTTAGATGCCATGTGGCAACCAACATCTT	2220
Qy	2297	CAATAGTGTCTATCCGGAACATCTCAAGTCCAAGACAGTCTCTGTTGTTATACCCACCAAGT	2356
Db	2221	CAATAGTGTCTATCCGGAACATCTCAAGTCCAAGACAGTCTCTGTTGTTATACCCACCAAGT	2280
Qy	2357	ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAGACGGCTGTATTACGGGAAG	2416
Db	2281	ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAGACGGCTGTATTACGGGAAG	2340
Qy	2417	AGGCACCCATGAGGAACCTCATGAATTTAAATGGTGACTATGCTACCAATTTTTTAACCT	2476
Db	2341	AGGCACCCATGAGGAACCTCATGAATTTAAATGGTGACTATGCTACCAATTTTTTAACCT	2400
Qy	2477	GTTGCTGGGAGACACCCGCCAGTTGAGATCAATTTCAAAAAAGAAACCAAGTGGTTCACA	2536
Db	2401	GTTGCTGGGAGACACCCGCCAGTTGAGATCAATTTCAAAAAAGAAACCAAGTGGTTCACA	2460
Qy	2537	GAGAGAGTCACAGACAGGGTCTTAAACAGGATCAGTAAAGAAAGAAAGACGAGTAAA	2596
Db	2461	GAGAGAGTCACAGACAGGGTCTTAAACAGGATCAGTAAAGAAAGAAAGACGAGTAAA	2520
Qy	2597	GCCAGAGGAAGGCAGCTTGTGCAGCTCGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC	2656
Db	2521	GCCAGAGGAAGGCAGCTTGTGCAGCTCGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC	2580
Qy	2657	AGTATATGTTGTCTACATCCAGGCTGTGGGGGGCCCTTGGCATTCCTGGTTATTATGCG	2716
Db	2581	AGTATATGTTGTCTACATCCAGGCTGTGGGGGGCCCTTGGCATTCCTGGTTATTATGCG	2640
Qy	2717	CCTTTTCATGCTGAATGTAGGCAGCACCGCTTCAGACACCTGGTGGTTGAGTTACTGGAAT	2776
Db	2641	CCTTTTCATGCTGAATGTAGGCAGCACCGCTTCAGACACCTGGTGGTTGAGTTACTGGAAT	2700
Qy	2777	CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGAACAGACACCTCGGTGAGTGACAG	2836
Db	2701	CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGAACAGACACCTCGGTGAGTGACAG	2760
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Qy	2897	CATGCTGATCTTGAAGCATTCGAGAGTTGTCTTTGTCAAGGGCAGCTCGGAGCTTC	2956
Db	2821	CATGCTGATCTTGAAGCATTCGAGAGTTGTCTTTGTCAAGGGCAGCTCGGAGCTTC	2880
Qy	2957	CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA	3016
Db	2881	CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA	2940
Qy	3017	CAGACCCCCACAGGAGGATCTCAACAGTTTTTCCAAGACATGATGAATGATGACGT	3076
Db	2941	CAGACCCCCACAGGAGGATCTCAACAGTTTTTCCAAGACATGATGAATGATGACGT	3000
Qy	3077	GCGGCTGCCGTTCCAGGCGGAGATGTTTCATCCAGAAGCTTATCTGGTGTTCTTCGTGT	3136
Db	3001	GCGGCTGCCGTTCCAGGCGGAGATGTTTCATCCAGAAGCTTATCTGGTGTTCTTCGTGT	3060
Qy	3137	GGGAATGATCGCAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGGCCCTTGTCATCCT	3196
Db	3061	GGGAATGATCGCAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGGCCCTTGTCATCCT	3120
Qy	3197	CTTTTCAGTCTGACATNTGCTCCAGGGTCCCTGATTCGGGAGCTGAAGCGTCTGACAA	3256
Db	3121	CTTTTCAGTCTGACATNTGCTCCAGGGTCCCTGATTCGGGAGCTGAAGCGTCTGACAA	3180

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DB	3301	CCAAGCTCCTTTTTTTTGTATTACGTGTCGGATGCGGTGGCTGGCTGCGGCTGGACCT	3360
QY	3437	CATCAGCATCGCCCTCATCACACACAGGGGTGATGATGCTTTATGACACGGGCAGAT	3496
DB	3361	CATCAGCATCGCCCTCATCACACACAGGGGTGATGATGCTTTATGACACGGGCAGAT	3420
QY	3497	TCGCCAGCCTATGCGGGTCTCGCCATCTTTATGCTGTCCAGTTAACGGGGCTGTTCCA	3556
DB	3421	TCGCCAGCCTATGCGGGTCTCGCCATCTTTATGCTGTCCAGTTAACGGGGCTGTTCCA	3480
QY	3557	GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTTCGATTCACCTTCGGTGAGAGGATCAA	3616
DB	3481	GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTTCGATTCACCTTCGGTGAGAGGATCAA	3540
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DB	3541	TCACTACATTAAGACTCTCTCCTTAAAGAAAGTATCCTTCACGATCAAACTTAAGAGAAAGATTGG	3600
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DB	3841	CGACCTCCGAAGCAAACTCTCATCTTCAAGAGCCGGTGTCTTCAGTGGCACTGT	3900
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DB	3901	CAGATCAAAATTTGGACCCCTTCAACACGATACACTGAAGACACAGATTTGGATGCCCTGGA	3960
QY	4037	GAGGACACATGAAGAATGTTATGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGTAT	4096
DB	3961	GAGGACACATGAAGAATGTTATGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGTAT	4020
QY	4097	GGAGAAATGGGATAACTTCTCAGTGGGGAAAGCGGACGCTTTGTGATAGCTAGAGCCCT	4156
DB	4021	GGAGAAATGGGATAACTTCTCAGTGGGGAAAGCGGACGCTTTGTGATAGCTAGAGCCCT	4080
QY	4157	GCTCGCCACTGTAAAGTTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC	4216
DB	4081	GCTCGCCACTGTAAAGTTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC	4140
QY	4217	AGACTTATTTGATTCAGAGACCATTCGGAGAAGCATTTGCAGACTGTACCATGCTGACCAT	4276
DB	4141	AGACTTATTTGATTCAGAGACCATTCGGAGAAGCATTTGCAGACTGTACCATGCTGACCAT	4200
QY	4277	TGCCCATCGCCTGCACAGGTTCTAGGCTCCGATAGGATTATGGTGTGCGCCACGGGACA	4336
DB	4201	TGCCCATCGCCTGCACAGGTTCTAGGCTCCGATAGGATTATGGTGTGCGCCACGGGACA	4260
QY	4337	GGTGTGGAGTTTGACACCCCATCGCTCTCTGTGCCAACGACAGTTTCCGATTTCTATGC	4396

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Db 4261 GGTGTGAGTTGACACCCATCGCTCTTGTCTCAACACAGTCCCGCATTCATGC 4320
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Qy 4816 TGTGCTAATAACA 4828
Db 4741 TGTGCTAATAACA 4753
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RESULT 4

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US-08-463-092B-3
; Sequence 3, Application 05/08463092B
; Patent No. 5766880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,092B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-WAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-463-092B-3

Query Match      8.7%; Score 510; DB 1; Length 5011;
Best Local Similarity 52.2%; Pred. No. 3.7e-121;
Matches 1360; Conservative 0; Mismatches 1185; Indels 59; Gaps 8;

Qy 1821 CACATCCACTCGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGCATC 1880
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Db 2200 CCCGAAGGTGCTTTGGTGGCGGTGGCCAGGTGGCTGGCGAAGTGTCCCTGCTC 2259
Qy 1941 TCAGCCATTTTAGGCCAGATGAGCGCTTTCAGAGGGCAGCATTCGATCAGTGGAACTTC 2000
Db 2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGCAGCTGCTGATCAAGGGCTCCGTG 2319
Qy 2001 GCTTATGTGCGCCAGCAGCGCTGAGTCCCAATGCTACTCTGAGAGACACATCTCTGTTT 2060
Db 2320 GCCTATGCGCCACAGCAGCGCTGGATTTCAGATGATTTCTCGGAGAAACATCTCTTTT 2379
Qy 2061 GGAAGAGATATGATGAAGAAAGATACAACTCTGTCTGAAACAGTCTGCTCGAGGCCCT 2120
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Qy 2121 GACCTGGCCATTTCTCCAGCAGCAGCGCTGACGGAGATTGGAGAGCGAGGAGCCACCTG 2180
Db 2440 GACCTGGAAATCCTGCCAGTGGGGATCGACAGAGATTGGCGAAGAGCGGTGAACCTG 2499
Qy 2181 AGCGGTGGCAGCGCCAGAGGATCAGCCTTGCCCGGCCCTTGATAGTGACAGGAGCATC 2240
Db 2500 TCTGGGGGACAGAACGAGCGCGTGAGCCCTGGCGGGCGCTGTATCCCAACGCTGACAT 2559
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Db 2680 ATGAGCTACTTGGCGGAGTGGACATCATCTGATGCTGGCGGCAAGATCTCTGAG 2739
Qy 2415 AGAGGCACCATGAGGAAGTGAATTTAAATGGTGACTATCTACCATTTTTTAATAAC 2474
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Qy 2475 CTGTTGCTGGGAGAGACACCGCGAGTT--GAGATCAATTTCAAAAAAGGAACACCGTGGT 2531
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Db 2800 TATCCAGCAGAGCAGGAGCAGGATGCGAGAGAACGGGGTTCACGGGGCTCAGCGGT 2859
Qy 2332 TCACAGAAGAGTTCACAGACA-----AGGGTCTCTAAAA 2565
Db 2860 CCAGGAAGGAAGCAAGCAATGAGCAATGGCATGGTGTGAGCGACAGTGCAGGGAAG 2919
Qy 2566 CAGGATCAGTAAGAAAGAAAGCAGTAAGCCAGAGGAAGGCGAGCTTGTGAGCTGG 2625
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Db 3920 TGCATGCTTCTGTTGCTGCCCTGTTTGGCGGTGATCTCCAGGCAACGCTCAGTGTGGC 3879
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Db 4000 GAGACTGAGAA---GGAGGGCCCTGGCAATCCAGGAGACAGCTCCGCCACAGCTGG 4056
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Qy 3987 TTGGACCCCTTCAACAGTACACTGAAGACAGATTTGGGATGCTTGGAGGAGACAC 4046
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Qy 4287 CTGCACAGGTTTAGGCTCCGATAGGATTTATGTTGGTGGCCCGGAGGAGTGGTGGAG 4346
Db 4657 CTCAACACCATCTAGGACTACAAAGGATGATCGTCTTGGCAAGAGGAGAAATCCAGGAG 4716
Qy 4347 TTTGACACCCCATCGTCTCTCTG 4370
Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 5

US-08-462-109A-3

: Sequence 3, Application US/08462109A

: Patent No. 5882875

: GENERAL INFORMATION:

: APPLICANT: Cole, Susan P.C.

: APPLICANT: Deeley, Roger G.

: TITLE OF INVENTION: METHODS FOR IDENTIFYING

: TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS

: NUMBER OF SEQUENCES: 6

: CORRESPONDENCE ADDRESS:

: STREET: 60 State Street, suite 510

: CITY: Boston

QY 2739 AGCAGCGCTTCAGCAGCTGGTGGTGTAGTTACTGATCAACAGAGGAGCGGAACACC 2798
 DB 3100 GCCATCGGAGCTTCTCATCTCTCTCAGCATCTTCCCTTTTCATGTGTAAACATGTGTCC 3159
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 QY 2853 CATATGCACTACTATGCGAGCATCTACGCCCTCTCCATGGGAGTCAATGCTGATCTGAAA 2912
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RESULT 8
 US-08-461-384B-3
 ; Sequence 3, Application US/08461384B
 ; Patent No. 6025473
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; APPLICANT: Delevy, Roger G.
 ; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
 ; STREET: Queen's University at Kingston
 ; CITY: Kingston
 ; STATE: Ontario
 ; COUNTRY: CANADA
 ; ZIP: K7L 3N6
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/461.384B
 ; FILING DATE: 05-JUN-95
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/966,923
 ; FILING DATE: 27-OCT-1992
 ; APPLICATION NUMBER: 08/029,340
 ; FILING DATE: 8-MAR-1993
 ; APPLICATION NUMBER: 08/141,893
 ; FILING DATE: 26-OCT-1993
 ; APPLICATION NUMBER: 08/407,207
 ; FILING DATE: 20-MAR-1995

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 QY 4347 TTTGACACCCCATCGGCTCTTCTG 4370
 Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 10
 US-08-463-092B-1
 ; Sequence 1, Application US/08463092B
 ; Patent No. 5766880
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; APPLICANT: Deeley, Roger G.
 ; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
 ; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 ; NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston

[illegible]

QY 3147 GCAGGAGTCTTCCGCTGCTTGTGGCAGTGGGGCCCTTGTGTCATCTCTTTTTCAGTC 3206
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Db 3940 CGATGTCATCTGAATGGAACCAACATCTGTGGCGCTGGAGAGGCTCAAGGATATTCA 3999
QY 3627 AGACTCTGCTTGAAGCAGCTGCCAGATTAAGAACAGGCTCCCTCCCTGACTGG 3686
Db 4000 GAGACTGAGAA--GGAGCGCCCTGGCAATCCAGGAGACAGCTCCGCCAGCAGCTGG 4056
QY 3687 CCCCAGGAGGAGTGTACCTTTGAGAACGAGAGATGAGTACCGAGAAACCTCCCT 3746
Db 4057 CCCCAGTGGCGGAGTGAATTCGGAACTACTGCTCGCTTACCGAGAGACCTGGAC 4116
QY 3747 CTGTCTTAAAGAAATATCTTTCAGATCAACCTTAAAGAGAAATGTCATTTGGGG 3806
Db 4117 TTCGTTCTCAGGCACATCAATGTCAGATCAATGGGGAGAAAGTGGCATCGTGGGG 4176
QY 3807 CGGACGAGTACGAGGAGTCTCGCTGGGATGGCCCTTCCGCTGTGGGATGATCT 3866
Db 4177 CGGACGGGAGCTGGGAAGTCTGCTGACCCCTGGGCTTATTTCCGATCAACGAGTCTGC 4236
QY 3867 GGAGGCTGATCAAGATGATGAGTGAAGTCAAGTATGAGTATGAGTATGAGTATGAGT 3926
Db 4237 GAAGGAGATCATCATGATGATGATCAACATCGCCAGATCGGCTGACAGCTCCGC 4296
QY 3927 AGCAACTCTTATCATCTTCAAGAGCGGCTGCTGTTTCAGTGGCAGTGTGATCAAT 3986
Db 4297 TTAAGATCAACCATCATCCCGCAGGACCTGTTTGTGTTTTCGGTTCCTCCGATGAC 4356
QY 3987 TTGGACCCCTTCAACAGTACTAGACAGATTTGGGATGCTTGGAGGAGACAC 4046
Db 4357 CTGGACCCATTGAGCAGTACTCGATGAAGAGTCTGGACGCTCCCTGGAGTGGCCAC 4416
QY 4047 ATGAAGATGATTTGCTCAGTCTCTCTGAACCTTGAATGATGATGATGATGATGAT 4106
Db 4417 CTGAAGGACTTCTGCTCAGCCCTTCTCTGACAGCTAGACCATGATGATGATGATGATG 4476
QY 4107 GATACTTCTCAGTGGGGAAGCGGAGCTTCTTGTGATAGCTAGAGCCCTGCTCGCCAC 4166
Db 4477 GAGAACCTCAGTGTGCGGAGCGCCAGCTTGTGCTGCTAGCCCGGCTGCTGAGGAG 4536
QY 4167 TGTAAAGTCTGATTTTATGATGAAGCCAGCTGCTGATGAGACAGACAGATTTATG 4226
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QY 4287 CTCACACAGGTTCTAGCTCCGATAGGATTTGCTGGCCCGGACAGTGGTGGAG 4346
Db 4657 CTCAACACCATCATGAGTACACAAAGGTGATCTCTTGGACAAAGGAATCCAGAG 4716
QY 4347 TTTGACACCCATCGGTCCTCTG 4370
Db 4717 TAGGGCGCCCATCGGACCTCTG 4740

RESULT 11
US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Dealey, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-462-109A-1

Query Match 8.7%; Score 505.2; DB 2; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;
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Qy 3627 AAGACTCTGCTTGGAAAGCCTCCAGAAATTAAGAAAGGCTCCCTCCCTGACTGG 3686
Db 4000 GAGACTGAGAA---GGAGGCGCCCTGGCAATCCAGGAGACAGTCCGCCACGAGCTGG 4056
Qy 3687 CCCAGAGGAGGAGGTGACCTTTGAGAACACAGAGATGAGTACCGGAAACCTCCCT 3746
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Qy 3807 CCGACAGGATCAGGAAGTCTCGTGGGATGGCCCTCTTCCGCTCTGGTGAGTATATCT 3866
Db 4177 GGGAGGAGGTGGGAAGTCTGCTCCCTGACCTTATTTCCGATCAACGAGCTGCCC 4236
Qy 3867 GGAGGCTCATCAAGATTGAGTGGAGTGAATCAGTGAATATGGCTTCCGACCTCCGA 3926
Db 4237 GAAGGAGATCATCATCGATGGCATCAACATCGCAAGATCGGCTCGACGACCTCCGC 4296
Qy 3927 AGCAAACTCTTATCATCTTCAAGAGCGGTGCTGTTTCACTGAGTGTGCTGATCAAT 3986
Db 4297 TTCAAGATCATCATCCCCCAGGACCTGTTTGTGTTTTCGGGTTTCCCTCCGATGAAC 4356

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QY 3987 TTGGACCCCTTCAACACAGTACACTGAAGACCAAGATTGGGATGCCCTGGAGGAGACACAC 4046
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Db 4717 TACGGCGCCCATCGGACTCTG 4740

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RESULT 12

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US-08-460-907B-1
; Sequence 1, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki

```

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; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196...4788
; US-08-460-907B-1

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Query Match      8.7%; Score 505.2; DB 2; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

QY 1821 CACATCCACTGGGCCACCTTACAGAGGACACTGCACAGACATCGATCTGGAGATC 1880
Db 2142 CACATTCACCTGGGCCA--GGAGCGACCCCTCCACACTGAATGSCATCACCTTCTCCATC 2199
QY 1881 CAAGAGGTAAACTGTTGGAATCTCGGCGAGTGTGGGAAGTGGAAAAAACCCTCTCTCAT 1940
Db 2200 CCCGAAGTGCTTTGGTGGCCGTTGGTGGCCAGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259
QY 1941 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGGAGCAGCATTCGAATCACTGGACCTC 2000
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QY 2001 GCTTATGTGGCCAGCAGCCCTGGATCTCAATGCTACTCTGAGACACAACTCTCTGTT 2060
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,179A

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/966,923

FILING DATE: 27-OCT-1992

APPLICATION NUMBER: 08/029,340

FILING DATE: 8-MAR-1993

APPLICATION NUMBER: 08/141,893

FILING DATE: 26-OCT-1993

APPLICATION NUMBER: 08/407,207

FILING DATE: 20-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PQI-002CP8

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5011 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 196..4788

US-08-463-179A-1

Query Match 8.7% Score 505.2; DB 3; Length 5011;
Best Local Similarity 52.1%; Pred. No. 63e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

QY 1821 CACATCCACCTGGGCCACCTGGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1880
DB 2142 CACATTCACCTGGGGCA--GGAGCGACCTCCACACTGAATGGCATCACCTTCTCCATC 2199
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DB 2200 CCCGAAGGTGTTGGTGGCCGTGTGGGCCAGGTGGGCTCGGAAAGTGTGCCCTGCTC 2259
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DB 2260 TCAGCCCTTTGGCTGAGATGACACAAAGTGGAGGGCAGCTGCTATCAAGGGCTCCGTG 2319
QY 2001 GCTTATGTCGCCAGCGCCCTGGATCCTCAATGCTACTCTGAGACAAACATCCTGTTT 2060
DB 2320 GCCTATGTGCCACAGCGCCCTGGATTCAGAATGATTTCTCCGAGAAACATCCTTTT 2379
QY 2061 GGGAGGATATGATGACAAAGATACAACTCTGCTGTAACAGCTGCTGCTGAGGCT 2120
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QY 3327 AATAAGGCGGAGTCTTGCACAGATACACAGGAGCTGCTGATGACAAACAGTCTCT 3386
DB 3700 GAGGAGGAGGCGCTTTCATCCACAGAGTGAAGTGGAGGAGGAGGAGGAGGAGG 3759
QY 3387 TTTTGTGTTTACGTGTGCGATGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 3446

Db 3760 TATTACCCACGATCGTGGCCAAACAGGTGGCTGGCGGTGGAGTGTGTGGGCAAC 3819
Qy 3447 GCCCTATCACCACACAGGGGCTGATGATCGTTTATGACAGGGCAGATCCCCCAGCC 3506
Db 3820 TGCATCGTCTGTTTGTGGCTGCTTTGGGTGATCTCCAGGCACAGCCTCAGTCTGGC 3879
Qy 3507 TATCGGCTCTCGCATCTTATGCTGCTCCAGTTAAGGGGCTCTCCAGTTTACGTC 3566
Db 3880 TTGGTGGCCTCTCAGTGTCTTACTCATGTGAGGTACACGTAATGAACTGGCTGTT 3939
Qy 3567 AGACTGGCATCTGACAGAGAAGCTCGATTCACCTCGGTGGAGAGATCAATCACTACAT 3626
Db 3940 CGGATGTCATGAAATGGAAACCAACATCGTGGCGGTGGAGAGCTCAAGAGTATCA 3999
Qy 3627 AAGACTGTCTTGGAGACACTGCGCAGAAATTAAGAACAGGCTCCCTCCCTGACTGG 3686
Db 4000 GAGACTGAGAA--GGAGGGCCCTGCAATTCAGGAGACACGTCCGCCCCAGCAGCTGG 4056
Qy 3687 CCCAGGAGGAGAGGTGACCTTTGAGAACGACAGATGAGGTACCCGAGAAACCTCCCT 3746
Db 4057 CCCAGGTGGCCGAGTGGAAATCCGGAATCTGCTGCTACCCGAGAGACTGGAC 4116
Qy 3747 CTGTCTCTAAGAAAGTATCTCTCACGATCAAACTTAAAGAGAAGATGGCATTTGGGG 3806
Db 4117 TTCGTCTCAGGCACATCAATGTCAAGATCAATGGGGAGAAAGGTGGCATCGTGGG 4176
Qy 3807 CGGACAGATCAGGAAGTCTCCTCGCTGGGATGCGCTTCTTCCCTGTGGTGGATTAAT 3866
Db 4177 CGGACGGAGGTGGGAAGTCTCCTGACCTGCGCTTATTCGGATCAACGAGTCTGCC 4236
Qy 3867 GGAGTCTCATCAAGATGATGAGTGTGAGTATGATGATGATGATGATGATGATGAT 3926
Db 4237 GAAGGAGATCATCATCGATGGGATCAACATCCCAAGATCGCGCTGACGACCTCCG 4296
Qy 3927 AGCAACTCTCTATCTCTCAAGAGCGGTGCTGTTGAGTGGCACTGTGATGATCAAT 3986
Db 4297 TTCAAGATCACCATCATCCCCAGGACCTCTTTGTTTCGGGTCCCTCCGATGAC 4356
Qy 3987 TTGACCCCTTCAACAGTACATGAGACAGATTTGGGATGCGCTGGAGAGGACACAC 4046
Db 4357 CTGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGAGTCTGCGTGGAGTGGCC 4416
Qy 4047 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4106
Db 4417 CTGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4476
Qy 4107 GATAACTTCTCAGTGGGGAACGAGCTCTTGTGCTAGTAGAGCCTGCTCGGCCAC 4166
Db 4477 GAGAACCTCAGTGTGGGACGCGCAGCTTGTGTGCTAGTCCCGGCGCTGCTGAGGAG 4536
Qy 4167 TGTAAATCTGATTTAGATGAAGCCACAGCTGCCATGCCATGACAGACAGATTAATG 4226
Db 4537 ACGAAGATCTTGTGTGGATGAGGCCACGAGCTGGACCTGGAAACGAGGACCTC 4596
Qy 4227 ATCAAGAGACATCCGAGAGATTTGACAGTGTACCATGCTGACCATGCTGCTGCTG 4286
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Qy 4287 CTGACACGCTTCTAGGCTCCGATGATGATGATGATGATGATGATGATGATGATGAT 4346
Db 4657 CTCAACACCATCATGACTACACAGGATGATGATGATGATGATGATGATGATGATGAT 4716
Qy 4347 TTTGACACCCATCGGCTCTCTG 4370
Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 14

US-08-461-384B-1
; Sequence 1, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-461-384B-1

Query Match

Best Local Similarity 8.7%; Score 505.2; DB 3; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

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Db 2142 CACATTCACCTGGGCCA--GGAGCGACCTCCACACCTGAATGGCATCACCITCTCCATC 2199
Qy 1881 CAAGAGGTAACCTGGTTGGATCTGGCGCAGTGTGGGAAGTGGGAAAAACCTCTCTCAT 1940
Db 2200 CCCGAAGTGTCTTGGTGGCGCTGGTGGCGCAGGTGGCGGAAAGTTGCCCTGCTC 2259
Qy 1941 TCAGCATTTTAGGCGACATGACGCTTCTAGAGGCGAGCATTCATGATGATGATGAT 2000
Db 2260 TCAGCCCTCTTGGCTGAGATGACAAAGTGGAGGGGACGCTGCTATCAAGGCTCCGTG 2319
Qy 2001 GCTTATGTGGCCAGCAGGCTGATCTCTCAATGCTACTCTGAGAGACAAACATCTCTGTT 2060
Db 2320 GCTTATGTGGCCAGCAGGCTGATTCAGATGATTCCTCCGAGAAACATCTCTTTT 2379
Qy 2061 GGAAGGAATATGATGAAGAAATACAACTCTGTGTAACAGCTGTGCTGAGGCT 2120
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Qy 2121 GACCTGGCCATCTTCCAGGAGCGACCTGACGAGATTTGGAGAGGAGGAGGACCTG 2180
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Db 4657 CTCAACACCATCATGGAGTACACAAGGGTGTCTCTTGGACAAGAGGAATCCAGGAG 4716
QY 4347 TTTGACACCCCATCGGTCCTTCG 4370
Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 15

US-08-407-207A-1
; Sequence 1, Application US/08407207A
; Patent No. 6063621
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,207A
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: 01512
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196...4788
US-08-407-207A-1

Query Match 8.7%; Score 505.2; DB 3; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

QY 1821 CACATCCACCTGGCCACCTCGGCTTACAGAGACACTGCACAGCATCGATCTGGAGATC 1880
Db 2142 CACATTCACCTGGGCA--GGAGCGACCCCTCCACACTGAATGGCATCACCTTCTCCATC 2199
QY 1881 CAAGAGGTAACCTGGTTCGATCTCGGCAGTGGGAGTGGGAAACCTCTCTCATTT 1940
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Db 3220 CAGGAGCACAGAAAGTCCGCTGAGCTCTATGAGGCCCTGGGCACTTTCACAGGAGATC 3279
QY 2913 GCATTCGAGG-----AGTTGCTTTTCAAGGGCAGCTGCGAGCTTCTCCCGGCTG 2966
Db 3280 GCGGTGTTGGCTACTCCATGGCGGTGTCATCGGGGAGTCTTGGCTTCCCGCTGCTG 3339
QY 2967 CATGAGGAGCTTTTCGAAGGATCTTCGAAGCCCTATGAAGTTTGTGACACACACCCC 3026
Db 3340 CAGTGGACCTGCTGCACAGCATCTCGGGTCAACCCATGAGCTTCTTTGAGCGGACCCCC 3399

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	4791	82.1	4847	19	AAZ5682
5	4724.2	80.9	4781	22	AAZ85287
6	1936.4	33.2	2167	18	AAZ94055
7	1676	28.7	1761	18	AAZ94054
8	925.8	15.9	4101	22	AAZ14909
9	790.6	13.5	4008	22	AAZ14912

10	766.4	13.1	4149	22	AAF83643	Novel human transp
11	759.4	13.0	3660	22	AAZ14910	Human transporter-
12	757.8	13.0	4074	24	AAZ36023	Human adenosine tr
13	753.2	12.9	3753	22	AAZ14911	Human transporter-
14	727	12.5	3055	23	ABV21036	Human prostate exp
15	727	12.5	3055	23	ABV26879	Human prostate exp
16	723.8	12.4	3189	22	AAF83637	Novel human transp
17	723.8	12.4	4638	24	AAZ92270	Human ATP-binding
18	722.2	12.4	4427	24	ABK92211	Prostate cancer-as
19	537.8	9.2	1698	22	AAZ14913	Human transporter-
20	522	8.9	3549	23	AAZ90084	DNA encoding novel
21	510	8.7	5011	19	AAV31498	Human MRP variant
22	510	8.7	5011	20	AAZ19818	Human multidrug re
23	510	8.7	5011	20	AAZ21977	Human MDR variant
24	510	8.7	5011	21	AAZ94741	Human ATP binding
25	510	8.7	5011	21	AAZ90193	Multidrug resistan
26	510	8.7	5011	21	AAZ39556	Human MRP variant
27	510	8.7	5011	24	ABK92125	Prostate cancer-as
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31	505.2	8.7	5011	17	AAZ17173	cDNA encoding mult
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34	505.2	8.7	5011	20	AAZ21976	Multidrug resistan
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36	505.2	8.7	5011	21	AAZ90192	Human multidrug re
37	505.2	8.7	5011	21	AAZ39555	Human TRICH-2 CDNA
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45	435.8	7.5	6140	22	AAH93829	

ALIGNMENTS

RESULT 1
AAZ30079

ID AAZ30079 standard; cDNA; 5838 BP.

XX AAZ30079;

AC AAZ30079;

XX 26-JAN-2000 (first entry)

DE cDNA encoding a human MPR-related ABC transporter designated MOAT-C.

XX Human; MPR-related ABC transporter; MOAT protein; MOAT-C;

KW MOAT mediated transport; anticancer drug sensitivity;

KW transporter mediated cellular efflux; anticancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 126..4439

FT /*tag= a

FT /product= "MOAT-C"

FT /note= "MPR-related ABC transporter"

XX WO9949735-A1.

PD 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06644.

XX 27-MAR-1998; 98US-0079759.

XX 03-AUG-1998; 98US-0095153.

XX (FOXC-) FOX CHASE CANCER CENT.

XX Kruh G, Lee K, Belinsky M, Bain L;
XX WPI; 1999-610812/52.
XX P-PSDB; AAY43542.
XX New transporter gene useful for screening for anti-cancer drugs
XX Claim 11; Page 134-135; 153pp; English.
XX The present sequence encodes a human MPR-related ABC transporter (MOAT)
CC protein, designated MOAT-C. The protein comprises a multi-domain
CC structure including a tandem repeat of nucleotide binding folds
CC appended C-terminal to a hydrophobic domain, having Walker A and B ATP
CC binding sites and several potential membrane spanning domains. The MOAT
CC nucleic acids are useful for screening a test compound for inhibition of
CC MOAT mediated transport, indicated by restoration of anticancer drug
CC sensitivity, which in turn causes a reduction of transporter mediated
CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
CC probes to detect the presence or expression of genes encoding MOAT
CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
CC MOAT proteins.
XX
XX Sequence 5838 BP; 1422 A; 1432 C; 1509 G; 1475 T; 0 other;
Query Match 100.0%; Score 5838; DB 20; Length 5838;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5838; Conservative 0; Mismatches 0; Indels 0; Gaps
QY 1 CCGGGCAGGTGGCTCATGCTCGGGACGCTGGTTGAGCGGCTGGCGGGTGTCTCTGGAGC 60
DB 1 CCGGGCAGGTGGCTCATGCTCGGGACGCTGGTTGAGCGGCTGGCGGGTGTCTCTGGAGC 60
QY 61 AGGGGGCCAGGAATTCGTATGTGAAACTAACAGTCTGTGAGCCCTGGAACTCCGCTCAG 120
DB 61 AGGGGGCCAGGAATTCGTATGTGAAACTAACAGTCTGTGAGCCCTGGAACTCCGCTCAG 120
QY 121 AGAAGATGAAGATATCGACATAGGAAAGAGTATATCATCCCCAGTCTCGGTATAGAA 180
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QY 241 GGAGAACTCGACCGTTGGAAATGCCAAGATGCTTGGAAACAGACGCCGAGCCGAGGGCC 300
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QY 301 TCTCTCTTGATGCCTCCATGCATTCTCAGCTCAGAAATCCTGGATGAGAGCATCCCAAGG 360
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QY 421 ACCCAGTGACAAATGCTGGGCTTTTTTCTGTATGACTTTTTTCTGTGGCTTTCTTCTCTGG 480
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QY 481 CCCGTGTGCCCAACAAGAGGGGAGCTCTCAATGGAAGACGTGTGGTCTGTCTCCCAAGC 540
DB 481 CCCGTGTGCCCAACAAGAGGGGAGCTCTCAATGGAAGACGTGTGGTCTGTCTCCCAAGC 540
QY 541 ACCAGTCTTCTGACGTGAATCGCAAGAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG 600
DB 541 ACCAGTCTTCTGACGTGAATCGCAAGAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG 600
QY 601 AAGTTGGGCCAGACGCTGCTTCCCTCGAAGGGTTGTGTGGATCTTCTGCCGACACGAGC 660
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QY ACAGCATCGATCTGGAGATCCAGAGGGTAAACTGGTGGAAATCTGGGAGGTGGGAA 1920
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Db 2521 AAACCAAGTGTTCACAGAAGAGTCAACAGCAAGGGTCTTAAACAGGATCAGTAAAGA 2580
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Db 2581 AGAAAAGCAGTTAAGCCAGAGAGGCGAGCTTGTGACGCTGGAAGAAAGGCGAGG 2640
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Db 2641 GTTCAGTGCCTGTGCTAGTATGTTGCTCTACATCCAGGCTGCTGGGGGCCCTTTGGCAT 2700
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Db 2701 TCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGAGCAGCCCTTCAGCACCTGGT 2760
QY GGTGAGTTACTGATCAAGCAGAGGAGCGGACCACTGTGACTCGAGGGAACGAGA 2820
Db 2761 GGTGAGTTACTGATCAAGCAGAGGAGCGGAGCACTGTGACTCGAGGGAACGAGA 2820
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Db 2821 CCTCGGTGAGTGACAGCATGAAGGACAAATCTCTATATGAGTACTATGCCACATCTACG 2880
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Db 3541 TAACGGGCTGTTCCAGTGTACGCTGAGCTGCGATCTGAGACAGAGCTCGATTCACCT 3600
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QY 4141 GCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCCTGATTTAGATGAAGCCACAGCTG 4200
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QY 5821 AAAAAAATAAAAAA 5838
Db |||||||
QY 5821 AAAAAAATAAAAAA 5838
Db |||||||
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RESULT 2
AA294745
ID AA294745 standard; cDNA; 5838 BP.
XX
AC AA294745;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human ATP binding cassette ABC5 (MRP5) cDNA.
XX
KW ABC5; ATP binding cassette; human; cholesterol; lipid disorder;
KW atherosclerosis; lipid disorder; dyslipidemia; psoriasis;
KW lupus erythematosus; diagnosis; gene therapy; MRP5;
KW multidrug resistance associated protein; chromosome 3q25-27;
KW Dubin Johnson syndrome; hyperbilirubinemia; ss.
XX

OS Homo sapiens.
XX WO200018912-A2.
PN XX
PD 06-APR-2000.
XX 21-SEP-1999; 99WO-EP06991.
XX 25-SEP-1998; 98US-0101706.
PR (FARB) BAYER AG.
XX
XX Schmitz G, Klucken J;
XX WPI; 2000-293151/25.
DR XX
XX Adenosine triphosphate binding proteins useful for identifying agents
PT for treating atherosclerosis and other inflammatory disorders -
PT
XX
PS Claim 9; Page 123-125; 154pp; English.
XX
CC The present sequence is that of human ATP binding cassette
CC subfamily C protein ABC5 cDNA. The cDNA was identified using a
CC differential display method in which monocytes from peripheral
CC blood were subjected to macrophage differentiation and cholesterol
CC loading with acetylated low density lipoproteins and subsequent
CC deloading with high density lipoprotein (HDL3) to identify
CC cholesterol sensitive genes. The gene maps to chromosome 3q25-27
CC and is also termed MRP5 (multidrug resistance associated protein).
CC This is the gene locus for Dubin-Johnson syndrome, a disorder
CC associated with mild chronic conjugated hyperbilirubinemia.
CC The invention provides cholesterol-sensitive ABC genes (see
CC AA294734-63). These genes, and polypeptides encoded by them,
CC can be used for diagnostic and therapeutic applications, and for
CC biochemical or cell-based assays to screen for pharmacologically
CC active modulator compounds useful for the treatment of lipid
CC disorders, atherosclerosis or other inflammatory diseases such as
CC psoriasis and lupus erythematosus.
XX
SQ Sequence 5838 BP; 1422 A; 1432 C; 1509 G; 1475 T; 0 other;

Query Match 100.0%; Score 5838; DB 21; Length 5838;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGCAGGTGGCTCATGCTCGGAGCGGTGGTGGAGCGGTGGCGGGTGTCTCTGAGC 60
DB 1 CCGGGCAGGTGGCTCATGCTCGGAGCGGTGGTGGAGCGGTGGCGGGTGTCTCTGAGC 60

QY 61 AGGGGCGCAGGAATCTGATGTGAACACTACAGTCTGTGAGCCCTGGAACCTCGGCTCAG 120
DB 61 AGGGGCGCAGGAATCTGATGTGAACACTACAGTCTGTGAGCCCTGGAACCTCGGCTCAG 120

QY 121 AGAAGTGAAGGATATCGACATAGGAAACAGATATATCATCCCGAGTCCTGGGTATAGAA 180
DB 121 AGAAGTGAAGGATATCGACATAGGAAACAGATATATCATCCCGAGTCCTGGGTATAGAA 180

QY 181 GTGTGGGGAGAGAACCCAGCACTCTCTGGGACGCACAGAGCCGCTGAAGATTCGAAGTTCA 240
DB 181 GTGTGGGGAGAGAACCCAGCACTCTCTGGGACGCACAGAGCCGCTGAAGATTCGAAGTTCA 240

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DB 241 GGAGAACTCGACCGTTGGAAATGCAAGATGCTTGGAAACAGAGCCCGAGCCGAGGGCC 300

QY 301 TCTCTCTTGATGCTCCATCCTCAGCTCAGATCTGAGTCCAGATCTCGGATGAGGATCCCAAGG 360
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DB 361 GAAAGTACCATCATGCGTCTGAGTCTGAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 420

QY 421 ACCCAGTGGACAATGCTGGGCTTTTCTCTGATGACTTTTCTCGTGGCTTTCTCTCTCG 480
DB 421 ACCCAGTGGACAATGCTGGGCTTTTCTCTGATGACTTTTCTCGTGGCTTTCTCTCTCG 480

QY 481 CCCGTGTGGCCACACAAGAGGGGAGCTCTCAATGGAAGACAGTGTGGTCTCTGTCTCAAGC 540
DB 481 CCCGTGTGGCCACACAAGAGGGGAGCTCTCAATGGAAGACAGTGTGGTCTCTGTCTCAAGC 540

QY 541 ACGAGTCTTCTGAGCTGAACCTGCAAGAGCTAGAGAGCTGTGCAAGAGAGCTGAATG 600
DB 541 ACGAGTCTTCTGAGCTGAACCTGCAAGAGCTAGAGAGCTGTGCAAGAGAGCTGAATG 600

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DB 601 AAGTTGGCCAGAGCTGCTTCCCTGCCAAGGGTGTGTGGATCTTCTGCCACCAAGC 660

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DB 1141 TCAGAGCATATTTCCAGGAGAAATGCGTGGCGCCGACGAGTGAACGTGTCCAGAGATGA 1200

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[illegible]

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2641	Db		2700
2641	Db	GTTCACTGCCCTCGTCAGATATATGGTGTCTACATCAGAGCTGCTGGGGGCCCTTGGCAT	2700
2701	Qy	TCTCGTTATTATGGCGCCCTTTTCATGCTGAATGTAGGCACACCGCCTTCAGCACCTGGT	2760
2701	Db	TCTCGTTATTATGGCGCCCTTTTCATGCTGAATGTAGGCACACCGCCTTCAGCACCTGGT	2760
2761	Qy	GGTTGAGTTACTGGATCAGCAAGGAAGCGGGGAACACCACTGTGACTCGAGGGAACGAGA	2820
2761	Db	GGTTGAGTTACTGGATCAGCAAGGAAGCGGGGAACACCACTGTGACTCGAGGGAACGAGA	2820
2821	Qy	CCTCGTGTAGTGACAGCATGAAGSACAATCCTCATATGCAGTACTATGCCAGCATCTACG	2880
2821	Db	CCTCGTGTAGTGACAGCATGAAGSACAATCCTCATATGCAGTACTATGCCAGCATCTACG	2880
2881	Qy	CCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTGTCTTTGTCAAGG	2940
2881	Db	CCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTGTCTTTGTCAAGG	2940
2941	Qy	GCACGCTGCGAGTTCCTCCCGCTCGATGACAGAGTCTTTCCGAAGGATCCTTCGAAGCC	3000
2941	Db	GCACGCTGCGAGTTCCTCCCGCTCGATGACAGAGTCTTTCCGAAGGATCCTTCGAAGCC	3000
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3001	Db		3060
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3121	Db	TGGTGTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCOCGTGTTCTTGTGGCAGTGG	3180
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3181	Db	GGCCCTCTGCATCCCTTTTTCAGTCCGACATTTGTTCCAGGGTCTTGATTCGGGAGC	3240
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3241	Db	TGAAGCGCTGGACRATATCAGCAGTCACCTTTCCTCTCCCACATCAGTCCAGCATAC	3300
3301	Qy	AGGGCTTCCACCATCCAGCGCTACAAATAAGGGCAGGAGTTTCTGCAGATACCAGG	3360
3301	Db	AGGGCTTCCACCATCCAGCGCTACAAATAAGGGCAGGAGTTTCTGCAGATACCAGG	3360
3361	Qy	AGCTGTGTGATGACAAACAGCTCCTTTTTTTTGTAGTGTGAGTCCGGTGCCTGG	3420
3361	Db	AGCTGTGTGATGACAAACAGCTCCTTTTTTTTGTAGTGTGAGTCCGGTGCCTGG	3420
3421	Qy	CTGTGGCGTGGACCTTCATCAGCATCGCCCTCATCACACCACGGGGCTGATCGTTTC	3480
3421	Db	CTGTGGCGTGGACCTTCATCAGCATCGCCCTCATCACACCACGGGGCTGATCGTTTC	3480
3481	Qy	TTATGCACGGGCAGATTCCCCAGCGCTATGCGGGTCTCGCCATCTCTTATGCTGTCAGT	3540
3481	Db	TTATGCACGGGCAGATTCCCCAGCGCTATGCGGGTCTCGCCATCTCTTATGCTGTCAGT	3540
3541	Qy	TAAACGGGCTGTTCAGTTTACGGTTCAGACTGGCATCTGACAGAGAGTCTGCATTCACCT	3600
3541	Db	TAAACGGGCTGTTCAGTTTACGGTTCAGACTGGCATCTGACAGAGAGTCTGCATTCACCT	3600
3601	Qy	CGGTGGAGAGGATCAATCACTACTATTAAGACTCTGTGCTTGGAAAGCACCTGCCAGAAATTA	3660
3601	Db	CGGTGGAGAGGATCAATCACTACTATTAAGACTCTGTGCTTGGAAAGCACCTGCCAGAAATTA	3660
3661	Qy	AGAACAAAGCTCCCTCCCTGACTGCCCCAGGAGGAGGAGTGTGACCTTTTGAAAGCGCAG	3720
3661	Db	AGAACAAAGCTCCCTCCCTGACTGCCCCAGGAGGAGGAGTGTGACCTTTTGAAAGCGCAG	3720

QY 3721 AGATGAGTACCGAGAAACCTCCCTCTGTGCTTAAGAAAGTATCCTTCACGATCAAAAC 3780
DB 3721 AGATGAGTACCGAGAAACCTCCCTCTGTGCTTAAGAAAGTATCCTTCACGATCAAAAC 3780
QY 3781 CTAAGAGAAAGATTGGGATTTGGGGCGGACAGGATCAGGAAAGTCCCTCGCTGGGGATGG 3840
DB 3781 CTAAGAGAAAGATTGGGATTTGGGGCGGACAGGATCAGGAAAGTCCCTCGCTGGGGATGG 3840
QY 3841 CCCCTCTCCGCTGTGGAGTTATCTGAGGCTGCATCAAGATTGATGAGTGAAGATCA 3900
DB 3841 CCCCTCTCCGCTGTGGAGTTATCTGAGGCTGCATCAAGATTGATGAGTGAAGATCA 3900
QY 3901 GTGATATTGGCTTGGCCGACCTCGAAGCAAACTCTCTATCATTTCTCCTCAAGAGCCGGTGC 3960
DB 3901 GTGATATTGGCTTGGCCGACCTCGAAGCAAACTCTCTATCATTTCTCCTCAAGAGCCGGTGC 3960
QY 3961 TGTTCAGTGGGACCTGTGATCAAAATTGGACCCCTTCAACAGTACACTGAAGACCAGA 4020
DB 3961 TGTTCAGTGGGACCTGTGATCAAAATTGGACCCCTTCAACAGTACACTGAAGACCAGA 4020
QY 4021 TTTGGGATGCCCTGGAGAGGACACATGAAAGAAATGTTGCTCAGCTACCTCTGAAC 4080
DB 4021 TTTGGGATGCCCTGGAGAGGACACATGAAAGAAATGTTGCTCAGCTACCTCTGAAC 4080
QY 4081 TTGAATCTGAAGTATGGGATGGGATTAACCTTCTAGTGGGGAGCCGAGCTCTTGT 4140
DB 4081 TTGAATCTGAAGTATGGGATGGGATTAACCTTCTAGTGGGGAGCCGAGCTCTTGT 4140
QY 4141 GCATAGCTAGAGCCCTGCTCGGCACCTGAAGATTCTCATTTTACATCAAGCCACAGCTG 4200
DB 4141 GCATAGCTAGAGCCCTGCTCGGCACCTGAAGATTCTCATTTTACATCAAGCCACAGCTG 4200
QY 4201 CCATGGACACAGACAGACTTATTGATTTCAAGAGACCATCCGAGAAGCAATTTGAGACT 4260
DB 4201 CCATGGACACAGACAGACTTATTGATTTCAAGAGACCATCCGAGAAGCAATTTGAGACT 4260
QY 4261 GTACATGCTGACCATGCTGCTGCACAGGTTCTAGGCTCCGATAGGATTATGG 4320
DB 4261 GTACATGCTGACCATGCTGCTGCACAGGTTCTAGGCTCCGATAGGATTATGG 4320
QY 4321 TGCTGGCCAGGACAGGTGGTGGATTGACACCCATCGCTCTGCTCAACAGACA 4380
DB 4321 TGCTGGCCAGGACAGGTGGTGGATTGACACCCATCGCTCTGCTCAACAGACA 4380
QY 4381 GTTCCCGATTCTATGCCATGTTGCTGCTGCAGAGAACAGGTGCTGCAAGGCTGAC 4440
DB 4381 GTTCCCGATTCTATGCCATGTTGCTGCTGCAGAGAACAGGTGCTGCAAGGCTGAC 4440
QY 4441 TCCTCCCTGTTGAGAGTCTCTTTTCTTTAGAGATTGCCATTCCTGCTGGGGCGGG 4500
DB 4441 TCCTCCCTGTTGAGAGTCTCTTTTCTTTAGAGATTGCCATTCCTGCTGGGGCGGG 4500
QY 4501 CCCCTCATCGCTCTCCTACCGAAACCTTCCTTCGATTTTATCTTCGACAGCA 4560
DB 4501 CCCCTCATCGCTCTCCTACCGAAACCTTCCTTCGATTTTATCTTCGACAGCA 4560
QY 4561 GTTCCGGATTGGCTGTGTTTTCACCTTTAGGGAGAGTCTATTTTGAATTTATTTT 4620
DB 4561 GTTCCGGATTGGCTGTGTTTTCACCTTTAGGGAGAGTCTATTTTGAATTTATTTT 4620
QY 4621 ATTCCATATTGATGAACAAATTTAGTTTGTCTTAATTGCACCTTAAGAGTTCA 4680
DB 4621 ATTCCATATTGATGAACAAATTTAGTTTGTCTTAATTGCACCTTAAGAGTTCA 4680
QY 4681 GGGAACTGTTATTAATTGATCAGAGGCTTAAATGAAGCTTTATACGTAGCTATA 4740
DB 4681 GGGAACTGTTATTAATTGATCAGAGGCTTAAATGAAGCTTTATACGTAGCTATA 4740
QY 4741 TCTATATATATCTGTACATAGCCTATATTACAGTGAAGTGAAGCTGTTATTTTA 4800
DB 4741 TCTATATATATCTGTACATAGCCTATATTACAGTGAAGTGAAGCTGTTATTTTA 4800

QY 4801 TATTAATAAAGCACTGTCTAATAACAGTGCATATTTCTTTCTATCATTTTGTACAGT 4860
DB 4801 TATTAATAAAGCACTGTCTAATAACAGTGCATATTTCTTTCTATCATTTTGTACAGT 4860
QY 4861 TTGCTGTACTAGAGATCTGTTTTTGTATTAGACTGTAGGAAGTAGCATTTTCATTTT 4920
DB 4861 TTGCTGTACTAGAGATCTGTTTTTGTATTAGACTGTAGGAAGTAGCATTTTCATTTT 4920
QY 4921 CTCCTAGCTGGTGGTTTTCAGGTCGCCAGGTTTCTGGGTGCTCCAAAGAAAGACGTG 4980
DB 4921 CTCCTAGCTGGTGGTTTTCAGGTCGCCAGGTTTCTGGGTGCTCCAAAGAAAGACGTG 4980
QY 4981 ATAGTGGGCCCCCAGACAGCCCTCTGCGGCTCCACAGCCGCTCCAGGGGTGGCTG 5040
DB 4981 ATAGTGGGCCCCCAGACAGCCCTCTGCGGCTCCACAGCCGCTCCAGGGGTGGCTG 5040
QY 5041 GAGAGGGTGGGCGGTGGAGCCATGACAGAGCCGCTGAGTTTCTCAGGGCTCTCTGCTT 5100
DB 5041 GAGAGGGTGGGCGGTGGAGCCATGACAGAGCCGCTGAGTTTCTCAGGGCTCTCTGCTT 5100
QY 5101 CTGCTCTGCTGCTACTTACTGTTTCTGTCAGGAGAGAGCGGGGCGAAGCCAGGCCCT 5160
DB 5101 CTGCTCTGCTGCTACTTACTGTTTCTGTCAGGAGAGAGCGGGGCGAAGCCAGGCCCT 5160
QY 5161 TTTCACTCCCTCCATCAAGAAATGGGATCACAGAGACATTTCTCCAGAGCCGGGAGTTTC 5220
DB 5161 TTTCACTCCCTCCATCAAGAAATGGGATCACAGAGACATTTCTCCAGAGCCGGGAGTTTC 5220
QY 5221 TTTTCTGCTCTCTTTCTTTTGTGTTTCTTAAACAAGAAATCAGTCTATATCCACAGAG 5280
DB 5221 TTTTCTGCTCTCTCTTTTGTGTTTCTTAAACAAGAAATCAGTCTATATCCACAGAG 5280
QY 5281 TCCCCTGCTCAGGTTTCTATGGCTGGCCACTGACAGAGCTCTCCAGTCCCAAGACCT 5340
DB 5281 TCCCCTGCTCAGGTTTCTATGGCTGGCCACTGACAGAGCTCTCCAGTCCCAAGACCT 5340
QY 5341 GTTGGTTTCAAGCCCTGGAGCCAACTGCTGCTTTTGGAGTGGCACTTTTTCATTTGCTT 5400
DB 5341 GTTGGTTTCAAGCCCTGGAGCCAACTGCTGCTTTTGGAGTGGCACTTTTTCATTTGCTT 5400
QY 5401 ATTCCACACCTCCACAGTTTCTAGTGGCAGGCTCAGGATTTTCTGGGCTCTGTTTCTT 5460
DB 5401 ATTCCACACCTCCACAGTTTCTAGTGGCAGGCTCAGGATTTTCTGGGCTCTGTTTCTT 5460
QY 5461 CTCACGCGAGTGTGCGACAGTCTCTCTCTCTCCCTCAAAGTCTGCAACTTTAAG 5520
DB 5461 CTCACGCGAGTGTGCGACAGTCTCTCTCTCTCTCCCTCAAAGTCTGCAACTTTAAG 5520
QY 5521 CAGCTCTTCTAATCAGTCTCTCACACTGGCGTAGAAGTTTGTACTGTAAAGAGACCT 5580
DB 5521 CAGCTCTTCTAATCAGTCTCTCACACTGGCGTAGAAGTTTGTACTGTAAAGAGACCT 5580
QY 5581 ACCTCAGGTTGCTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5640
DB 5581 ACCTCAGGTTGCTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5640
QY 5641 GGGGCTGTAGCTCAGGTGGGGTGGTCTGCTGCTCAATCAGTTGAATGGTCAAGCTTGC 5700
DB 5641 GGGGCTGTAGCTCAGGTGGGGTGGTCTGCTGCTCAATCAGTTGAATGGTCAAGCTTGC 5700
QY 5701 ATGCTGTGACCAACTAGACATTTCTGCTGCTTAGAGATTTTGTGCTGAACCTTTGTGAAG 5760
DB 5701 ATGCTGTGACCAACTAGACATTTCTGCTGCTTAGAGATTTTGTGCTGAACCTTTGTGAAG 5760
QY 5761 CAAAAATCTGAATGTGAATAAAAATTTTGGATTTTGTAAAAAATAAAAAA 5820
DB 5761 CAAAAATCTGAATGTGAATAAAAATTTTGGATTTTGTAAAAAATAAAAAA 5820
QY 5821 AAAAAAATAAAAAA 5838
DB 5821 AAAAAAATAAAAAA 5838

RESULT 3
 AAA40481
 ID AAA40481 standard; cDNA; 4847 BP.
 XX
 AC AAA40481;
 DT 23-NOV-2000 (first entry)
 XX
 DE Human MRP-beta cDNA.
 XX
 KW MRP-beta; multidrug-resistance associated protein; human; cytostatic;
 KW chemotherapy; cancer cell; drug discovery; cytotoxic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 116..4429
 FT /*tag= a
 FT /product= "MRP-beta"
 XX
 FT US6077936-A.
 PN 20-JUN-2000.
 XX
 PF 16-APR-1998; 98US-0061400.
 XX
 PR 16-APR-1997; 97US-0843459.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Shyjan A;
 XX
 DR WPI; 2000-430613/37.
 DR P-PSDB; AAB10225.
 XX
 PT Model multidrug-resistance associated polypeptide useful for improving
 PT the effectiveness of a chemotherapeutic regimen to eradicate
 PT multidrug-resistant transformed cells especially cancer cells -
 XX
 PS Claim 6; Fig 1A-D; 43pp; English.
 XX
 CC This invention describes a novel model multidrug-resistance associated
 CC polypeptide, MRP-beta (I) which has cytostatic activity. Inhibitors of
 CC (I) are useful for improving the effectiveness of a chemotherapeutic
 CC regimen to eradicate multidrug-resistant transformed cells, especially
 CC cancer cells, from the body of a mammal, preferably human. (I) is also
 CC useful for drug discovery, especially to the design of novel
 CC chemotherapeutic drugs that are cytotoxic to cells expressing (I). This
 CC sequence encodes the human MRP-beta protein which is described in the
 CC method of the invention.
 XX
 SQ Sequence 4847 BP; 1226 A; 1178 C; 1263 G; 1180 T; 0 other;
 Query Match 82.1%; Score 4792.6; DB 21; Length 4847;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
 QY 11 GGCTCATGCTGGGAGCGTGGTGGAGCGGTGGCGCGGTGGTCTCTGGAGCGGGCGAG 60
 DB 1 GGCTCATGCTGGGAGCGTGGTGGAGCGGTGGCGCGGTGGTCTCTGGAGCGGGCGAG 60
 QY 71 GAATTCGATGTGAACTACAGTCTGTAGCCCTGGAACCTCGGCTCAGAGAAGATGAA 130
 DB 61 GAATTCGATGTGAACTACAGTCTGTAGCCCTGGAACCTCGGCTCAGAGAAGATGAA 120
 QY 131 GGATATCGACATAGGAAAGAGTATATCATCCCGAGTCCTGGGTATAGAGTGTGAGGGA 190
 DB 121 GGATATCGACATAGGAAAGAGTATATCATCCCGAGTCCTGGGTATAGAGTGTGAGGGA 180
 QY 191 GAGAACGACGACTTCTGGGACGACAGAGCCGTGGAAGATTCCAAGTTCCAGGAACTCG 250
 DB 181 GAGAACGACGACTTCTGGGACGACAGAGCCGTGGAAGATTCCAAGTTCCAGGAACTCG 240

QY 251 ACCGTTGGAATGCCAAGATGCTTGGAAACACGACGCCGAGCCGAGGGCCTCTCTTGA 310
 DB 241 ACCGTTGGAATGCCAAGATGCTTGGAAACACGACGCCGAGCCGAGGGCCTCTCTTGA 300
 QY 311 TGCCTCCATGCAATCTCAGCTCAGAAATCCTGGATGAGGAGCATCCCAAGGGAAGTACCA 370
 DB 301 TGCCTCCATGCAATCTCAGCTCAGAAATCCTGGATGAGGAGCATCCCAAGGGAAGTACCA 360
 QY 371 TCATGGCTGAGTGTCTGAAGCCCATCCGGACTACTTCCAAACACACAGCACCAGTGA 430
 DB 361 TCATGGCTGAGTGTCTGAAGCCCATCCGGACTACTTCCAAACACACAGCACCAGTGA 420
 QY 431 CAATCTGGGCTTTTCTCTGATGACTTTTCGTCGGCTTCTCTCTGGCCCGTGTGC 490
 DB 421 CAATCTGGGCTTTTCTCTGATGACTTTTCGTCGGCTTCTCTCTGGCCCGTGTGC 480
 QY 491 CCACAAGAGGGGAGCTCTCAATGGAAGAGCTGTGGTCTCTGTCCAAAGCAGCTCTTC 550
 DB 481 CCACAAGAGGGGAGCTCTCAATGGAAGAGCTGTGGTCTCTGTCCAAAGCAGCTCTTC 540
 QY 551 TGACGTGAAGTGCAGAGACTAGAGACTGTGGCAAGAGAGCTGAATGAAGTTGGGCC 610
 DB 541 TGACGTGAAGTGCAGAGACTAGAGACTGTGGCAAGAGAGCTGAATGAAGTTGGGCC 600
 QY 611 AGACGCTGCTTCCCTGCGAAGGTTGTGTGGATCTTCTGCGCCACACAGGCTCATCTGTC 670
 DB 601 AGACGCTGCTTCCCTGCGAAGGTTGTGTGGATCTTCTGCGCCACACAGGCTCATCTGTC 660
 QY 671 CATCGTGTGCTGATGATCAGCAGCTGGCTGGCTTCAAGTGACAGCAGCTTCAATGGTGA 730
 DB 661 CATCGTGTGCTGATGATCAGCAGCTGGCTGGCTTCAAGTGACAGCAGCTTCAATGGTGA 720
 QY 731 ACACCTTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTGTAGT 790
 DB 721 ACACCTTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTGTAGT 780
 QY 791 GCTGGGCTCTCTCTGAGGAAATCGTCGGCTTGTGGTCTGCTGACATGACTTGGGCATT 850
 DB 781 GCTGGGCTCTCTCTGAGGAAATCGTCGGCTTGTGGTCTGCTGACATGACTTGGGCATT 840
 QY 851 GAATTCAGAACCGGTGTCCGCTTGGGGGGGCATCTCAACCTAGGCTTAAAGAAAT 910
 DB 841 GAATTCAGAACCGGTGTCCGCTTGGGGGGGCATCTCAACCTAGGCTTAAAGAAAT 900
 QY 911 CCTTAAGTTAAGAACATTAAGAGAAATCCCTGGGTGAGCTATCAACATTTGCTCCAA 970
 DB 901 CCTTAAGTTAAGAACATTAAGAGAAATCCCTGGGTGAGCTATCAACATTTGCTCCAA 960
 QY 971 CGATGGGCGAGAGATGTTTGGAGCAGCAGCGTTGGCAGCCTGCTGGGAGGACCGGT 1030
 DB 961 CGATGGGCGAGAGATGTTTGGAGCAGCAGCGTTGGCAGCCTGCTGGGAGGACCGGT 1020
 QY 1031 TGTGGCATCTTAGGCATGATTATTAATGTAATTTCTGGGACCAACAGGCTTCTCTGGG 1090
 DB 1021 TGTGGCATCTTAGGCATGATTATTAATGTAATTTCTGGGACCAACAGGCTTCTCTGGG 1080
 QY 1091 ATCAGCTGTTTTATPCCTCTTTTACCCAGCAATGATGTTTGCATCAGGCTCAGAGATA 1150
 DB 1081 ATCAGCTGTTTTATPCCTCTTTTACCCAGCAATGATGTTTGCATCAGGCTCAGAGATA 1140
 QY 1151 TTTCCAGGAGAAATGCGTGGCGCCACCGATGAACGCTGCCAGAGATGAATGAAGTTCT 1210
 DB 1141 TTTCCAGGAGAAATGCGTGGCGCCACCGATGAACGCTGCCAGAGATGAATGAAGTTCT 1200
 QY 1211 TACTTACATTAATTTATCAAAATGATGCTGGTCAAGCATTTCTCAGAGTGTTC 1270
 DB 1201 TACTTACATTAATTTATCAAAATGATGCTGGTCAAGCATTTCTCAGAGTGTTC 1260
 QY 1271 AAAAATCCGAGGAGGAGCGTCGATATTGAAAAAGCCGGTACTTCCAGGCTATCAC 1330
 DB 1261 GAAAATCCGAGGAGGAGCGTCGATATTGAAAAAGCCGGTACTTCCAGAGCATCAC 1320
 QY 1331 TGTGGGTGTGCTCCCATTTGTTGGTGAATGGCCAGCGTGTGACCTTCTCTGTTTCAAT 1390

Db 1321 TGTGGGTGTGGCTCCCAATTCGTGTGTGATGTCAGCGTGGTACCTTCTCTGTTCATAT 1380
 QY 1391 GACCTGGGCTTCGATCTGACAGACAGCAGGCTTTCACAGTGTGTGACAGTCTTCAATTC 1450
 Db 1381 GACCCCTGGGCTTCGATCTGACAGCAGCAGCAGGCTTTCACAGTGTGTGACAGTCTTCAATTC 1440
 QY 1451 CATGACCTTTTGTCTTGAAGCTAACACCGTTTTCAGTAAAGTCCCTCTCAAGAGCCTCAGT 1510
 Db 1441 CATGACCTTTTGTCTTGAAGCTAACACCGTTTTCAGTAAAGTCCCTCTCAAGAGCCTCAGT 1500
 QY 1511 GGCTGTGTACAGATTTAAGAGTTTGTCTTAATGGAGAGGTTTCACATGATAAAGACAA 1570
 Db 1501 GGCTGTGTACAGATTTAAGAGTTTGTCTTAATGGAGAGGTTTCACATGATAAAGACAA 1560
 QY 1571 ACCAGCAGTCTCACATCAAGTAGAGATGAAATGCCACCTTGGCATGGGACTCCTC 1630
 Db 1561 ACCAGCAGTCTCACATCAAGTAGAGATGAAATGCCACCTTGGCATGGGACTCCTC 1620
 QY 1631 CCACTCCAGTATCCAGAACTCGCCAGCTGACCGTGCACCCCAAAATGAAAAGACAGAGGGC 1690
 Db 1621 CCACTCCAGTATCCAGAACTCGCCAGCTGACCGTGCACCCCAAAATGAAAAGACAGAGGGC 1680
 QY 1691 TTCCAGGGCAAGAAAGAGAGGTGAGGCAAGCTGCAGCGCACTGAGCATCAGGGCGTGTCT 1750
 Db 1681 TTCCAGGGCAAGAAAGAGAGGTGAGGCAAGCTGCAGCGCACTGAGCATCAGGGCGTGTCT 1740
 QY 1751 GGCAGAGCAAGAGGCCACCTCTCTCTGGACAGTGACAGCGGCCCCAGTCCCGAAGAGGA 1810
 Db 1741 GGCAGAGCAAGAGGCCACCTCTCTCTGGACAGTGACAGCGGCCCCAGTCCCGAAGAGGA 1800
 QY 1811 AGAAGCAAGCAACATCCACTGGCCGACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1870
 Db 1801 AGAAGCAAGCAACATCCACTGGCCGACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
 QY 1871 TCTGGAGATCCAAAGAGGGTAACTGTTGGAATCTGCGGCAAGTGTGGAAAGTGGAAAAAC 1930
 Db 1861 TCTGGAGATCCAAAGAGGGTAACTGTTGGAATCTGCGGCAAGTGTGGAAAGTGGAAAAAC 1920
 QY 1931 CTCTCTCATTTAGCCCATTTAGCCCATGAGCGTCTTACAGAGGCAAGCATTCGAATCAG 1990
 Db 1921 CTCTCTCATTTAGCCCATTTAGCCCATGAGCGTCTTACAGAGGCAAGCATTCGAATCAG 1980
 QY 1991 TGAACCTTCGCTTATGTGCCCCAGAGCGCTGATCTCAATGCTACTCTGAGAGACAA 2050
 Db 1981 TGAACCTTCGCTTATGTGCCCCAGAGCGCTGATCTCAATGCTACTCTGAGAGACAA 2040
 QY 2051 CATCTCTTTTGGGAAGGAATATGATGAAGAAAGATACAATCTGTCTGAACAGCTGCTG 2110
 Db 2041 CATCTCTTTTGGGAAGGAATATGATGAAGAAAGATACAATCTGTCTGAACAGCTGCTG 2100
 QY 2111 CTTGAGCGCTGACCTGGCCATTTCTCCAGACGCGCTGACGAGATTGGAGCGAGG 2170
 Db 2101 CTTGAGCGCTGACCTGGCCATTTCTCCAGACGCGCTGACGAGATTGGAGCGAGG 2160
 QY 2171 AGCCAACTTCAGCGGTGGGCGAGCGCAGAGATCAGCGTTCGCCGCGCTGTGATAGTGA 2230
 Db 2161 AGCCAACTTCAGCGGTGGGCGAGCGCAGAGATCAGCGTTCGCCGCGCTGTGATAGTGA 2220
 QY 2231 CAGGAGCATCTACATCTTGGACACCGCCCTCAGTGCCTTAGATGCCCATGTGGSCAACCA 2290
 Db 2221 CAGGAGCATCTACATCTTGGACACCGCCCTCAGTGCCTTAGATGCCCATGTGGSCAACCA 2280
 QY 2291 CATCTTCAATAGTGTATTCGGAAACATCTCAAGTCCAAAGACAGTCTGTGTTGTTACCCA 2350
 Db 2281 CATCTTCAATAGTGTATTCGGAAACATCTCAAGTCCAAAGACAGTCTGTGTTGTTACCCA 2340
 QY 2351 CCAGTTACAGTACTGTTGACCTGATGAAGTATCTTCAATGAAGGGCTGTATTAC 2410
 Db 2341 CCAGTTACAGTACTGTTGACCTGATGAAGTATCTTCAATGAAGGGCTGTATTAC 2400
 QY 2411 GGAAGAGGCGACCATCAGGAACATGATGAATTTAAATGGTGACTATCTACCATTTTAA 2470

Db 2401 GGAAGAGGCGCCCATGAGGAACGTGATGAATTTAAATGGTGACTATGCTACCATTTTAA 2460
 QY 2471 TAACTGTTTGTGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAGGAACACAGTGG 2530
 Db 2461 TAACTGTTTGTGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAGGAACACAGTGG 2520
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 Db 2521 TTAACAGAAAGTACACAAAGACAAAGGTCCTAAAACAGATCAATAAAGAAAGAAAGC 2580
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 Db 2581 AGTAAAGCAGAGGAAGGCGCAGCTTGTGAGCTGGAAGAAAGGCGAGGTTCACTGCGC 2640
 QY 2651 CTGGTCACTATATGCTGTCTACATCCAGGCTGCTGGGGCCCCCTTGGCATTTCTGTTAT 2710
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 QY 2711 TATGGCCCTTTTCACTGCTGAATGTAGGAGCAGCACCCCTTCAGACCTGGTGTGATTA 2770
 Db 2701 TATGGCCCTTTTCACTGCTGAATGTAGGAGCAGCACCCCTTCAGACCTGGTGTGATTA 2760
 QY 2771 CTGATCAAGCAAGGAAGGCGGGAACACCACTGTGACTCGAGGGAACAGACCTCGGTGAG 2830
 Db 2761 CTGATCAAGCAAGGAAGGCGGGAACACCACTGTGACTCGAGGGAACAGACCTCGGTGAG 2820
 QY 2831 TGACAGCATGAAGGACAATCTCATATGACGTACTATGCCAGCATCTACGCCCTCTCCAT 2890
 Db 2821 TGACAGCATGAAGGACAATCTCATATGACGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
 QY 2891 GGCAGTCACTGCTGATCTCTGAAGCCATTCGAGGAGTTGTCTTTGTCAGGGGACGCTGCG 2950
 Db 2881 GGCAGTCACTGCTGATCTCTGAAGCCATTCGAGGAGTTGTCTTTGTCAGGGGACGCTGCG 2940
 QY 2951 AGCTTCTCTCCGGCTGCTGATGACGAGCTTTTCCGAAGGATCTCTCGAAGCCCTATGAAGTT 3010
 Db 2941 AGCTTCTCTCCGGCTGCTGATGACGAGCTTTTCCGAAGGATCTCTCGAAGCCCTATGAAGTT 3000
 QY 3011 TTTTGAACAGACCCCGCAGGAGGATTCCTCAACAGGTTTCCAAAGACATGGATGAAGT 3070
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 Db 3121 CTGTGTGGGAATGATCGCAGAGGCTTCCCGTGTGCTTCTGTCAGTGGGCGCCCTTGT 3180
 QY 3191 CATCTCTTTTCACTGCTGCAATGCTTCCAGGCTCTGATTCGGGAGCTGAAGCGCT 3250
 Db 3181 CATCTCTTTTCACTGCTGCAATGCTTCCAGGCTCTGATTCGGGAGCTGAAGCGCT 3240
 QY 3251 GGCAATATACAGCAGTCACTTCTTCCACATCAGTCCACGATACAGGCGCTTGC 3310
 Db 3241 GGCAATATACAGCAGTCACTTCTTCCACATCAGTCCACGATACAGGCGCTTGC 3300
 QY 3311 CACCATCCAGCCTTACATAAAGGCGAGGTTTCTGCACAGATACAGGAGCTGCTGGA 3370
 Db 3301 CACCATCCAGCCTTACATAAAGGCGAGGTTTCTGCACAGATACAGGAGCTGCTGGA 3360
 QY 3371 TGACAAACAAGCTCTTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGTGCGGCT 3430
 Db 3361 TGACAAACAAGCTCTTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGTGCGGCT 3420
 QY 3431 GGACCTCATCAGCATCGCCCTCATCACACCGCGGCTGATGCTGCTTATGCACGG 3490
 Db 3421 GGACCTCATCAGCATCGCCCTCATCACACCGCGGCTGATGCTGCTTATGCACGG 3480
 QY 3491 GCAGTTTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAACGGGCT 3550
 Db 3481 GCAGTTTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAACGGGCT 3540

QY	3551	GTTCAGGTTTACGGTCAGACTGCGATCTCAGACAGAAGCTCGATTTCACCTCGGTGGAGAG	3611
DB	3541		3600
QY	3611	GATCAATCACTACATTAAGAAGCTCTGTCCTTTGGAAGCACTGCGAGAATTAAAGAACAAAGGC	3670
DB	3601		3660
QY	3671	TCCCTCCCTTACTGCGCCCGAGAGGGAGAGTGACCTTTGAGAACGCGAGAGATGAGGTA	3730
DB	3661		3720
QY	3731	CCGAGAAACCTCCCTTTGTCTTAAGAAAGCTATCTCTTCAGATCAAACTCAAGAGAA	3790
DB	3721		3780
QY	3791	GATTGGCATTGTGGGCGGACAGGATCAGGGAAGTCTCGCTGGGGATGGCCCTCTTCCG	3850
DB	3781		3840
QY	3851	TCGTGGGAGTATCTGGAGGCTGCATCAAGAATTGATGGAGTGAGAACTCAGTGATATGG	3910
DB	3841		3900
QY	3911	CCTTGGCGACCTCGAAGCAAACTCTATATCTCTCAAGACCGGTGCTGTTCAGTGG	3970
DB	3901		3960
QY	3971	CACGTGCAGATCAAAATTTGGACCCCTTCAACCACTACACTGAAGACCCAGATTTGGGATGC	4030
DB	3961		4020
QY	4031	CTCTGGAGAGGACACATGAAAGATGTATGCTCAGCTACCTCTGAAACTTGAATCTGA	4090
DB	4021		4080
QY	4091	AGTGATGGAGATGGGATTAACCTCTCAGTGGGGAAACGGCAGCTCTGTGTCATAGCTAG	4150
DB	4081		4140
QY	4151	AGCCCTGCTCCGCCACTGTAAGATTTCTGATTTAGATGAAGCCACAGCTGCCATGGACAC	4210
DB	4141		4200
QY	4211	AGAGACAGACTTATGATTTCAAGACACATCCGAGAGCAATTTCCAGACTGTACATGCT	4270
DB	4201		4260
QY	4271	GACCATTGCCCATCGCTCCACACAGGTTCTAGGCTCCGATAGGATTAATGCTGCTGGCCCA	4330
DB	4261		4320
QY	4331	GGACAGGTGGTGGATTTGACACCCCATCGCTCTCTGTCTGTCCAACGACAGTTCCCGATT	4390
DB	4321		4380
QY	4391	CTATGCCATGTTTGTCTGTCGAGAGAACAGGTGCTGTCAAGGGCTGACTCTCCCTGT	4450
DB	4381		4440
QY	4451	TGACGAAGTCTCTTTTCTTAGAGCATTTGCCATTCCTGCTGGGGGGGGCCCC-TCATC	4509
DB	4441		4500
QY	4510	GCCTCCTCTACCGAAACCTTGCCCTTCTCGATTTATCTTTTCGCACAGCAGTTCCGGAT	4569
DB	4501		4560
QY	4570	TGCGTTGTGTGTTTTCATTTTATAGGAGAGTCAATATTTTGTATTAATGATTTATTCATAT	4629
DB	4561		4620

QY	4630	TCATGTAACAACAATTTAGTTTGTCTTAATTCGACTCTAAAGGTTTCAGGGAACCGT	4680
DB	4621	TCATGTAACAACAATTTAGTTTGTCTTAATTCGACTCTAAAGGTTTCAGGGAACCGT	4680
QY	4690	TATTATAAATGTATCAGAGGCTTATATGAAGCTTTTATAGCTGCTAGCTATATCTATATAT	4749
DB	4681	TATTATAAATGTATCAGAGGCTTATATGAAGCTTTTATAGCTGCTAGCTATATCTATATAT	4740
QY	4750	AATTCGTGATACAGCCCTATATTTACAGTGAATAATGTAAGCTGTTTATTTTATATTTAAAT	4809
DB	4741	AATTCGTGATACAGCCCTATATTTACAGTGAATAATGTAAGCTGTTTATTTTATATTTAAAT	4800
QY	4810	AAGCACTGTGCTTAATAACA 4828	
DB	4801	AAGCACTGTGCTTAATAAAA 4819	
RESULT 4			
AAV65682			
ID	AAV65682 standard; cDNA; 4847 BP.		
AC	AAV65682;		
XX			
DT	02-FEB-1999 (first entry)		
XX			
DE	Human multidrug resistance-associated protein cDNA.		
KW	Multidrug resistance-associated protein; MRP-beta; human; cancer;		
KW	tumour; chemotherapy; therapy; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	116..4429	
ET		/*tag= a	
XX			
PN	WO9846736-A1.		
XX			
PD	22-OCT-1998.		
XX			
PF	16-APR-1998; 98WO-US07673.		
XX			
PR	16-APR-1997; 97US-0843459.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Shyjan A;		
XX			
DR	WPI; 1998-568724/48.		
DR	P-PSDB; AAW80597.		
XX			
PT	New isolated multidrug resistance-associated polypeptide - used to		
PT	develop products for modulating multidrug resistance, particularly		
PT	for reducing resistance of tumours to chemotherapeutic drugs		
XX			
PS	Claim 1; Page 54-59; 93pp; English.		
XX			
CC	This nucleotide sequence codes for novel human multidrug resistance		
CC	associated protein (MRP-beta, see AAW80597), over-expression of which		
CC	is thought to be associated with the emergence and/or persistence		
CC	of a multidrug-resistance phenotype in transformed mammalian cells,		
CC	including carcinoma and adenocarcinoma cells. A unique fragment		
CC	(see AAV65683) of the MRP-beta gene was identified by computer		
CC	assisted searching of a nucleic acid database corresponding to a		
CC	human endothelial cell (HUMVEC) expression library. It was used		
CC	to screen the HUMVEC expression library. This yielded a 4.78 kb		
CC	clone, designated fohd013a05m (deposited as ATCC 98409). Two		
CC	independent cDNA clones comprising approximately 60 residues		
CC	upstream from fohd013a05m were isolated by hybridisation screening		
CC	of human brain and liver cDNA libraries using a probe from the 5'		
CC	end of fohd01305m. The presented sequence of MRP-beta cDNA		
CC	comprises fohd01305m and 66 additional upstream nucleotides. The		
CC	invention provides compositions and methods for improving the		

effectiveness of chemotherapeutic regimens to eradicate
multidrug-resistant transformed cells from the body of a mammal,
especially a human. the disclosed compositions include MRP-beta
nucleic acids, including probes and antisense oligonucleotides
(see also AAV65684-88), MRP-beta polypeptides and antibodies,
MRP-beta expressing host cells, and non-human mammals that are
transgenic or nullizygous for MRP-beta. The disclosed methods
include methods for attenuating aberrant MRP-beta gene expression,
protein production and/or protein function, and for improving the
effectiveness of chemotherapy for a mammal afflicted with a
multidrug-resistant tumour, wherein the tumour is of mammary,
respiratory tract, urogenital tract, endocrine system or immune
system origin. In addition, methods are disclosed for identifying
and using a modulator, such as an inhibitor, that is cytotoxic to
cells expressing MRP-beta.

xx
SQ Sequence 4847 BP; 1225 A; 1179 C; 1263 G; 1180 T; 0 other;

Query Match 82.1%; Score 4791; DB 19; Length 4847;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4808; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 11 GGCTCATGCTCGGAGCGTGGTGGAGCGGCTGGCGGCTGCTCGTGGAGCGGCGGAG 70
DB 1 GGCTCATGCTCGGAGCGTGGTGGAGCGGCTGGCGGCTGCTCGTGGAGCGGCGGAG 60

QY 71 GAATTCGTGTGAACCTACAGTCTGTGAGCCCTGGAACCTCGCTCAGAGAGATGAA 130
DB 61 GAATTCGTGTGAACCTACAGTCTGTGAGCCCTGGAACCTCCTCAGAGAGATGAA 120

QY 131 GGATTCGACATAGAAAGAGTATATCATCCCGAGTCTGGGTATAGAACTGTGAGGA 190
DB 121 GGATTCGACATAGAAAGAGTATATCATCCCGAGTCTGGGTATAGAACTGTGAGGA 180

QY 191 GAGAACAGACATCTCTGGGAGCGACAGAGACCGTGAAGATTCAGAGAGAACTCG 250
DB 181 GAGAACAGACATCTCTGGGAGCGACAGAGACCGTGAAGATTCAGAGAGAACTCG 240

QY 251 ACCGTGGATGCCAAGATGCTTGGAAACAGAGCCGCGAGCCGAGGCGCTCTCTTTGA 310
DB 241 ACCGTGGATGCCAAGATGCTTGGAAACAGAGCCGCGAGCCGCGCTCTCTTTGA 300

QY 311 TGCTCCATCATCTCTCAGTCTCAGATCTGATGAGGAGCATCCCAAGGGAAGTACCA 370
DB 301 TGCTCCATCATCTCTCAGTCTCAGATCTGATGAGGAGCATCCCAAGGGAAGTACCA 360

QY 371 TCATGGCTTGAGTGTCTGAAGCCCATCCGAGTCTACTTCCAAACACAGCAGCCAGTGA 430
DB 361 TCATGGCTTGAGTGTCTGAAGCCCATCCGAGTCTACTTCCAAACACAGCAGCCAGTGA 420

QY 431 CAATGCTGGCTTTTTCCTGTATGACTTTTCTGCTGGCTTCTTCTCTGGCCGCTGTGC 490
DB 421 CAATGCTGGCTTTTTCCTGTATGACTTTTCTGCTGGCTTCTTCTCTGGCCGCTGTGC 480

QY 491 CCACAAAGAGGGGAGCTCTCAATGGAAGAGAGTGTGTCTCTGTCACAGCAGAGTCTTC 550
DB 481 CCACAAAGAGGGGAGCTCTCAATGGAAGAGAGTGTGTCTCTGTCACAGCAGAGTCTTC 540

QY 551 TGAGCTGAATCGAAGAGCTAGAGAGTGTGGCAAGAGAGTGAATGAAGTTGGGCC 610
DB 541 TGAGCTGAATCGAAGAGCTAGAGAGTGTGGCAAGAGAGTGAATGAAGTTGGGCC 600

QY 611 AGAGCTGCTTCCCTGGAAGGTTGTGTGATCTTCTGCGCAGCAGGCTCATCCTGTC 670
DB 601 AGAGCTGCTTCCCTGGAAGGTTGTGTGATCTTCTGCGCAGCAGGCTCATCCTGTC 660

QY 671 CATCGTGTGCTGTATGATCATCGAGTGGCTGGCTTCAGTGGACAGCAGCTTCATGGTGA 730
DB 661 CATCGTGTGCTGTATGATCATCGAGTGGCTGGCTTCAGTGGACAGCAGCTTCATGGTGA 720

QY 731 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTTAACCTGACAGTACAGCTTGTGTAGT 790
DB 721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTTAACCTGACAGTACAGCTTGTGTAGT 780

QY 791 GCTGGCCCTCTCTCGACGGAATCGTGGGCTTGGTCTGCTGCACTGACTTTGGGCAT 850
DB 781 GCTGGCCCTCTCTCGACGGAATCGTGGGCTTGGTCTGCTGCACTGACTTTGGGCAT 840

QY 851 GAATTAACGAACCGGTGCTCGCTTGGGGGGGCGCATCTTAACCATGSCATTTAAGAAGAT 910
DB 841 GAATTAACGAACCGGTGCTCGCTTGGGGGGGCGCATCTTAACCATGSCATTTAAGAAGAT 900

QY 911 CTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 970
DB 901 CTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960

QY 971 CGATGGGAGAGAAATGTTTGGGCGAGCAGCCGTTGGCAGCCGCTGCTGGTGGAGGACCGT 1030
DB 961 CGATGGGAGAGAAATGTTTGGGCGAGCAGCCGTTGGCAGCCGCTGCTGGTGGAGGACCGT 1020

QY 1031 TGTTCGCCATCTTAGCATGATTATAATCTAATTTCTGGGACCAACAGGCTTCTCTGG 1090
DB 1021 TGTTCGCCATCTTAGCATGATTATAATCTAATTTCTGGGACCAACAGGCTTCTCTGG 1080

QY 1091 ATCAGCTGTTTATCTCTCTTTTACCCAGCAATGATGTTTGCATCAGGCTCACAGCAT 1150
DB 1081 ATCAGCTGTTTATCTCTCTTTTACCCAGCAATGATGTTTGCATCAGGCTCACAGCAT 1140

QY 1151 TTTTCCAGGAGAAATCGGTGGCGCCGACGGATGAACGTGTCCAGAAAGTGAATGAAATCT 1210
DB 1141 TTTTCCAGGAGAAATCGGTGGCGCCGACGGATGAACGTGTCCAGAAAGTGAATGAAATCT 1200

QY 1211 TACTTACATTAATTTATCAAAATGATGCTGGGTGGAAGCATTTTTCAGAGTGTTC 1270
DB 1201 TACTTACATTAATTTATCAAAATGATGCTGGGTGGAAGCATTTTTCAGAGTGTTC 1260

QY 1271 AAAATCCGCGAGGAGCGCTCGGATATTGGAAGGCGGCTACTTCCAGGCTATCAC 1330
DB 1261 GAAATCCGCGAGGAGCGCTCGGATATTGGAAGGCGGCTACTTCCAGGCTATCAC 1320

QY 1331 TGTGGGTGGCTCCCATGTTGGTGTGATGCGCAGCGTGGTGAACCTCTCTGTTTCAAT 1390
DB 1321 TGTGGGTGGCTCCCATGTTGGTGTGATGCGCAGCGTGGTGAACCTCTCTGTTTCAAT 1380

QY 1391 GACCTGGCTTCGATCTGACAGCAGCAGCTTTTACAGTGGTGACAGTCTTCAATTC 1450
DB 1381 GACCTGGCTTCGATCTGACAGCAGCAGCTTTTACAGTGGTGACAGTCTTCAATTC 1440

QY 1451 CATGACTTTTGTGTTGAAGTAAACCGCTTTTTCAGTAAAGTCCCTCTCAGAAAGCTCAGT 1510
DB 1441 CATGACTTTTGTGTTGAAGTAAACCGCTTTTTCAGTAAAGTCCCTCTCAGAAAGCTCAGT 1500

QY 1511 GGCTGTTGACAGATTAAAGATTGTTTCTAATGGAAGAGTTCACATGATAAAGAACAA 1570
DB 1501 GGCTGTTGACAGATTAAAGATTGTTTCTAATGGAAGAGTTCACATGATAAAGAACAA 1560

QY 1571 ACCAGCCAGTCTCATCAAGATAGAGATGAAATGCACTTGGCATGGGACTCCCTC 1630
DB 1561 ACCAGCCAGTCTCATCAAGATAGAGATGAAATGCACTTGGCATGGGACTCCCTC 1620

QY 1631 CCATCTCCAGTATCCAGAACTCGCCCAAGTGAACCCCAAAATGAAAGAGAGAGGCG 1690
DB 1621 CCATCTCCAGTATCCAGAACTCGCCCAAGTGAACCCCAAAATGAAAGAGAGAGGCG 1680

QY 1691 TTCCAGGCGCAAGAGAGAGAGTGGGAGCTGAGCAGCTGAGCCGCTGAGCATCAGGCGTGT 1750
DB 1681 TTCCAGGCGCAAGAGAGAGAGTGGGAGCTGAGCAGCTGAGCCGCTGAGCATCAGGCGTGT 1740

QY 1751 GCGAGCAGAGAAAGCCGCTCTCTCTGACAGTGAACAGGCGCCAGTCCCGAAGAGGA 1810
DB 1741 GCGAGCAGAGAAAGCCGCTCTCTCTGACAGTGAACAGGCGCCAGTCCCGAAGAGGA 1800

QY 1811 AGAAGGCAAGCAGATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1870
DB 1801 AGAAGGCAAGCAGATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860

QY	1871	TC	TGGAGATCC	AAGAGG	TAACTG	TTGGAATCTCGG	GAGTGTGG	AAAGTGG	AAAAAC	1930						
DB	1861	TC	TGGAGATCC	AAGAGG	TAAACT	TGGTTTGG	AATCTCGG	CAGTGTGG	AAAGTGG	1920						
QY	1931	CT	CTCTCA	TTTCAG	CCATTTT	AGGCCAG	ATGACG	CTTCTAG	AGGCGAGCAT	TGCATTCAG	1990					
DB	1921	CT	CTCTCA	TTTCAG	CCATTTT	AGGCCAG	ATGACG	CTTCTAG	AGGCGAGCAT	TGCATTCAG	1980					
QY	1991	TG	GAACCT	TCGCTT	ATGTG	GGCCAC	GACGAG	CCCTGG	ATGCTTCA	ATGTCTAG	GAGACAA	2050				
DB	1981	TG	GAACCT	TCGCTT	ATGTG	GGCCAC	GACGAG	CCCTGG	ATGCTTCA	ATGTCTAG	GAGACAA	2040				
QY	2051	CAT	CTCTG	TTTGG	GAAGGA	ATATG	ATGA	AGAAAG	ATACAA	CTCTGT	GCTGAACAG	CTGCTG	2110			
DB	2041	CAT	CTCTG	TTTGG	GAAGGA	ATATG	ATGA	AGAAAG	ATACAA	CTCTGT	GCTGAACAG	CTGCTG	2100			
QY	2111	CCT	GAGGCT	GTACCT	TGGCCAT	TTCTT	CCCAG	CAGCAG	CACTTG	ACGGAG	ATTGG	GAGCGAGG	2170			
DB	2101	CCT	GAGGCT	GTACCT	TGGCCAT	TTCTT	CCCAG	CAGCAG	CACTTG	ACGGAG	ATTGG	GAGCGAGG	2160			
QY	2171	AG	CCAACT	GAGCGT	TGG	CGCAG	CGCAG	AGGATC	AGCCTT	GC	CGGCGCTT	GTATAGTGA	2230			
DB	2161	AG	CCAACT	GAGCGT	TGG	CGCAG	CGCAG	AGGATC	AGCCTT	GC	CGGCGCTT	GTATAGTGA	2220			
QY	2231	CAG	GAGCAT	CTAC	ATCCT	GGACG	ACCCCT	TCAGT	GCCTT	AGAT	GCCCAT	TGTGGGCAACCA	2290			
DB	2221	CAG	GAGCAT	CTAC	ATCCT	GGACG	ACCCCT	TCAGT	GCCTT	AGAT	GCCCAT	TGTGGGCAACCA	2280			
QY	2291	CAT	CTTCA	ATG	TGCTAT	CCGGA	AACAT	CTCA	AGTCC	AAGAC	AGTTC	TCTGTTGTACCA	2350			
DB	2281	CAT	CTTCA	ATG	TGCTAT	CCGGA	AACAT	CTCA	AGTCC	AAGAC	AGTTC	TCTGTTGTACCA	2340			
QY	2351	CC	AGTTAC	AGTAC	CTTGT	TGACT	GTATG	AACTG	ATCTT	CATGA	AGAGG	CGCTGTATATAC	2410			
DB	2341	CC	AGTTAC	AGTAC	CTTGT	TGACT	GTATG	AACTG	ATCTT	CATGA	AGAGG	CGCTGTATATAC	2400			
QY	2411	GGA	AGAGG	CA	CCCAT	ATGAG	GA	ACTGAT	GAATTT	AAAT	GTG	ACTATGCT	TACCATTTTTAA	2470		
DB	2401	GGA	AGAGG	CA	CCCAT	ATGAG	GA	ACTGAT	GAATTT	AAAT	GTG	ACTATGCT	TACCATTTTTAA	2460		
QY	2471	TAA	CTGTT	GTG	GGAGAG	ACAC	CCCG	AGTT	CTCAG	ATCA	TTTCA	AAAAAG	GAACCACTGG	2530		
DB	2461	TAA	CTGTT	GTG	GGAGAG	ACAC	CCCG	AGTT	CTCAG	ATCA	TTTCA	AAAAAG	GAACCACTGG	2520		
QY	2531	TTC	CAGA	AGAG	TCCACA	AGAC	CAAGG	GTCTT	AAAA	CAGAT	CAGT	TAAAG	AAAGGAAAAAGC	2590		
DB	2521	TTC	CAGA	AGAG	TCCACA	AGAC	CAAGG	GTCTT	AAAA	CAGAT	CAGT	TAAAG	AAAGGAAAAAGC	2580		
QY	2591	AG	TAAAG	CCAG	AG	GAAGG	CGACT	TTG	CGAG	CTGGA	AGAGA	AGGCG	AGGGTTCAGTGC	2650		
DB	2581	AG	TAAAG	CCAG	AG	GAAGG	CGACT	TTG	CGAG	CTGGA	AGAGA	AGGCG	AGGGTTCAGTGC	2640		
QY	2651	CT	GTG	CACT	ATAT	GTGT	CTAC	ATCC	AGGCT	GCTGG	GGCCCTT	TGGCAT	TTCCTGTTAT	2710		
DB	2641	CT	GTG	CACT	ATAT	GTGT	CTAC	ATCC	AGGCT	GCTGG	GGCCCTT	TGGCAT	TTCCTGTTAT	2700		
QY	2711	TAT	GGCCCT	TTTT	CAT	GC	TGA	ATG	TAG	GAG	CA	CCCGCTT	CAGCACT	TGTGTTGAGTTA	2770	
DB	2701	TAT	GGCCCT	TTTT	CAT	GC	TGA	ATG	TAG	GAG	CA	CCCGCTT	CAGCACT	TGTGTTGAGTTA	2760	
QY	2771	CT	GAT	CAAG	GAAG	CGG	GAAC	CA	CCACT	TGT	ACT	CGAGG	AAACG	AGACCTCGGTGAG	2830	
DB	2761	CT	GAT	CAAG	GAAG	CGG	GAAC	CA	CCACT	TGT	ACT	CGAGG	AAACG	AGACCTCGGTGAG	2820	
QY	2831	TG	CAGCAT	GAAG	CA	ATCT	CA	TATG	CAGT	ACTAT	GCC	AGCAT	TAC	GCCCTCTCCAT	2890	
DB	2821	TG	CAGCAT	GAAG	CA	ATCT	CA	TATG	CAGT	ACTAT	GCC	AGCAT	TAC	GCCCTCTCCAT	2880	
QY	2891	GG	CAGT	CA	TGCT	GA	AGCC	ATTC	GAG	AGCTT	GT	CTT	GTG	CAAGG	CGACGCTGG	2950
DB	2881	GG	CAGT	CA	TGCT	GA	AGCC	ATTC	GAG	AGCTT						

[illegible]

Db 2581 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCTTGGCATTCCTGGTTATTATGGC 2640
 QY 2717 CTTTTCATGCTGAATGTAGGACAGCACCCTTCAGCACCTGGTGGTTAGTTACTGGAT 2776
 Db 2641 CTTTTCATGCTGAATGTAGGACAGCACCCTTCAGCACCTGGTGGTTAGTTACTGGAT 2700
 QY 2777 CAAGCAAGGAAGCGGGAACCACTGTGACTTCAGAGGAACAGACCTTCGGTGGAGTGACAG 2836
 Db 2701 CAAGCAAGGAAGCGGGAACCACTGTGACTTCAGAGGAACAGACCTTCGGTGGAGTGACAG 2760
 QY 2837 CATGAAGGCAATCCTCATATGCACTACTATGCCAGCATTCAGCCCTCTCCATGGCAGT 2896
 Db 2761 CATGAAGGCAATCCTCATATGCACTACTATGCCAGCATTCAGCCCTCTCCATGGCAGT 2820
 QY 2897 CATGCTGATCCTGAAGCCATTCGAGGAGTTGCTTTGTCAAGGGACGCTCGCAGCTTC 2956
 Db 2821 CATGCTGATCCTGAAGCCATTCGAGGAGTTGCTTTGTCAAGGGACGCTCGCAGCTTC 2880
 QY 2957 CTCGGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTGTGA 3016
 Db 2881 CTCGGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTGTGA 2940
 QY 3017 CACGACCCCCACAGGAGGATTCACAGGTTTTCACAGACATGATGAAGTTGACGT 3076
 Db 2941 CACGACCCCCACAGGAGGATTCACAGGTTTTCACAGACATGATGAAGTTGACGT 3000
 QY 3077 GCGGCTGCCCTTCAGGCCGAGATGTTATCCAGAGCTTATCCGTTGCTGCTGCTGTGT 3136
 Db 3001 GCGGCTGCCCTTCAGGCCGAGATGTTATCCAGAGCTTATCCGTTGCTGCTGCTGCTGTGT 3060
 QY 3137 GGAATGATCGCAGGAGCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTGTGTCATCCT 3196
 Db 3061 GGAATGATCGCAGGAGCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTGTGTCATCCT 3120
 QY 3197 CTTTTCAGTCTGCACATGCTCTCCAGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3256
 Db 3121 CTTTTCAGTCTGCACATGCTCTCCAGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3180
 QY 3257 TATCAGCAGTCACTTTTCTTCCACATCAGTCCAGCATACAGGGCTTGGCCACCAT 3316
 Db 3181 TATCAGCAGTCACTTTTCTTCCACATCAGTCCAGCATACAGGGCTTGGCCACCAT 3240
 QY 3317 CCAGCCTACAATAAAGGCGAGGTTCTGACAGATACAGAGCTGCTGGATGACAA 3376
 Db 3241 CCAGCCTACAATAAAGGCGAGGTTCTGACAGATACAGAGCTGCTGGATGACAA 3300
 QY 3377 CCAAGCTCCTTTTTTTTGTGTACGTGCGATGCGGTGGCTGGCTGGGGCTGGACCT 3436
 Db 3301 CCAAGCTCCTTTTTTTTGTGTACGTGCGATGCGGTGGCTGGCTGGGGCTGGACCT 3360
 QY 3437 CATCAGATCGCCCTCATCACACAGCGGGCTGATGATCGTTTATGACAGGGGACAGAT 3496
 Db 3361 CATCAGATCGCCCTCATCACACAGCGGGCTGATGATCGTTTATGACAGGGGACAGAT 3420
 QY 3497 TCCCCAGCCTATGCGGGTCTCCCATCTCTTATGCTGTCAGTTAACGGGCTGTTCCA 3556
 Db 3421 TCCCCAGCCTATGCGGGTCTCCCATCTCTTATGCTGTCAGTTAACGGGCTGTTCCA 3480
 QY 3557 GTTTACGGTCAGACTGCGCATCTGAGACAGAGCTTCGATTCACCTCGGTGGAGAGGATCAA 3616
 Db 3481 GTTTACGGTCAGACTGCGCATCTGAGACAGAGCTTCGATTCACCTCGGTGGAGAGGATCAA 3540
 QY 3617 TCACTACATTAAGACTCTGTCTTGGAGCACCTGCGCAGATTAAGAACAGGCTCCCTC 3676
 Db 3541 TCACTACATTAAGACTCTGTCTTGGAGCACCTGCGCAGATTAAGAACAGGCTCCCTC 3600
 QY 3677 CCTGACTGCCCCAGGAGGAGGTTGACCTTTGAGAACGCGCAGATGAGGTACCCAGA 3736
 Db 3601 CCTGACTGCCCCAGGAGGAGGTTGACCTTTGAGAACGCGCAGATGAGGTACCCAGA 3660
 QY 3737 AAACCTCCCTCTGTCTCTAAAGAAAGTATCCTTCACCATCAAAAGCTAAAGAGAGATTGG 3796
 Db 3661 AAACCTCCCTCTGTCTCTAAAGAAAGTATCCTTCACCATCAAAAGCTAAAGAGAGATTGG 3720

QY 3797 CATTTGGGGCGGACAGGATCAGGGAAGTCTCTCGCTGGGATGGCCCTCTTCCGCTCTGT 3856
 Db 3721 CATTTGGGGCGGACAGGATCAGGGAAGTCTCTCGCTGGGATGGCCCTCTTCCGCTCTGT 3780
 QY 3857 GGAGTTATCTCGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3916
 Db 3781 GGAGTTATCTCGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3840
 QY 3917 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCGGCTGCTTTCAGTGCGACTGT 3976
 Db 3841 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCGGCTGCTTTCAGTGCGACTGT 3900
 QY 3977 CAGATCAAAATTTGGACCCCTTCAACCACTACACTGAAGACAGATTTGGGATGCGCTGGA 4036
 Db 3901 CAGATCAAAATTTGGACCCCTTCAACCACTACACTGAAGACAGATTTGGGATGCGCTGGA 3960
 QY 4037 GAGGACACACATGAAGAATGTTATGCTCAGTCTCCTGAACTTGAATCTGAAGTGAT 4096
 Db 3961 GAGGACACACATGAAGAATGTTATGCTCAGTCTCCTGAACTTGAATCTGAAGTGAT 4020
 QY 4097 GGAGAATGGGATAAATCTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4156
 Db 4021 GGAGAATGGGATAAATCTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4080
 QY 4157 GCTCCGCCACTGTAAAGATTCTGATTTAGTGAAGCCACAGCTGCCATGGACACAGAGAC 4216
 Db 4081 GCTCCGCCACTGTAAAGATTCTGATTTAGTGAAGCCACAGCTGCCATGGACACAGAGAC 4140
 QY 4217 AGACTTATGATTCAGAGACCATCCGAGAGCATTTGCAGACTGTACCATCTGACCAT 4276
 Db 4141 AGACTTATGATTCAGAGACCATCCGAGAGCATTTGCAGACTGTACCATCTGACCAT 4200
 QY 4277 TGCCCATCGCTGCACACGGTTCTAGGCTCCGATAGGATTATGTTGCTGGCCCGAGGACA 4336
 Db 4201 TGCCCATCGCTGCACACGGTTCTAGGCTCCGATAGGATTATGTTGCTGGCCCGAGGACA 4260
 QY 4337 GGTGGTGGAGTTTGACACCCCATCGGCTCTTGTCACACAGACTTCCCGATTCTATGC 4396
 Db 4261 GGTGGTGGAGTTTGACACCCCATCGGCTCTTGTCACACAGACTTCCCGATTCTATGC 4320
 QY 4397 CATGTTTGTCTGTCAGAGAACAGGTCGCTGTCAGGCTGACCTCCCTCTGTTGACGA 4456
 Db 4321 CATGTTTGTCTGTCAGAGAACAGGTCGCTGTCAGGCTGACCTCCCTCTGTTGACGA 4380
 QY 4457 AGTCTCTTTCTTTAGAGCATTCCTGCTGCTGGGGCGGCGCC--TCATCGCGTCC 4515
 Db 4381 AGTCTCTTTCTTTAGAGCATTCCTGCTGCTGGGGCGGCGCCCTTCATCGCGTCC 4440
 QY 4516 TCCTACCGAAACCTTGCCTTCTCGATTTTATCTTTCCGACAGAGTTCGGGATGGCTT 4575
 Db 4441 TCCTACCGAAACCTTGCCTTCTCGATTTTATCTTTCCGACAGAGTTCGGGATGGCTT 4500
 QY 4576 GTGTTGTTTCACTTTTAGGAGAGTCATATTTGATTATTGATTATTATTCATATTCATCT 4635
 Db 4501 GTGTTTCACTTTTAGGAGAGTCATATTTGATTATTGATTATTATTCATATTCATCT 4560
 QY 4636 AAACAAATTTAGTTTTTGTCTTAATTCGACTCTTAAAGGTTTCAGGGAACCGTTATTAT 4695
 Db 4561 AAACAAATTTAGTTTTTGTCTTAATTCGACTCTTAAAGGTTTCAGGGAACCGTTATTAT 4620
 QY 4696 AATTGTATCAGAGGCTTATTAAGCTTTTATACGTGTAGCTATATCTATATATATTCCT 4755
 Db 4621 AATTGTATCAGAGGCTTATTAAGCTTTTATACGTGTAGCTATATCTATATATATTCCT 4680
 QY 4756 GTACATAGCCTTATTTACAGTGAAGTAAAGCTGTTTATTTATATTAATAAAGCAGC 4815
 Db 4681 GTACATAGCCTTATTTACAGTGAAGTAAAGCTGTTTATTTATATTAATAAAGCAGC 4740
 QY 4816 TGTGCTTAATAACA 4828
 Db 4741 TGTGCTTAATAACA 4753

RESULT 6
 AAT94055
 ID AAT94055 standard; cDNA; 2167 BP.
 XX AC AAT94055;
 XX DT 01-APR-1998 (first entry)
 XX DE Human multidrug resistance-associated protein 5 (MRP5) cDNA sequence 2.
 KW Canalicular multispecific organic anion transporter protein;
 KW cMOAT protein; ATP-binding cassette transporter family; ABC transporter;
 KW hepatobiliary excretion; multidrug resistance-associated protein; MRP5;
 KW cMOAT protein activity; multidrug resistance-related protein; MDR-1;
 KW Dubin-Johnson disease; Rotor disease; ss.
 XX OS Homo sapiens.
 XX PN WO9731111-A2.
 XX PD 28-AUG-1997.
 XX PF 21-FEB-1997; 97WO-NL00079.
 XX PR 22-FEB-1996; 96EP-0200460.
 XX PA (MED-1) ACAD MEDISCH CENT AMSTERDAM.
 XX PA (HETN-) HET NEDERLANDS KANKER INST.
 XX PA (INTR-) INTROGENE BV.
 XX PI Borst P, Bosma PJ, Evers R, Oude Elferink RPJ,
 PI Paulusma CC;
 DR WPI: 1997-435163/40.
 XX
 PT DNA encoding human and rat canalicular multispecific organic anion
 PT transporter proteins - useful for diagnosis and treatment of
 PT Dubin-Johnson disease and Rotor disease
 XX
 PS Disclosure; Fig 19B; 106pp; English.
 XX
 CC The present cDNA sequence encodes a human multidrug resistance-associated
 CC protein 5 (MRP5). The MRP5 gene has been localised to chromosome 3. The
 CC MRP5 protein is a member of the ATP-binding cassette (ABC) transporter
 CC family of anorganic anion transporters. MRP5 is a 4 domain protein, with
 CC 2 ATP-binding domains, and 2 domains with transmembrane proteins. The
 CC protein is a homologue of MRP1, which is involved in ATP-dependent
 CC transport of glutathione conjugates such as dinitrophenyl glutathione.
 CC These substrates are also transported by a novel canalicular
 CC multispecific organic anion transporter (cMOAT) protein. The ATP
 CC dependent cMOAT transporter system mediates hepatobiliary excretion in
 CC the liver. cMOAT may be a liver-specific homologue of multidrug
 CC resistance-associated protein. The nucleic acids are used to provide
 CC cells with cMOAT protein activity. cMOAT protein activity in cells can
 CC be enhanced by increasing the level of glutathione, glucuronide and/or
 CC sulphate. Antisense constructs, especially derived from another multidrug
 CC resistance (MDR)-related protein, e.g. MDR-1, to the nucleic acids and
 CC vectors can be used to decrease the level of cMOAT in a cell. The nucleic
 CC acids and proteins can be used especially in diagnosis of Dubin-Johnson
 CC disease, Rotor disease or another disease involving cMOAT. The cMOAT gene
 CC may also be used as a selectable marker gene.
 XX
 SQ Sequence 2167 BP; 494 A; 511 C; 511 G; 626 T; 25 other;

Query Match 33.2%; Score 1936.4; DB 18; Length 2167;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 2069; Conservative 9; Mismatches 47; Indels 14; Gaps 10;

QY 3692 GGAGGGAGGAGTACCTTTGAGAACCCAGAGATGAGGTACCCAGAAAAACCTCCCTCTGT 3751
 DB 29 GSAGAKKRACCNCTCATKAGAGGAACARAAGATGGGTACSGAGAACTCTCTTTTAT 88

QY 3752 CCTAAA--GAAAGTATCTCTCAGCATCAAACTAAAGAGAAGATTGGCATTTCTGGGCGG 3809
 DB 89 CCTAAAAGAAGATATCTCTCAGCATCAAACTAAAGAGAAGATTGGCATTTCTGGGCGG 148
 QY 3810 ACAGGATCAGGGAAGTCTCTCGTGGGATGGCCCTCTTCCCTCTCTGGTGGAGTTATCTGA 3869
 DB 149 ACAGGATCAGGGAAGTCTCTCGTGGGATGGCCCTCTTCCCTCTCTGGTGGAGTTATCTGA 208
 QY 3870 GGCTGCATCAAGATTGATGGAGTGAGATCAGTATGATTTGGCCCTTCCGACCTCCGAAGC 3929
 DB 209 GGCTGCATCAAGATTGATGGAGTGAGATCAGTATGATTTGGCCCTTCCGACCTCCGAAGC 268
 QY 3930 AAATCTCTATCATCTCTCAAGAGCCGCTGCTGTTCACTGGCAGCTGTCAGATCAAAATTG 3989
 DB 269 AAATCTCTATCATCTCTCAAGAGCCGCTGCTGTTCACTGGCAGCTGTCAGATCAAAATTG 328
 QY 3990 GACCCCTTCAACCACTACACTGAAGACAGATTGGGATGCCCTGGAGAGACACACATG 4049
 DB 329 GACCCCTTCAACCACTACACTGAAGACAGATTGGGATGCCCTGGAGAGACACACATG 388
 QY 4050 AAAGATGATTTGCTCAGCTACCTCTGAACCTTGAATCTGAATGATGAGAAATGGGAT 4109
 DB 389 AAAGATGATTTGCTCAGCTACCTCTGAACCTTGAATCTGAATGATGAGAAATGGGAT 448
 QY 4110 AACTTCTCAGTGGGGAAGCGCAGCTCTTGTGCATAGCTAGAGCCCTCTCCGCCACTGT 4169
 DB 449 AACTTCTCAGTGGGGAAGCGCAGCTCTTGTGCATAGCTAGAGCCCTCTCCGCCACTGT 508
 QY 4170 AAGATTTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGACAGACTTATTGAT 4229
 DB 509 AAGATTTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGACAGACTTATTGAT 568
 QY 4230 CAAGAGACCATCCAGAGAGCAATTTGCAGACTGTACCATGTCGATGCCATGCCCTG 4289
 DB 569 CAAGAGACCATCCAGAGAGCAATTTGCAGACTGTACCATGTCGATGCCATGCCCTG 628
 QY 4290 CACACGGTCTTAGGCTCCGATAGGATTTGCTGCTGCCAGAGGACAGCTGGCTGAGTTT 4349
 DB 629 CACACGGTCTTAGGCTCCGATAGGATTTGCTGCTGCCAGAGGACAGCTGGCTGAGTTT 688
 QY 4350 GACACCCCATCGGTCTTCTGTCACAGGACAGTTTCCCGATTCTATGTCATGTTTGGCTGCT 4409
 DB 689 GACACCCCATCGGTCTTCTGTCACAGGACAGTTTCCCGATTCTATGTCATGTTTGGCTGCT 748
 QY 4410 GCAGAGAACAAAGTCTGCTGTCAGGGCTGACTCTCCCTGTTGACGAAGTCTCTTTTCTT 4469
 DB 749 GCAGAGAACAAAGTCTGCTGTCAGGGCTGACTCTCCCTGTTGACGAAGTCTCTTTTCTT 808
 QY 4470 TAGAGCATTCGCATTCCTCCCTGGGGGGGGCCCTCATCGCGTCCCTACCGAAACCT 4529
 DB 809 TAGAGCATTCGCATTCCTCCCTGGGGGGGGCCCTCATCGCGTCCCTACCGAAACCT 868
 QY 4530 TGCTTTTCTCGATTTTATCTTTTCCACAGCAGATTTCGGGATTGGCTTGTGTTTCACTTT 4589
 DB 869 TGCTTTTCTCGATTTTATCTTTTCCACAGCAGATTTCGGGATTGGCTTGTGTTTCACTTT 928
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 DB 929 TAGGAGAGTCATATTGTTGATTTATTTATTTCCATATTTCTATGTAACAAAAATTTAGT 988
 QY 4650 TTTTGTCTTTAATTTGCACTCTAAAGGTTTCAGGGAACCGTTTATTTATTTATGATCAGG 4709
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 QY 4710 CCTATATGAAGCTTTATAGCTGATATCTATATATATATATATATATATATATATATAT 4769
 DB 1049 CCTATATGAAGCTTTATAGCTGATATCTATATATATATATATATATATATATATAT 1108
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 DB 1109 TTTACAGTGAAGTGAAGCTGTTTATTTTATTTATTTAAATAAGCACTGTGCTAATAACAG 1168
 QY 4830 TGCATATCTCTTCTATCATATTTTGTACAGTTTGTGCTACTAGAGATCTGGTTTGTCTAT 4889

Dbb 120 GAACAGCTGCTGCTGAGGCGCTGACCTGGCCATTTCTCCACGACGCGACCTGACGGAGAT 179
QY 2159 TGGAGAGCAGGAGCAACCTGAGCGGTGGCAGCGCCAGAGGATCAGCCTTGCCCGGCG 2218
Dbb 180 TGGAGAGCAGGAGCAACCTGAGCGGTGGCAGCGCCAGAGGATCAGCCTTGCCCGGCG 239
QY 2219 CTTGTATAGTGACAGGAGCACTTACATCCTTGAGAGACCCCTCAGTGCTTTAGATGCCA 2278
Dbb 240 CTTGTATAGTGACAGGAGCACTTACATCCTTGAGAGACCCCTCAGTGCTTTAGATGCCA 299
QY 2279 TGTGGCAACACATCTTCAATAGTGTATCCGGAACATCTCAAGTCCAGACAGATTCT 2338
Dbb 300 TGTGGCAACACATCTTCAATAGTGTATCCGGAACATCTCAAGTCCAGACAGATTCT 359
QY 2339 GTTTT---GTTTACCACAGTTTACAGTACTGCTGTTGACTGTGATGAAGTGATCTTCATGAA 2395
Dbb 360 GTTTNNNGTTACCCACAGTTTACAGTACTGCTGTTGACTGTGATGAAGTGATCTTCATGAA 419
QY 2396 AGAGGGCTGTATTACGGAAGAGGACCCCATGAGGAAGTGTATGAATTTAAATGTTGACTA 2455
Dbb 420 AGAGGGCTGTATTACGGAAGAGGACCCCATGAGGAAGTGTATGAATTTAAATGTTGACTA 479
QY 2456 TGCTTACCATTTTTAAATACCTGTTGCTGGGAGACACCCGAGTTGAGATCAATTCAAA 2515
Dbb 480 TGCTTACCATTTTTAAATACCTGTTGCTGGGAGACACCCGAGTTGAGATCAATTCAAA 539
QY 2516 AAAGGAAACCACTGTTTACAGAAAGAGTCAACAGCAAGGCTCTTAAACAGGATCAGT 2575
Dbb 540 AAAGGAAACCACTGTTTACAGAAAGAGTCAACAGCAAGGCTCTTAAACAGGATCAGT 599
QY 2576 AAAGGAAACCACTGTTTACAGAAAGAGTCAACAGCAAGGCTCTTAAACAGGATCAGT 2635
Dbb 600 AAAGGAAACCACTGTTTACAGAAAGAGTCAACAGCAAGGCTCTTAAACAGGATCAGT 659
QY 2636 GCAGGGTTCAGTCCCTGGTGCAGTATATGTTGTTCTATCCAGGCTGCTGGGGGCCCTT 2695
Dbb 660 GCAGGGTTCAGTCCCTGGTGCAGTATATGTTGTTCTATCCAGGCTGCTGGGGGCCCTT 719
QY 2696 GGCA-TTCCCTGGTTATTATGCGCCCTTTTCATG--CTGAATGTAGCAGCAGCGCTTCAG 2752
Dbb 720 GGCA-TTCCCTGGTTATTATGCGCCCTTTTCATG--CTGAATGTAGCAGCAGCGCTTCAG 779
QY 2753 CACCTGTGTGTGTTGAGTTACTGATCAAGCAAGGAGGCGGGAACCACTGTGACTCGAGG 2812
Dbb 780 CACCTGTGTGTGTTGAGTTACTGATCAAGCAAGGAGGCGGGAACCACTGTGACTCGAGG 839
QY 2813 GAAGGAGACCTCGGTGAGTGACAGCATGAAGCAATCTCTATGAGTACTATGCGAG 2872
Dbb 840 GAAGGAGACCTCGGTGAGTGACAGCATGAAGCAATCTCTATGAGTACTATGCGAG 899
QY 2873 CATCTAGCCCTCTCCATGGCAGTCACTGCTGATCCTGAAAGCCATTCGAGGAGTTGCTT 2932
Dbb 900 CATCTAGCCCTCTCCATGGCAGTCACTGCTGATCCTGAAAGCCATTCGAGGAGTTGCTT 959
QY 2933 TGTCAGGGCAGCGTGGGAGCTTCTCCCGCTGCATGACAGAGCTTTTCCGAGGATCCT 2992
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QY 3053 CAAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGCCGAGATGTTTCATCCAGAA 3112
Dbb 1080 CAAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGCCGAGATGTTTCATCCAGAA 1139
QY 3113 CGTTATCCTGGTCTTCTGTTGTTGGAATGATGCGAGGAGTCTTCCCGTGGTTCTTGT 3172
Dbb 1140 CGTTATCCTGGTCTTCTGTTGTTGGAATGATGCGAGGAGTCTTCCCGTGGTTCTTGT 1199
QY 3173 GGCAGTGGGGCCCCCTGTCATCTCTTTTTCAGTCTGCACATGCTTCCAGGGTCTGAT 3232
Dbb 1200 GGCAGTGGGGCCCCCTGTCATCTCTTTTTCAGTCTGCACATGCTTCCAGGGTCTGAT 1259

QY 3233 TCGGGAGCTGAAGCGCTCTGGACAATATCAGCAGTCACTTCTCTCCACATCAGCTC 3292
Dbb 1260 TCGGGAGCTGAAGCGCTCTGGACAATATCAGCAGTCACTTCTCTCCACATCAGCTC 1319
QY 3293 CAGCATACAGGCGCTTGGCCACCATCCACGCTTACATAAAGGCGAGGTTTCTGCACAG 3352
Dbb 1320 CAGCATACAGGCGCTTGGCCACCATCCACGCTTACATAAAGGCGAGGTTTCTGCACAG 1379
QY 3353 ATACAGGAGCTGCTGGATGACAAACAAGCTCTTTTTTTTACGTGTGCGATGCG 3412
Dbb 1380 ATACAGGAGCTGCTGGATGACAAACAAGCTCTTTTTTTTACGTGTGCGATGCG 1439
QY 3413 GTGGCTGGCTGCGGCTGACCTCATCAGCATCGCCCTCATCACCACCGGGCTGAT 3472
Dbb 1440 GTGGCTGGCTGCGGCTGACCTCATCAGCATCGCCCTCATCACCACCGGGCTGAT 1499
QY 3473 GATCTTCTTATGACGGGAGATTCCCGCAGCTATCGGGTCTCGCCATCTCTTATGCG 3532
Dbb 1500 GATCTTCTTATGACGGGAGATTCCCGCAGCTATCGGGTCTCGCCATCTCTTATGCG 1559
QY 3533 TGTCCAGTTAAGCGGCTCTTCCAGTTTACGTTACGACTGGCATCTGAGACAGAACTCG 3592
Dbb 1560 TGTCCAGTTAAGCGGCTCTTCCAGTTTACGTTACGACTGGCATCTGAGACAGAACTCG 1619
QY 3593 ATTACCTCGGTGGAGAGGATCAATCACTACATTAAGACTGTCTTGAAGCACTCG 3652
Dbb 1620 ATTACCTCGGTGGAGAGGATCAATCACTACATTAAGACTGTCTTGAAGCACTCG 1679
QY 3653 CAGAAATTAAGAAAGGCTCCCTCCCTGACCTGGCCCGAGGAGGAGG 3702
Dbb 1680 CAGAAATTAAGAAAGGCTCCCTCCCTGACCTGGCCCGAGGAGGAGG 1729

RESULT 8

AAD14909

ID AAD14909 standard; cDNA; 4101 BP.

XX AC AAD14909;

XX DT 01-NOV-2001 (first entry)

XX DE Human transporter-related protein #22 cDNA.

XX KW Human; transporter-related protein; metabolite transporter;
XX KW organic cation transporter; multi-drug resistance; MDR; gene therapy;
XX KW cellular transporter; sodium-glucose cotransporter; diagnosis; screening;
XX KW symptomatic; phenotypic manifestation; biological condition; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..4101

XX FT /*tag= a

XX FT /product= "Human transporter-related protein"

XX FT /transl_except= (pos:3025..3039, aa:Thr-Thr)

XX FT /transl_except= (pos:3370..3372, aa:Xaa)

XX FT /note= "Xaa can be any amino acid"

XX PN WO200157214-A2.

XX PD 09-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US03646.

XX PR 03-FEB-2000; 2000US-0179973.

XX PR 14-FEB-2000; 2000US-0182422.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Turner CA, Mathur B, Wang X, Abuin A, Friedrich G, Zambrowicz B;

XX PI Sands AT;

DR WPI: 2001-514599/56.
DR P-PSDB; AAE08075.
XX Novel polynucleotides encoding novel human proteins with structural
PT similarity to cellular transporters for the diagnosis of disease and
PT use in gene therapy -
XX
XX
PS Claim 4; Page 60-61; 91pp; English.
XX
CC The present sequence is a human transporter-related protein cDNA.
CC The human transporter-related protein share structural similarity with
CC mammalian metabolite or organic cation transporters, multi-drug
CC resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
CC other cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
CC manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
CC biological conditions.
XX
SQ Sequence 4101 BP; 1046 A; 1023 C; 1048 G; 983 T; 1 other;
Query Match 15.9%; Score 925.8; DB 22; Length 4101;
Best Local Similarity 54.0%; Pred. No. 1e-213;
Matches 2159; Conservative 0; Mismatches 1707; Indels 129; Gaps 8;
QY 421 ACCAGTGTGACAAATGCTGGGCTTTTCCCTGTATGACTTTTTCGTGGCTTCTCTCTCG 480
DB 131 ACCCGGTGGATGATCGCGGCTACTCTCCCTGCCACATTTTCTGGCTCACGCCGGTGA 190
QY 481 CCGGTGGGCCACAGAAGGGGAGCTCTCAATGGAAGAGGTGTGTCTCTGTCCAAAGC 540
DB 191 TGGTGAAGGCTACCGGCAAG--GCTGACCGTAGACACCTGCCCCCATTTGTGACAT 247
QY 541 ACAGTCTTCTGACGTGAAGTCTGAGAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG 600
DB 248 ATGACTCATCTGACACCAATGCCAAGATTTTCGAGTCTTGGATGAAGAGGTAGCAA 307
QY 601 AAGTGGGCCAGAGCTGTCTCCCTGGGAAGGTTGTGTGATCTTCTGCGCCACCAAGC 660
DB 308 GGGTGGGCTCTGAGAAGGCTCTCTGAGCCACGTTGTGTGAAATTCAGAGGACAGCG 367
QY 661 TCATCTGTCCATCGTGTGCTGATGATACGAGCTGGCTGGCTTCAGTGGACAGCCT 720
DB 368 TGTGTGAGCATCTGGGCCAACATCTGTGATCATCATGGCAGCCATAGGGCCGACAG 427
QY 721 TCATGTGAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACTGCAGTACAGCT 780
DB 428 TTCTCATTCACCAATCTCTCAGCAGACTGAGAGGACCTCTGGGAAGTCTGGGTGGCA 487
QY 781 TGTGTGTAGTGTGGGCTCTCTCCTGACGAAATCGTGGGCTGTGTGCTGTGCTGCACTGA 840
DB 488 TTGGACTGTGCATAGCCCTTTTGGCCACCGAGTTTACCAAGTCTTCTTTTGGGCCCTTG 547
QY 841 CTGGGCATTAATACCGAACCGTGTCCGCTTGGGGGGCCATCTTAACCATGSCAT 900
DB 548 CTGGGCCATCAACTACCGCACCGGCATCCGTTTGAAGGTGGGCTCTCCACCTTGTGTT 607
QY 901 TTAAGAAGATCCCTTAAGTTAAAGAAATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
DB 608 TTCAAAACCTAGTGTCTTCAAGACATGACCCACATCTCTGTGGGAGGTGCTCAATA 667
QY 961 TTTGTCCACAGATGGCAGAGAATGTTGAGGACAGCCGTGGCAGCCTGCTGGCTG 1020
DB 668 TACTGTCAAGTATAGTATTTCTTTTGTGTTGAAGTGTCTTTTGTGCTTTGGCCAGCCA 727
QY 1021 GAGGACCGGTGTGGCATCTTAGCATGATTTATATGTAATTTCTGGGACCAACAG 1080
DB 728 CCATCCCGATCCCTAAATGGTCTTTTGTGGCGGTACGCCCTTTTTCATTTCTGGGCCACAG 787
QY 1081 GCCTCTCGGATCAGCTGTTTATCTCTTTTACCCAGCAATGATGCTTTTGCATCAGGC 1140

DB 788 CTCTCATCGGATATCATGTATGTATCATATTCATACCCGCTCCAGATGTTTATGGCCAAAGC 847
QY 1141 TCACAGCATATTTTCAGGAGAAATCGGTGGCCGCCACGGATGAACCTGTCCAGAGATGA 1200
DB 848 TCAATTCAGCTTTCCGAAGGTCAGCAATTTTGGTGACACAGCAGGATTCAGACAATGA 907
QY 1201 ATGAAGTCTTACITACATTAATTTATCAAAATGTATGCCCTGGGTCAAGCAATTTTCTC 1260
DB 908 ATGAGTTTCTGACCTGCATCAGCTGATCAAAATGTATGCCGGGAGAAATCTTTTACCA 967
QY 1261 AGAGTGTTCAAAATAATCCGAGGAGGAGCGTCGGATATTGGAAGAAAGCCGGTACTTCC 1320
DB 968 ACAGTATCCAGATATAGAAGGAGGAAAGAAATTTACTGGAAGAAAGCTGGATTTGTCC 1027
QY 1321 AGGTATCACTGTGGGTGTGGCTCCCATTTGTGTGGTGTGATTCAGCGTGGTGCCTTCT 1380
DB 1028 AAGTGGAAACTCTGCCCTGGCCCTCGTGTCCACCATAGCCATCGTGTGACATTTAT 1087
QY 1381 CTGTTCAATGACCTGGGCTTCGATCTGACAGCAGCAGCAGGCTTTCACAGTGGTGACAG 1440
DB 1088 CTGCCACATCTCTGAGACGCAAACTCACCGCACCCCTGGCATTTAGTGTGATGGCA 1147
QY 1441 TCTTCAATTCATGACTTTTGGCTTTGAAAGTAACACCGTTCAGTAAAGTCCCTCTCAG 1500
DB 1148 TGTTAATGTAATGAAGTTTCCATGTCAATCTTGCCCTTCTCCATCAAGCAATGGCTG 1207
QY 1501 AAGCTCTAGTGGCTTTGACAGATTTAAGAGTGTGTTTCTTAATGGAAGAGGTTTCACATGA 1560
DB 1208 AAGCAATGTCTCTAAGGAGAAATGAAGAAATTTCTCATAGTAAACCCCCCATCTT 1267
QY 1561 TAAAGAACAAACAGCCAGTCTCTACATCAAGATAGAGATGAAGAAATGCCACTTGGCAT 1620
DB 1268 ACATCACCACCAAGCAGACAGCAGTACTGTCTGCTTTTAGCAATGTCACCTTGACAT 1327
QY 1621 GGGACTCTCCACTCCAGTATCCAGAACTCCGCCCAAGCTGACCCCAAAATGAAAAAG 1680
DB 1328 GGG-----AGCATGAAGCCAGCAGAAAGTA 1354
QY 1681 ACAAGAGGCTTCCAGGGCAAGAAAGAGAGGTGAGCGACTGCGCCACTGAGCATC 1740
DB 1355 CCCCAAGAAATTCAGAACCAAGAAAGCATTTATGCAAGAACAGAGGTGACAG---- 1410
QY 1741 AGGCGGTCTGCGCAGCAGAAAGCCACCTCTCTCTGACAGTACGAGCGGCCAGTC 1800
DB 1411-----GCATACAGTGAGAGGAGTCCACC-----AGCCAAGGAGGACCTG 1450
QY 1801 CCGAAGAGAAAGAGGCAAGCAGCATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGC 1860
DB 1451 GCCCAGAGGACAAAGTGACAGCCCTCAATCG-----TTCTGC 1489
QY 1861 ACAGCATCGATCTGGAGATCCAAAGAGGTAAACTGGTTGGAATCTGCGSCAGTGGGAA 1920
DB 1490 ACAGCATAAAGCTTGTGTGAGAAAGGGAAGATCTTGGGAATATGTGGAAATGTGGAA 1549
QY 1921 GTGGAAGAACTCTCTCATTTACGCCATTTTAGGCCAGATGACGCTTCTAGAGGCGAGCA 1980
DB 1550 GTGGAAGAGCTCCCTCTCTGACGCTCTCTAGGACAGATGACGATGCAAGAGGCTGG 1609
QY 1981 TTGCAATCAGTGAACCTTCTGCTTATGTGGCCACAGCGCTTGGATCTCTCAATGCTACTC 2040
DB 1610 TGGCAGTCAATGGAACCTTGGCTTACGTTTACAGCAGGCTGGATCTTTCATGGAATG 1669
QY 2041 TGAGAGACAACATCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGA 2100
DB 1670 TGAGAGAAAACATACTCTTTGGAGAAAAGATGATCAACCAAGAGTATCAGCACAGTCC 1729
QY 2101 ACAGCTGCTGCTGAGGCTCACCTGCGCCATCTTCCAGCAGCAGCACTGACGGAGATTG 2160
DB 1730 CGCTCTGTGGCTCCAGAAAGACCTGAGCAACCTCCCTTATGGAGACCTGACTGAGATTG 1789
QY 2161 GAGAGCAGGAGCCAACTGAGCGGTGGCAGCGCCAGAGGATCAGCTTGGCCCGGCT 2220
DB 1790 GGGAGCGGGCTCAACCTCTCTGGGGGCGCAGAGGATTAGCCTTGGCCCGGCTG 1849

QY 2221 TGTATAGTGACAGGAGCATCTACATCCTGTGACGACGCCCTCAGTGTAGATGCCCATG 2280
DB 1850 TCTACTCCGACCGTCACTCTACTCTGTGACGACGCCCTGTGCGCGTGGAGCCGACG 1909
QY 2281 TGGGCAACACATCTTCAATAGTGTATCCGGAACATCTCAAGTCCAAAGACAGATCTGT 2340
DB 1910 TGGGGAAGCAGCTTTTGAGGAGTGCATTAAGAAGACGCTCAGGGGAAAGACAGTCGTCC 1969
QY 2341 TTGTTACCACAGTTTACAGTACCTGGTTGACTGTGATGAAGTATCTCATGAAAGAGG 2400
DB 1970 TGGTGACCCACCAAGCTACAGTTCTTATAGAGTCTGTGATGAAGTTATTTATAGAAGATG 2029
QY 2401 GCTGTATTACGGAAGAGACCCATAGAGCACTGATGAATTTAAATGTGACTATGCTA 2460
DB 2030 GAGAGATTTGTGAAGAGAACCCACAGAGATTATGAGAGAGAGGGCGCTATGCAA 2089
QY 2461 CCATTTTTAATACCTGTGTCTGGGAGACACCGCCAGTTGAGATCAATTCAAAAAAGG 2520
DB 2090 AACTGATTACAACTTCGAGGATTTCAGTTCAAGGATCCTGAACACCTTTACAATGCAG 2149
QY 2521 AAACAGTGGTTACAGAGAAGTAC-----AAGACAGGGTCTCTAAACAGGAT 2571
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QY 2572 CAGTAAAGAGAAAGCAGTAAGCCAGAGAA----- 2606
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DB 2330 AAACATATCACAGCTACATTAAGGCTTCTGAGAGGTACCTCTTCTCTCACTGTGT 2389
QY 2716 CCCTTTTCATGTGAATGTAGGACGACCGCTTCAGCACTGGTGGTTGAGTTACTGGA 2775
DB 2390 TCCTCTCTCTGATGATGGCGGCTGCTTCAGCACTGGTGGTGGTCTCTGCT 2449
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DB 2450 TGGACAAGGGCTCACGATGACCTGTGGGCCCCAGGGCAACAGGACCATGTGTGAGGTG 2509
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DB 2690 TTGACAGCACTCCCACTGGCAGGCTAATGAACCGTTTTCGAAGGATATGAGCAGCTGG 2749
QY 3073 AGTGGGTGCGGTTCAGGCGGAGATGTTTCATCCAGACGTTATCTCTGGTGTCTTCT 3132
DB 2750 ATGTGAGGCTGCGTTTCACGACAGAACTTCTCGACAGAGTTTTTATGGTGGTTTGA 2809
QY 3133 GTGTGGGAATGATCGAGAGTCTTCCCGTGGTTCCTGTGCGAGTGGGGCCCCCTGTCA 3192
DB 2810 TTCTCGTATCTTGTGCTGTGTTTCTCTGCTGCTCTTTAGTCTGCGCCACCTTGTG 2869
QY 3193 TCCTCTTTTCACTCTGACATGTCTCCAGGGTCTCTGATTCGGGAGTGGAAGCTGTGG 3252
DB 2870 TAGGCTTCTTCTGTTACGATTTTCCACAGAGGAGTCCAGGAGTCAAGAAGGTGG 2929

QY 3253 ACAATATCAGCAGTCACTTTTCTCTCCACATCAGTCCAGCATACAGGGCCTTGCCA 3312
DB 2930 AGATGTACCGGTACCGTGTGTTCACCCACATCACTCTCTCCATGCAGGGCCTTGGGCA 2989
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DB 2990 TCATTACGCTATGCGAAGAAGAGAGCTGCATCACTAGTTTAAAGACGCTAAACGACG 3049
QY 3373 ARAACAAAGTCTCTTTTGTGTAGGTGCGATGCGGTGGCTGGCTGTGCGGTGG 3432
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QY 3493 AGATTCCCCAGGCTATGCGGGTCTGCCATCTCTTATGTGTCCAGTTAAACGGGGTGT 3552
DB 3170 CCATCAGTACTTTCATCCAAAGGCTGTCTATTGTATACATCATCCAGCTGAGCGACTGC 3229
QY 3553 TCAGTTTACGGTACAGTGGCATCTGAGACAGAAGCTCGATTACCTCGGTGGAGAGA 3612
DB 3230 TCCAAGTGTGTGCGAAGCGGAACAGACAGCAAGCCAAATTCACCTCCGTGGAGCTGC 3289
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DB 3470 TCGGGATTTGGAAGAACAGGTTCCGGAAGATCATCGTTAGGAATGGCTTGTGTTCTC 3529
QY 3853 TGTGAGGTTATCTGGAGGCTGCATCAAGATTTGATGAGTGAAGATCAGTGATTTGGCC 3912
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QY 4033 TGGAGGAGACACATGAAAGAAATGATTTGCTCAGCTACCTCTGAAACTTTGAATCTGAAG 4092
DB 3710 TGCAGAGAACAATTCATGAGAGACACAATAATGAACCTCCCAAGAAATTAACAGCAGAAG 3769
QY 4093 TGATGAGAAATGGGGATACTTCTCAGTGGGGGAAGCGAGCTCTTGTGATAGTAGAG 4152
DB 3770 TCAGAAAATGAGAAAATCTTCTAGTAGGGGAAGCTGAGTCTTGTGTGGCCGAG 3829
QY 4153 CCGTGTCCGCCACTGAAGATTTCTGATTTAGATGAAGCCACAGCTGCCATGGACACAG 4212
DB 3830 CTCTCTCCGTAATTCAAAGATCATTTCTCTTGAATGAAGCCAGCGCTCTATGGATCCA 3889
QY 4213 AGACAGCTTATTGATTCAAGAGACCATCCGAGAAGCATTTGAGACTGTATACCTGTGA 4272
DB 3890 AGACTGACACCTGGTTCAAGACACCATCAAGATGCCITCAAGGCTGCACCTGTGCTGA 3949
QY 4273 CCATGCCCATGCCCTGACACAGGTTCTTAGGCTCCGATAGGATTAATGGTGTGCCCCAGG 4332
DB 3950 CCATGCCCATGCCCTCAACACAGTCTCAACTGCGATACGCTCTCTGTTTATGGAAAATG 4009
QY 4333 GACAGGTGGTGGATTTGACACCCCATCGTCTCTT 4367


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Db 4010 GGAAGGTGATTGAGTTGACAGCCTGAAGTCTT 4044
      | | | | | | | | | | | | | | | | | | | |
RESULT 9
AAD14912
ID AAD14912 standard; cDNA; 4008 BP.
XX
AC AAD14912;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human transporter-related protein #25 cDNA.
XX
KW Human; transporter-related protein; metabolite transporter;
KW organic cation transporter; multi-drug resistance; MDR; gene therapy;
KW cellular transporter; sodium-glucose cotransporter; diagnosis; screening;
KW symptomatic; phenotypic manifestation; biological condition; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4008
FT FT /tag= a
FT FT /product= "Human transporter-related protein"
FT FT /transl_except= (pos:3025..3039, aa:Thr-Thr)
FT FT /transl_except= (pos:3370..3372, aa:xaa)
FT FT /note= "Xaa can be any amino acid"
XX
XX W0200157214-A2.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03646.
XX
XX 03-FEB-2000; 2000US-0179973.
XX
XX 14-FEB-2000; 2000US-0182422.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Wang X, Abuin A, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI: 2001-514599/56.
XX P-PSDB; AAE08078.
XX
XX Novel polynucleotides encoding novel human proteins with structural
XX similarity to cellular transporters for the diagnosis of disease and
XX use in gene therapy
XX
XX Disclosure; Page 73-74; 91pp; English.
XX
XX The present sequence is a human transporter-related protein cDNA.
XX The human transporter-related protein share structural similarity with
XX mammalian metabolite or organic cation transporters, multi-drug
XX resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
XX other cellular transporters. The transporter-related protein DNA may be
XX used for the detection of mutant sequences or inappropriately expressed
XX sequences for the diagnosis of disease. They may also be used to screen
XX for drugs effective in the treatment of the symptomatic or phenotypic
XX manifestations of perturbing the normal functions of the sequences of the
XX invention in the body. They may also be used in gene therapy for treating
XX biological conditions.
XX
XX Sequence 4008 BP; 1018 A; 1005 C; 1022 G; 962 T; 1 other;
XX
XX Query Match 13.5%; Score 790.6; DB 22; Length 4008;
XX Best Local Similarity 52.7%; Pred. No. 6.3e-181;
XX Matches 2104; Conservative 0; Mismatches 1669; Indels 222; Gaps 9;
XX
XX 421 ACCCAGTGGACATGCTGGGCTTTTTCCTGATGACTTTTTCGTGGCTTCTTCTCTGG 480
      | | | | | | | | | | | | | | | | | | | |
XX 131 ACCGGTGGATGATGCGGGCTACTCTCTCGCCACATTTTCTGGCTCAGCCGGTGA 190

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QY 1561 TAAGAACAACACGAGCTCCTACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT 1620
Db 1268 ACATACCAACAGAGACCCAGATCTGCTTGTCTTTTAGCAAAATGCCACCTTGACAT 1327
QY 1621 GGGACTCTCCACTCCAGTATCCAGACTCGCCCAAGCTGACCCCAAAATGAAAAG 1680
Db 1328 GGG-----AGCATGAAGCCAGCAGGAAAAGTA 1354
QY 1681 ACAAGAGGGCTTCCAGGGCAAGAAAGAGAGTGTAGGCGAGCTGCAGCGCACTGAGCATC 1740
Db 1355 CCCAAGAAATTTGCAAGACCAAGAAAGGATTTATGCAAGAAACAGAGGTGACAG---- 1410
QY 1741 AGCGGTGTGGCAGACAGAAAGGCAACCTCTCTCTGGACAGTGTAGAGCGGCCAGTC 1800
Db 1411 -----GCATACGTGAGAGAGTCCACC-----AGCCAAGGGAGCCACTG 1450
QY 1801 CCGAAGAGAGAGGCAAGCAGCATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGC 1860
Db 1451 GCCAGAGGAGCAAGTGACAGCTCAAAATCGGT-----TCTGC 1489
QY 1861 ACAGCATCGATCTGGAGATCCAAAGAGGGTAAACTGTTGGAATCTGCGGCACTGGGAA 1920
Db 1490 ACAGCATAGCTTTGGTGAGAAAGGGAGATCTTGGGAATATGTGGGAATGTGGAA 1549
QY 1921 GTGAAAAACCTCTCAATTTACGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCA 1980
Db 1550 GTGAAAAGAGCTCCCTCTCTGACGCTCTCTAGGACAGATGACGCTGACAGAAAGGGGTG 1609
QY 1981 TTGCATCAGTGAACCTTCGCTTATGTGGCCAGCAGGCGCTGGATCTCAATGCTACTC 2040
Db 1610 TGGCAGCTCAATGGAACTTTGGCCCTAGCTTTTACAGAGGCGATGGATCTTTTATGGAAATG 1669
QY 2041 TGAGACACAACATCCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACCTCTGCTGA 2100
Db 1670 TGAGAAACAACATCTTTTGGGAAGGAATATGATCACAAGGATATCAGCACAGTCC 1729
QY 2101 ACAGCTGCTGCTGAGGCGCTGACCTGGCCATTTCTCCAGCAGCGACCTGACGAGATTG 2160
Db 1730 GCGTCTGTGGCTCCAGAAAGGACCTGAGCAACCTCCCTATGGAGACCTGACTGAGATTG 1789
QY 2161 GAGAGCGAGGACCACTTGAAGGGTGGGCGCCAGCGGAGGATCAGCTTGGCCGGGCT 2220
Db 1790 GGGAGCGGGGCTCAACCTCTCTGGGGGCGAGGAGGAGATTAGCCTGGCCCGGCTG 1849
QY 2221 TGTATAGTGACAGGAGCATCTACATCTCTGGACAGCCCTCTAGTGCCTTAGATGCCATG 2280
Db 1850 TCTACTCCGACCGTCACTCTACCTCTGAGCAGCCCTCTGCGGCGCTGGACGCCACG 1909
QY 2281 TGGCAACCAATCTTCAATAGTGTCTATCCGAAACATCTCAAGTCCAAAGACAGTCTGT 2340
Db 1910 TGGGAAGCACGCTTTGAGGAGTGCAATTAAGAAAGCGCTCAGGGGAAAGACAGTCTGTC 1969
QY 2341 TTGTTACCCACAGTTACAGTACCTGGTTGACTGTGATCAAGTGTATCTCATGAAGAGG 2400
Db 1970 TGGTGACCCACAGCTTCTTAGAGTCTTGTAGAGTCTTGTATGAAGTATTTATTAGAAGATG 2029
QY 2401 GCTGTATTACGGAAGACCCATGAGAACTGATGAATTTAAATGGTGAATGCTTA 2460
Db 2030 GAGAGATTGTGAAAAGGGAACCCCAAGAGTATATGAGGAGAGGCGCTATGCAA 2089
QY 2461 CCATTTTAAATACCTTGTGGGAGACACCGCCAGTGTGAGATCAATCAAAAAGG 2520
Db 2090 AACTGATTCAACAACCTGCGAGGATTGCACTTCAAGGATCCTGAACACCTTTACAATGCAG 2149
QY 2521 AAACAGTGGTTACAGAGAGATCAC-----AAGCAGGGTCTTAAACAGGAT 2571
Db 2150 CAATGGTGAAGCCTTCAAGAGAGCCCTGCTGAGAGAGAGGAGATGCTGTTTGGCTC 2209
QY 2572 CAGTAAGAGGAAAAAGCAGTAAGCCAGAGAA----- 2606
Db 2210 CAGGAATAGAAAGATGAGGAAGAAAGATCTGAACAGGCTCAGAAATTTGAGACAAA 2269
QY 2607 -----GGGCACTTTGTGACCTGGAAAGAAAGGGGAGGTTTCAGTGCCTGTGT 2655

Db 2270 AAGTTCTTGACCAAGCTCATCCAGACTGAATCCCCCAGGAAGAACCTGACCTGGA 2329
QY 2656 CAGTATATGGTGTACATCCAGGCTGCTGGGGCCCTTTGGCATTTCTGTTATATGG 2715
Db 2330 AAACATATCACACGTACATTAAGGCTTCTGGAGGTTACTCTCTCTCTACTGTGT 2389
QY 2716 CCCTTTTCACTGCTCAATGTAGGAGCAGCCGCTTTCAGCACCTGTTGTTGTTACTGGA 2775
Db 2390 TCCCTCTCTCTGATGATGGCAGCGTGCCTTTCAGCAACTGGTGGCTGCTCTGCT 2449
QY 2776 TCAAGCAAGGAAGCGGAAACACCACTGTGACTCGAGGAAGAGACCTCGGTGAGTGACA 2835
Db 2450 TGGCAAGGCTCACGATGACCTGTGGGCCAGGCAACAGACCATGTGTGAGGTGCG 2509
QY 2836 GCA---TGAAGGCAATCTCTCATATGCACTACTATGCCAGCATCTACGCCCTCTCCATGG 2892
Db 2510 GCGCGTGTGGCAGACATCGGTGACATGTGTACCACTGGGTGTACACTGCAAGCATGG 2569
QY 2893 CAGTCATGCTGATCTGAAAGCCATTCAGAGGTTGTCTTTGTCAAGGGCACGCTGCGAG 2952
Db 2570 TGTTCATGCTGGTGTGGCGTCAACAAAGCTTCGCTTCAACCAAGACCACTGATGG 2629
QY 2953 CTTCTCTCCGCTGCATGACGAGCTTTTCCGAAGGATCTTCGAAGCCCTATGAAGTTT 3012
Db 2630 CATCTCTCTCTGCATGACAGCTGTGTGATAGATCTTAAAGAGCCCAATGAGTTCT 2689
QY 3013 TTGACAGACCCCAAGGAGGATCTCAACAGTTTTCCTCAAGACATGATGATGAAGTTG 3072
Db 2690 TTGACAGACTCCCACTGGCAGGCTAATGAACGTTTTTCCAAAGGATATGACGAGCTGG 2749
QY 3073 ACCTGCGGCTGCGCTCCAGGCCGAGATGTTATCCAGAGGTTATCCTGGTGTCTTCT 3132
Db 2750 ATGTGAGGCTGCGCTTTCACGACAGAACTTCTGACAGAGTTTATGTTGTTGTTA 2809
QY 3133 GTGTGGAATGATCGCAGGAGTCTTCCCGTGTTCCTTGTGGCAGTGGGCCCTCTGCA 3192
Db 2810 TTCTCGTGTCTTGGCTGCTGTGTCTCTGCTGCTCTTTAGTCGGCCAGCTGCTG 2869
QY 3193 TCCTCTTTTCAGTCTGCAATGTCTCCAGGGTCTCTGATTCGGGAGCTGAAGCGTCTGG 3252
Db 2870 TAGGCTCTCTCTTCTGTTACGCAATTTTCCACAGAGAGTCCAGAGGCTCAAGAAGTGG 2929
QY 3253 ACAATATCAGCAGTCACTTCTCTCCACATCAGCTCCAGCATACAGGCTTCCCA 3312
Db 2930 AGATGTCACCGGTACCTGTTTCCACCATCACTCTCTCATGAGGGCTGGGCA 2989
QY 3313 CCATCCAGCCTTACAATAAAGGCGAGGTTTCTGCACAGATACCAAGAGCTGCTGATG 3372
Db 2990 TCATTCAGCGCTATGGCAAGAGAGAGTGCATCACTAGTTTAAAGACCTAAACGACG 3049
QY 3373 ACAACCAAGTCTCTTTTGTGTGTGAGTGTGGGTGCGGTGCTGCGGTGCTG 3432
Db 3050 AAAATCCAGTCACTCTCTTAACTGTGCTCTCAAGTGGTGTGGCTGAGAAATGG 3109
QY 3433 ACCTCATCAGCATCGCCTCATCAACACACGCGGTGTGATGCTTATGACCGGCG 3492
Db 3110 ATGCTCTCATGAACATCTTACCTTCACTGTGGCTTGTGGTGACCTGAGTTCTCCT 3169
QY 3493 AGATTCCTCCAGCTTATGCGGGTCTCGCCATCTCTTATGCTGCTCCAGTTAAACGGGCTG 3552
Db 3170 CCATCAGTACTTCAACAAAGGCTGTCTATTTGTCATACATCATCCAGCTGAGCGGCTG 3229
QY 3553 TCCAGTTTACGTCAGCTGGCATCTGAGACAGAGCTGATTCACCTCGGTGGAGGAGGA 3612
Db 3230 TCCAGTGTGTGTGCGAAGCGGAAACAGACGCAAGCAAAATTCACCTCCGTGGAGTGC 3289
QY 3613 TCAATCACTACATTAAGACTCTCTCTTGAACCACTGCCCAATTAAGAACAAGGCTC 3672
Db 3290 TCAGGAATACATTTTCGACCTGTGTTCCCTGAATGCACTCATCCCTCAAAGTGGGACCT 3349
QY 3673 CCTCCCTGACTGGCCCCAGGAGGAGGTGACCTTTGAGAACGACGAGATGAGGTACC 3732

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Db 3350 GTCCCAAGGACTGCGCCAGCYGTGGGAGATCACCTTCAGAGACTATCAGATGAGATACA 3409
QY 3733 GAGAAACCTCCCTCTTGTCTTAAGAAAGTATCTTCACGATCAAACTTAAGAGAGA 3792
Db 3410 GAGAAACACCCCTCTTGTCTTCAGACGCTTGAACCTTGAACATACAAAGTGGCGACAG 3469
QY 3793 TTGGCATTGTGGCGGAGATCAGGAAAGTCTCTGCTGGGATGCCCTCTTCCGTC 3852
Db 3470 TCGGATGTGGAGAACAGAGTCCGGAAGTATCATCTTAGGAATGGCTTTGTTCTGTC 3529
QY 3853 TGTGGAGTATCTGGAGGCTGCATCAAGATTTGATGGAGTCAAGATCAGTATGTCG 3912
Db 3530 TGTGGAGCAGCCAGTGGCAACTTTATTGATGAGTGGATATCTGCTCAAGT 3589
QY 3913 TTGGGACCTCCGAGCAAACTCTTATCATCTTCTCAAGACCCGCTGCTTCAAGTGA 3972
Db 3590 TGAAGACCTTCAGAACCAAGTCTGATGATCCACAGGATCTGCTCTGTT----- 3641
QY 3973 CTGTGAGATCAAAATTTGGACCCCTTCAACCACTACACTGAAGACCAAGATTTGGGATGCC 4032
Db 3642 ----- 3641
QY 4033 TGGAGAGCACACATGAAAGATGATTTGCTAGCTACCTCTGAAACTTGAATCTGAAG 4092
Db 3642 -----TATAATGAAACTCCCAAGAAATTTACAGGCAGAAG 3676
QY 4093 TGATGGAGATGGGATTAACCTCTCAGTGGGGAACGGCAGCTCTTGTGCAATAGTAGAG 4152
Db 3677 TCAGAGAAATGGAGAAACTCTCAGTAGGGGAACGCTCAGCTCTTGTGTGGCCCGAG 3736
QY 4153 CCTGCTCCGCACTGTAAGATCTGATTTAGATGAAGCCACAGCTGCCATGACACAG 4212
Db 3737 CTCCTCCGTAATCAAGATCAATCTCTTGAAGCCACCCGCTCTATGGACTCCA 3796
QY 4213 AGACAGACTTATTGATTAAGAGACCATCCGAGAGCATTTGCAGACTGTACCATGTGA 4272
Db 3797 AGACTGACACCTGGTTTCAGAACACCATCAAGATGCTTCAAGGGCTGCATGTGCTGA 3856
QY 4273 CCATTGCCATCGCTGCACACGGTCTTAGCTCCGATAGGATTTATGGTGTGCCCGAG 4332
Db 3857 CCATCGCCACCGCTCAACACAGTCTCACTGCGATCAGCTCTGTTATGGAATG 3916
QY 4333 GACAGTGTGGAGTTTGACACCCCATCGTTCCTT 4367
Db 3917 GGAAGTGATGATTTGACAGCCTGAAGTCTT 3951

RESULT 10
AAF83643
ID AAF83643 standard; cdna; 4149 BP.
XX AC AAF83643;
XX DT
XX 23-JUL-2001 (first entry)
XX Novel human transporter protein (NHP) encoding cdna.
XX Novel human protein; transporter protein; NHP; therapeutic; diagnostic;
KW gene therapy; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..4149
FT /*tag= a
FT 259..267
FT /*tag= b
FT /*note= "the amino acid residues encoded by the above 3
FT codons are not indicated in the corresponding
FT protein sequence"
XX WO200132706-A2.
PN
XX
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PD 10-MAY-2001.
XX
PF 31-OCT-2000; 200WO-US29852.
XX
PR 02-NOV-1999; 99US-0163018.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Harris M, Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
WPI: 2001-343477/36.
P-PSDB; AAB62555.
XX
Novel isolated human polynucleotide sequences encoding polypeptides
PT that share sequence similarity with mammalian multidrug resistance
PT proteins and cellular transporter proteins, useful as probe or primer
PT
XX
PS Disclosure: Page 44-46; 59pp; English.
XX
CC The invention relates to novel human transporter proteins (NHP) and
CC polynucleotides encoding the NHPs. fragments of NHP nucleotide sequences
CC can be used in conjunction with PCR to screen libraries, isolate clones
CC and prepare cloning and sequencing templates. The NHP oligonucleotides
CC can also be used as hybridization probes for screening libraries, for
CC assessing gene patterns and for preparing antisense nucleic acid
CC molecules. The NHP nucleotide sequences are also useful in screening
CC techniques for drugs which treats symptomatic or phenotypic
CC manifestations of perturbing the normal function of NHP in the body.
CC Sequences AAF83635-647 represent NHP nucleic acid sequences.
XX
SQ Sequence 4149 BP; 982 A; 1080 C; 1091 G; 996 T; 0 other;

Query Match 13.1%; Score 766.4; DB 22; Length 4149;
Best Local Similarity 50.9%; Pred. No. 4.7e-175;
Matches 2102; Conservative 0; Mismatches 1901; Indels 125; Gaps 7;

QY 294 GAGGCGCTCTCTTGTATGCCCTCCATGCTTCTAGCTCAGATCCTGATGAGGAGCAT 353
Db 118 GATGCGCCCTGGAGTCAGACAGAGAGAAATCTGAGGCTCCAGGGAGGSCAGCTGTCCCA 177
QY 354 CCCAAGGGAAGTACCATCATGCTTGTAGTCTCTGAGCCCATCCG-----GACTACT 407
Db 178 CCGTGGGGAAGTATGATGCTGCTTGAACACCATGATTCCTCCGTCGCCAAGCGGAGG 237
QY 408 TCCAAACACACAGACCCAGTGGACAAATGCTGGGCTTTTCTGTATGACTTTTCTGTGG 467
Db 238 TTTCTGCCCCCAGCCCTGGACAAATGCTGCCCTGTTCTTCTACCTACCGTGTATGG 297
QY 468 CTTTCTTCTGTGGCCCGTGTGGSCCAAGAAAGGGGAGCTCTCAATGGAAGA-CGTGTG 526
Db 298 CTCAC-----CCGCTCATGATCCAAAGCTTACGGAGTCGCTTAGATGAGAACACCATCC 353
QY 527 GTCTCTGTCCAAGACGAGTCTTCTGAGTGAACCTGACAGAACTAGAGAGACTGTGGCA 586
Db 354 TCCACTGTGATGCTGATGCTTCAGAAAAAATGTCAAAAGGCTTCAACCGCTTTGGGA 413
QY 587 AGAAGAGCTGAATGAAGTTGGGCCAGAGCTGCTTCCCTCCGAAAGGTTGTGTGATCTT 646
Db 414 AGAAGAGCTCAAGGCCGAGGATTTGAAAAGCTTCAAGCTTCTGCTGATGCTGAGGTT 473
QY 647 CTGCGGCACACGGCTCATCTCTGTCATGCTGCTGATGATGATGATGATGATGATGATG 706
Db 474 CCAGAGAACAAAGTTGATTTTCGATGCTTCTGCGCATCTCTTCTGATGCTGCTGCTG 533
QY 707 CAGTGGACACCCCTTCATGTTGAACACCTCTTGGAGTATATACCCAGGCAACAGAGTAA 766
Db 534 ACTCGGCAATATGATTATATACCAAGATCTGGAATATTCAGAAAGACAGTGTGGGAA 593
QY 767 CCTGCAGTACAGCTTGTGTTAGTGTGCTGCGCTCTCTGACGGAATCGTCCGCTTTG 826
Db 594 TGTTGTCCATGAGTGGAGTCTGCTTTGCCCTTTTCTCTCCGAATGTGTAAGTCTCT 653
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CC mammalian metabolite or organic cation transporters, multi-drug
CC resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
CC other cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
CC manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
CC biological conditions.

XX
SQ Sequence 3660 BP; 920 A; 915 C; 943 G; 881 T; 1 other;

Query Match 13.0%; Score 759.4; DB 22; Length 3660;

Best Local Similarity 52.9%; Pred. No. 2.2e-173;

Matches 1911; Conservative 0; Mismatches 1571; Indels 129; Gaps 8;

QY 421 ACCGAGTGCACATCTGGGCTTTTTCCTGTATGACTTTTTCGGGCTTCTCTCTGG 480
DB 131 ACCGGTGTGATGATCCGGGGCTACTCTCTTCGCCACATTTTTCCTGGCTCAGCGCGGTGA 190
QY 481 CCCGTGTGGCCACAAAGAGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCTCAAGC 540
DB 191 TGGTGAAGGCTACCGGCAAG--GCTACCGGTAGACACCTGCCCCCATTTGTGCAAT 247
QY 541 ACGAGTCTTCTGACGTGAATCTCAGAAGACTAGAGAGCTGTGGCAAGAGAGCTGAATG 600
DB 248 ATGACTCATCTGACACCAATGCAAAAGATTTTCGAGTCTTTTGGGATGAAGAGGTAGCAA 307
QY 601 AGTTGGGCCACACGCTGCTTCCCTCGGAGGGTGTGTGGATCTTCTCCCGCAGCAGCG 560
DB 308 GGGTGGGCTCTGAGAAGGCTCTCTGAGCCAGCTGTGGTGTGGAATTTCCAGAGGACACGG 367
QY 661 TCATCTGTGCCATCTGTGTCCTGTGATCACGACGTGCTGCTTCACTGGACACGCT 720
DB 368 TGTGTGACATCTGTGCCACATCTGTGATCATCATGACGACCATAGGCCGACAG 427
QY 721 TCATGGTGAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCACTACAGCT 780
DB 428 TTCTCATTCACCAATCTCTCCAGCAGACTGAGAGACCTCTGGGAAAGTCTGGTGGCA 487
QY 781 TGTGTGTAGTGTGGGCTCTCTGACGGAATCTGTGGGCTTGTGGCTGTGACATGA 840
DB 488 TTGGACTGTGCATAGCCCTTTTGGCCAGGAGTTTACCAAGATCTCTTTTGGGCCCTTG 547
QY 841 CTTGGGCATTTGAATTAACGAACGGTGTCCGCTTGGGGGGCCATCTTAACCATGGCAT 900
DB 548 CTGGGCCATCACTACCCAGCGGCATCCGTTGAAGTGGCGCTCTCCACCTTGGTTT 507
QY 901 TTAAGAAGATCCTTAAGTTAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
DB 608 TTGAAAACCTAGTGTCTCAAGACATTTGACCCACATCTCTGTGGCGAGGTGCTCAATA 667
QY 961 TTTGTCTCAACGATGGGAGAGAAATTTTGGAGGAGCAGCCGTTGGCAGCCTGTGGCTG 1020
DB 668 TACTGTGAAGTATAGCTATCTTTTGTGAAGCTGCGCTTGTGTCTTTTGGCCAGCA 727
QY 1021 GAGGACCCGTTGTGCCATCTTAGGCATGATTTAATGTAATTTCTGGGACCAACAG 1080
DB 728 CCATCCGATCCTAATGCTCTTTGTGGCGGTACGCGCTTTTTCATCTGGGGCCACAG 787
QY 1081 GCTTCTGGGATCAGCTGTTTTTATCTCTTTTACCCAGCAATGATGTTGATCAGCGC 1140
DB 788 CTTCTATCGGGATATCAGTGTATGTATATTCATACCCGTCACAGATGTTTATGCGCAAGC 847
QY 1141 TCACAGATATTTACGAGAAATGCGTGGCGCCGACCGATGACGTGTCCAGAGATGA 1200
DB 848 TCAATTCAGCTTTTCCGAAGGTACGAATTTTGGTGACAGACAGGCGAGTTCCAGACAATGA 907
QY 1201 ATGAAGTTCTTACTTACATTTAATTTTATCAAAATGTATGCTGCGTCAAGCATTTTCTC 1260
DB 908 ATGAGTTTCTGACCTGCATCAGGCTGATCAAAATGTATGCTGGGAGAAATCTTTTACCA 967
QY 1261 AGAGTGTTCAAAAAATCCGCGAGGAGGAGCGTGGATATTGGAATAAGCCGGGTACTTCC 1320

DB 968 ACATATCCAAAGATATAAAGAGGAGGAAAGAAATTTACTTGGAAAGAGCTGGATTTCTCC 1027
QY 1321 AGGTATCACTGTGGTGTGGCTCCCATTTGTGTGTGTGATTTGCCAGCGTGGTACCTTCT 1380
DB 1028 AAGTGTGAAACTGTGGCTGGCCCATCTGTGCCACATAGCATCGTGTGACATAT 1087
QY 1381 CTGTTTATATGACCTTGGCTTGTGACAGCAGCAGAGGCTTTCACAGTGGTGACAG 1440
DB 1088 CTTGCCACATCTCTTGAGAGCAAACTCACCGACCCGTGGCATTTAGTGTGATGCCA 1147
QY 1441 TCTTCAATTCATGACTTTTTCCTTTTGAAGTAAACACCGTTTTCAGTAAAGTCCCTCTCAG 1500
DB 1148 TGTTAATGTAATGAAGTTTTCATTTGCAATCTTGGCTTCTCCATCAAGCAATGCGCTG 1207
QY 1501 AAGCCTCAGTGGCTGTGTGACAGATTTAAGAGTTTGTGTTCTTAATGGAAGAGGTTTCACATGA 1560
DB 1208 AAGCGAATGTCTCTTAAGAGAAATGAAGAAATTTCTATAGATAAAAGCCGCCATCTT 1267
QY 1561 TAAAGAACAAACAGCAGCTCTCACATCAAGATAGAGATGAAGATGAAGATGCAAAATGAAAAAG 1620
DB 1268 ACATACCCAAACAGAGACCCAGATCTGTCTTGTCTTTAGCAAAATGCCCACCTTGACAT 1327
QY 1621 GGGACTCTCTCCACTCTCAGTATCCAGAACTCGCCCAAGCTGACCCCAATGAAAAAG 1680
DB 1328 GGG-----AGCATGAAGCCAGCAGGAAAAAGTA 1354
QY 1681 ACAAGAGGGCTTCCAGGGGCAAGAAAGAGTGAAGGAGCTGAGCGCAGCTGAGCATC 1740
DB 1355 CCCAAAGAAATTTGCAGAACCAAGAAAGCATTTATGCAAGAACAGAGGTCAGAG---- 1410
QY 1741 AGSCGCTGTGGCAGAGCAGAAAGGACCTCTCTCTGGACAGTGAAGCGGCGCCAGTC 1800
DB 1411 -----GCATACGTGAGAGGAGTCCACC-----AGCCAAGGAGGCCACTG 1450
QY 1801 CCAGAGGAGAAAGGCAAGCAGCATCCACTGGGCCACCTGCGCTTACAGAGGACACATGC 1860
DB 1451 GCCCAGAGGCAAGAGTGAAGCCTCAATCGG-----TTCGTC 1489
QY 1861 ACAGCATCATCTGGAGATCAAGAGGGTAAACTGGTGTGAATCTCGGGCAGTGTGGAA 1920
DB 1490 ACAGATAAGCTTTTGGTGTGAGAAAGGGAAGATCTTGGGAATATGTGGAAATGTGGAA 1549
QY 1921 GTGAAAAACCTCTCTCATTTTCAGCCATTTTAGCCAGATGACGCTTCTAGAGGCGAGCA 1980
DB 1550 GTGGAAGAGCTCCCTCTCTGAGCTCTCTTAGCAGATGACGCTGACAGAAAGGGTGG 1509
QY 1981 TTGCAATCAGTGGAACTCTTCTGCTTATGTGGCCAGCAGGCTTGATCTCAATCTACTC 2040
DB 1610 TGGCAGTCAATGGAACCTTTGGCCCTAGCTTTCACAGCAGGCAATGATCTTTCATGGAATG 1669
QY 2041 TGAGAGACAACATCTCTGTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGA 2100
DB 1670 TGAGAAAAACATCTCTTTTGGGAAGAAAGTATGATCACCAGGATATCAGCAGACAGTCC 1729
QY 2101 ACAGCTGCTGCTGAGGCTGACCTGCGCATTTCTCCAGCAGCAGCCTGACGAGATG 2160
DB 1730 GGGTCTGTGGCTCCAGAGGACCTGAGCACTCCCTCTATGGAGACCTGACGTGAGATTG 1789
QY 2161 GAGAGGAGGAGCCCACTTGAAGGTTGGCAGCGCAGGAGGATCAGCCTTGGCCGGGCT 2220
DB 1790 GGGAGGGGGCTCAACCTCTCTGGGGGCGAGAGGAGGATGATGCTGGCCGCGCTG 1849
QY 2221 TGTATAGTACAGGAGCATCTACATCTCTGGAGCAGCCCTCAGTGCCTTAGATGCCCCATG 2280
DB 1850 TCTACTCCGACGCTCAGCTCTACCTCTGTGGAGACCCCTCTGCGGCTGGAGCCACG 1909
QY 2281 TGGGAACACATCTTCAATAGTGTCTATCCGGAACATCTCAAGTCCAAAGACAGATCTGT 2340
DB 1910 TGGGAGACAGCTCTTTGAGGAGTGCATTTAAGAGACGCTCAGGGGAAAGACAGTCTGTC 1969
QY 2341 TTGTTACCCAGGATACAGTACCTGTTGACTGTGTGATGATGATCTTTCATGAAAGAGG 2400

Db 1970 TGGTGACCCACAGCTACAGTCTTGTAGAGTCTTGTGATGAAGTATTTTATTAGAAGATG 2029
QY 2401 GCTGTATTACGGAAAGAGGACCCATCAGAACTGATGAATTTAAATGGTGACTATGCTA 2460
Db 2030 GAGAGATTTGTGAAAGGGAACCCACAAAGAGATTAATGGAGGAGAGGCGCTATGCTCAA 2089
QY 2461 CCATTTTATAACCTGTTCTGGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAAGG 2520
Db 2090 AACTGATTCACACCTCGGAGGATTCAGTTCAAGGATCTGACACCTTTACATGCGAG 2149
QY 2521 AAACAGTGGTTTCACAGAAGAAGTAC-----AAGACAGGGTCCCTAAACAGAGAT 2571
Db 2150 CAATGGTGAAGCCTTCAAGAGAGAGCCCTGCTGAGAGAGAGGAAGATGCTGTTTGGCTC 2209
QY 2572 CACTAAGAGGAAAGACGATTAAGCCAGAGAGG----- 2609
Db 2210 CAGGAATGAGAAGATGAAGGAAAGAAATCTGAACAGAGCTCAGAAATTTGTAGACAA 2269
QY 2610 -----CAGCTTGTGACGTGGAAGAGAAAGGCGAGGTTTCAGTGCCCTGGT 2655
Db 2270 AAGTTCTGAGCACAGCTATCCAGCTGAATCCCCAGGAGAGAACCTGACCTGGA 2329
QY 2656 CAGTATATGCTGTACATCAGGCTGCTGGGGGCCCCCTTGGCATTCTCTGGTTATTATGG 2715
Db 2330 AAACATATCACAGTACATTAAGGCTTCTGGAGGGTACCTCTCTCTCTTCACTGCT 2389
QY 2716 CCGTTTTCATGCTGAATGTAGGAGACACCGCTTACAGACCTGGTGGTTGAGTTACTGGA 2775
Db 2390 TCCCTTCTCTCTGATGATTGGCAGGCTGCCCTTACGAACTGGTGGCTGGTCTCTGGT 2449
QY 2776 TCAAGCAAGGAGCGGACACACCTGTGACTCGAGGAGACGAGAC---TCGGTGAGTG 2832
Db 2450 TGGACAAGGCTCACGATGACATGTGGGCCCCAGGCAACAGACCATGTGTGAGTGC 2509
QY 2833 ACAGCATGAAGGACAACTCTCATATGACGACTATGCCAGCATCTAGCCCTCTCCATGG 2892
Db 2510 GCGCGTGTGCGACATCGGTGACATGTGTACCATGGTGGTACACTGCAAGCATGG 2569
QY 2893 CAGTATGCTGATCCGAAAGCATTCGAGGAGTTGTCTTGTCAAGGGCAGCTGCGAG 2952
Db 2570 TGTTCATGCTGGTGTGGCGTCAACAAAGGCTTCCGTCTTCAACCAAGACCACTGATGG 2629
QY 2953 CTTCCTCCGGCTGCTAGGAGCTTTTCGAAGGATCTTCGAAGCCCTATGAAGTTT 3012
Db 2630 CATCTCTCTCTGATGACACGGTGTGTGATGAATCTTAAGAGCCCAATGATTTCT 2689
QY 3013 TTGACACGACCCCGACAGGAGGATTTCAACAGGTTTCCAAAGACATGGATGAAGTTG 3072
Db 2690 TTGACACGACTCCACTGGCAGGCTAATGAACGGTTTTCGAAGGATATGGACGAGCTGG 2749
QY 3073 ACGTGGCTGCGTTCAGGCGGAGATGTTATCCAGACGTTATCCTGGTGTCTTCT 3132
Db 2750 ATGTAGGCTGCGGTTTCAGCGAGAACTTTCTGACGAGATTTTATGGTGGTGTGTTA 2809
QY 3133 GTGTGGGAATATGCGAGGAGTCTCCCGTGTTCTTGTGGCAGTGGGCGCCCTTCTCA 3192
Db 2810 TTTCTGATCTGGCTGTGCTGCTTCTCTCTTTAGTCGTGGCCAGCTTGTCTG 2869
QY 3193 TCCCTTTTTCAGTCTGACATTTCTCCAGGCTCTGATTCGGGAGCTGAAGCGTCTGG 3252
Db 2870 TAGGCTTCTTCTGTTACGATTTTCCACAGAGGAGTCCAGAGCTCAAGAGGTGG 2929
QY 3253 ACATATCAGCAGTACCTTTCTCTCCACATACGATCCAGCATACAGGGCTTCCCA 3312
Db 2930 AGAATCTCAGCGGTCACCTGGTTTCAACCCACATCACTCTCTCCATGCGAGGCTGGGCA 2989
QY 3313 CCATCCAGCCTACATAAAGGCGAGGTTTCTGCACAGATACCCAGGAGCTGCTGGATG 3372
Db 2990 TCATTCAGGCTATGCGACAGAGAGAGCTGCAATCACTAGTTTAAAGACCTAAACGAGC 3049
QY 3373 ACAACCAAGCTCTTTTTTTTGTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGG 3432
Db 3050 AAACCTCAGTACCTCTCTACTTTAACTGTCTCTCAGTGTGTTGGCTGAGATGG 3109

QY 3433 ACCTCATCAGCATCCCTCTCATCACCACCACGGGCTGATGATCTTCTTATGACGGGC 3492
Db 3110 ATGCTCTCATGAACATCCTTACCTTCACTGTGGCTTGTGGTACCCCTGAGTTTCTCCT 3169
QY 3493 AGATTCCCCAGCTATCGGGTCTCGCATCTCTTATGCTGCTCCAGTTAACGGGCTGT 3552
Db 3170 CCATCAGTACTTATCCAAAGGCTGTCTTGTCTATCATCATCCAGCTGACGGACTGC 3229
QY 3553 TCCAGTTTACGGTCAGACTGGCATCTTGAGACAGAAGCTCGATTACCTCGGTGGAGAGA 3612
Db 3230 TCCAAGTGTGTGGAACGGGAACAGACAGACGCAAGCAAAATTCACCTCCGTGGAGCTGC 3289
QY 3613 TCAATCACTACATTAAGACTCTGCTTGGGAAGCACTGCCAGAAATTAAGAACAAAGGCTC 3672
Db 3290 TCAGGGAATACATTTCCGACCTGTGTCTCTGAATGCATCTCCCTCAAGTGGGGACCT 3349
QY 3673 CCTCCCTGACTGGCCCGAGGAGAGGTGACCTTTGAGAAGCGCAGAGATGAGTACC 3732
Db 3350 GTCCCAAGGACTGGCCAGCTGTGGGAGATCACCTTCAGAGACTATCAGATGAGATACA 3409
QY 3733 GAGAAAACCTCCCTCTTCTCTTAAAGAAAGTATCCTTCACGATCAAACTTAAAGAGAAGA 3792
Db 3410 GAGACAACACCCCTTGTCTCGACAGCTGAACCTTGAACATACAAAGTGGGCAGACAG 3469
QY 3793 TTGCATTTGGGGCGGACAGGATCAGGAAAGTCTCTCGCTGGGATGGCCCTCTTCCGTC 3852
Db 3470 TCGGGATTTGGAAGAACAAGTCTCCGAAAAGTATCCTTTAGGAATGGCTTTGTTCCGTC 3529
QY 3853 TGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTCAATGATGATGATGATGGCC 3912
Db 3530 TGTGGAGCAGCCAGTGGCACAATCTTATGATGAGTGGATATCTGCATCTCAGCT 3589
QY 3913 TTGCGGACCTCCGAAGCAAACTCTATCATCTTCTCAAGAGCCGCTGTGTTCACTGGCA 3972
Db 3590 TGAAGACCTCAGAACAAGCTGATGATCCACAGGATCCTCTCTCTGTTGTAGGTA 3649
QY 3973 CTGTCAAGTCA 3983
Db 3650 CAGTAAGATAA 3660

RESULT 12
AAD36023
ID AAD36023 standard; cdna; 4074 BP.
XX
AC AAD36023;
XX
DT 09-AUG-2002 (first entry)
XX
DE Human adenosine triphosphate-binding cassette protein cDNA #1.
XX
DE Human; adenosine triphosphate-binding cassette; chemoprotectant; ATP;
KW ABC protein; gene therapy; breast proliferative fibrocystic disease;
KW breast adenocarcinoma; drug resistance; breast disorder; transgenic;
KW vaccine; gene; ABCP; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT 1..3996
FT /*tag= a
FT /product= "Human ABC protein"
XX
XX WO200224742-A2.
XX
XX PD 28-MAR-2002.
XX
XX PF 20-SEP-2001; 2001WO-US29455.
XX
XX PR 22-SEP-2000; 2000US-0668628.
XX
XX PA (INCY-) INCYTE GENOMICS INC.

2160 GGAGAGCAGGAGCCAACTGAGCGGTGGCGAGCGCCAGAGGATCAGCCTTCCCGGGCC 2219
1729 GGAGAGCGGGCCTCAACTCTCTGGGGGGGAGAAACAGAGGATCAGCCTGCCCGGGCC 1788
2220 TTGTATAGTACAGAGGAGATACATCTCTGGACGACCCCTCAGTGCCTTAGATGCCCAT 2279
1789 GTCTATTCGACCGTACAGTCTACCTGCTGGACGACCCCTCTGCTGTGGACGCCAC 1848
2280 GTGGCAACCAACATCTCAATAGTGTATCCGGAACATCTCAAGTCCAAAGACATTTG 2339
1849 GTGGGAAGACATTTTGGAGAGTGCATTAAGAAAGACACTCAGGGGAAGACGCTGCTC 1908
2340 TTTGTTACCCACCACTTACAGTACCTGCTGACTGTGATGAAGTCACTTTCATGAAGAG 2399
1909 CTGGTACCCACCACTGCACTACTTAGAATTTGTGGCCAGATCATTTTGTGGAAAT 1968
2400 GGCTGTATTACGGAAGAGGCCATCCATGAGGAACCTGATGAATTTAAATGGTGACTATGCT 2459
1969 GGGAAATCTGTGAAATGGAACCTCACAGTGAAGTTAATGCAGAAAAAGGGAAATATGCC 2028
2460 ACCATTTTAAATACCTGTTGCTGGGAGAGACACCGCCAGTGTAGATCAATTTCAAAAAG 2519
2029 CAACCTTATCCAGAGATCCAAAGGAAGCCACTTCGGACATGTTTCAGGACACAGCAAG 2088
2520 GAAACCACTGTTTACAGAAAGTCAAGAACAGGCTCTTAAACAGGATCACTAAAG 2579
2089 ATAGCAGAGAACCCAGGTAGAGTCAAGTCTGGGCCACTCCTCGAAGAGTCTCTC 2148
2580 AAGAAAAAGCAGTAAAGCCAGAGAGGAGGAGCTTGTGCAGCTGGAAGAAAGGGCAG 2639
2149 AAGGAAATGCTGT-----GCCGAGCATCAGCTCACACAGGAGGAGGATGAAGAA 2202
2640 GGTTCAGTCCCTGCTGATATATGCTCTACATCCAGGCTGCTGGGGGCCCTTTGGCA 2699
2203 GGCTCCTTGAGTGGAGGCTTACACCACTACATCCAGGAGCTGAGGTTTACATGCTC 2262
2700 TTCTGCTTATATGCGCCCTTTTATGCTGAATGTAGCAGCAGCCCTTCAGACCTGG 2759
2263 TCTGTCATAATTTCTTCTGCTGCTGCTGCTCTTCTTAAACGATCTTCAAGCTTCGG 2322
2760 TGGTTGAGTTACTGATCAAGAAAGGAGCGGACCACTGTGACTCGAGGGAACGAG 2819
2323 TGGCTGAGCTACTGTTGGACGAGGCTCGGGACCAATAGCAGCGGAGAGCAATGGA 2382
2820 ACTTCGGTGTGAGT---GACAGATGAGGAGCAATCTCTATATGCACTACTATGCCAGATC 2876
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2877 TAGCCCTCTCCATGGCAGTCTGATCTGATCTCTGAAAGCCATTCGAGGAGTGTCTTTGTC 2936
2443 TAGGGCTCAAGCCCTGCTCTCTGCTGTGGGGTCTGCTCTCAGGATTTTCACC 2502
2937 AAGGSCAGCTCGAGCTTCTCCCGGTGCTGATGACGAGCTTTTCCGAGGATCTCTGGA 2996
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2683 TTAATGGTATCGCGCTCTGTTGATGCTGAGTGTCTCTCCATATATCTGTTAATG 2742
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2803 GTGTTCAAGAGACTGGAGACTATAGCCGGTCTCTTTATTTCCCACTCTCAATTCT 2862
3297 ATACAGGGCCTTCCACCACCTACAGCCTTAAATAAAGGCGAGGTTTCTGCACAGATAC 3356
2863 CTGAGGGCCTGAGCTCCATCCATGCTATATGGAATAACCTGAAGACTTTCATCAGCCAGTTT 2922
3357 CAGGAGCTCTGGATGACAAACCAAGCTCTTTTGTGTTAGTGTGGGATGCGGTGG 3416
2923 AAGAGCTGACTGATGCGCAGAAATAACTCTGCTGTGTTTCTTCTTCCACACGATGG 2982
3417 CTGGCTGTGCGCTGACCTCATCAGCATCGCCCTCATCACCAACGAGGGGCTGATGC 3476
2983 ATGGCATTCAGCTGGAGATCATGACCAACCTTGTGACCTTGGCTGTGGCCCTGTCGTG 3042
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3103 CAGCTGGCGCTCAGCTTCCAGGCCACTGGCCGATTTGGCTTGGAGACAGAGGCACAGTTC 3162
3597 ACCTGGTGGAGAGGATCAATCACTACATTAAGACTCTGCTCTTGGAAAGCACTGCCAGA 3656
3163 ACGGCTGTAGAGAGGATCTGCAGTACATGAAGTGTGTCTCGGAAGCTCTCTTACAC 3222
3657 ATTAAGAACAAAGCTCCCTCCCTGACTGGCCCCAGGAGGAGAGTGTGACTTTTGAAGAC 3716
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3717 GCAGAGATGAGTACCGAGAAACCTCTCTTGTCTCTTAAAGAAAGTATCTTACAGATC 3776
3283 TATCATATGAATAACAGAGACAAACACCCACCGCTCTCACGGCATCAACCTGACCATC 3342
3777 AAACCTAAAGAAAGATTTGCGATTTGGGCGGACAGGATCAGGAGTCTCTCGCTGGGG 3836
3343 CCGGGCCAGAGTGTGGGATCTGTGGAGGACCGGGCTCTGGGAAGTCTCTTCTTGGGC 3402
3837 ATGGCCCTCTCCGCTGTGTGGAGTTATCTGGAGGCTGCATCAAGATTTGATGAGTGA 3896
3403 ATGGCTCTCTCCGCTGTGGAGCCATGCGAGCGGATTTCTCATTTGACGCGCTGGAC 3462
3897 ATCAGTGTATTTGGCTTCCGACCTCCGAGCAAACTCTCTATCATTTCTCTCAAGAGCG 3956
3463 ATTTGAGCATCGGCTGGAGGACTTGGCGTCCAGCTCTCAGTGTATCTCTCAAGATCCA 3522
3957 GTGCTGTTTCACTGGCACTGTGATCAAAATTTGGACCCCTTCAACAGTACACTGAAGAC 4016
3523 GTGCTGCTCTCAGGAACCATCAGATTCACCTAGATCCCTTTGACCGTCACTGACCCAG 3582
4017 CAGATTTGGATGCCCCGGAGGACACATGAAGAATGTATTTGCTCAGCTACCTCTG 4076
3583 CAGATCTGGATGCTTTGGAGAGGACATTTCTGACCAAGGCCATCTCAAAGTTTCCCAA 3642
4077 AAACCTGAATCTGAAGTGTGAGAGATGGGATAACTCTCAGTGGGGAACGGAGCTC 4136
3643 AAGCTGCATACAGATGTGGTGGAAAACGGTGGAAACTTCTCTGTGGGGAAGGAGCTG 3702
4137 TTGTGCATAGCTAGAGCCTGCTCCGCCACTGTAAAGATTTCTGATTTTATAGTGAAGCCACA 4196
3703 CTCTGATTTGCCAGGGCTGTGTTCCAACTCCAAAGATCATCTTATCATGAAGCCACA 3762
4197 GCTGCATGACACAGACAGACTTTATGATTTCAAGAGACCATCCGAGAAGCATTTGCA 4256
3763 GCCTCCATTTGACATGAGAGACACACCTGTATCCAGGACATTCCTGGAAGCTTCCAG 3822
4257 GACTGTACATCTGACCATTTGCCATCGCCTGCACAGGTTTCTAGGCTCCGATGAGAT 4316
3823 GGCTGACCGCTGCTGCTCATTTGCCACCGTGTCCACTGTGTGAACCTGTGACCGCATC 3882
4317 ATGGTGTGGCCCGGACAGAGTGTGGAGTTTGCACCCCTCTCTCTCTCTCTCTCTCAAC 4376

Db 3883 CTGGTTATGGCAATGGGAAGGTGGTAGAATTTATCGCGCGGAGTACTGCGGAAGAAG 3942
QY 4377 GACAGTTCGCCGATTCTATGCATGTTGCTGCTGC 4411
Db 3943 CTTGGGTCTATGTTCCGAGCCCTCATGGCCACAGC 3977

RESULT 13
AAD14911
ID AAD14911 standard; cDNA; 3753 BP.
XX
AC AAD14911;
XX
DT 01-NOV-2001 (first entry)
DE Human transporter-related protein #24 cDNA.
XX
KW Human; transporter-related protein; metabolite transporter;
KW organic cation transporter; multi-drug resistance; MDR; gene therapy;
KW cellular transporter; sodium-glucose cotransporter; diagnosis; screening;
KW symptomatic; phenotypic manifestation; biological condition; ss.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
CDS 1..3753
FT /*tag= a
FT /product= "Human transporter-related protein"
FT /transl_except= (pos:3025..3039, aa:Thr-Thr)
FT /transl_except= (pos:3370..3372, aa:Xaa)
FT /note= "Xaa can be any amino acid"
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XX WO200157214-A2.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03646.
XX
XX 03-FEB-2000; 2000US-0179973.
XX 14-FEB-2000; 2000US-0182422.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Wang X, Abuin A, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
XX WPI: 2001-514599/56.
XX P-PSDB; AAE08077.
XX
XX Novel polynucleotides encoding novel human proteins with structural
PT similarity to cellular transporters for the diagnosis of disease and
PT use in gene therapy
XX
XX Disclosure; Page 68-70; 91pp; English.
XX
XX The present sequence is a human transporter-related protein cDNA.
CC The human transporter-related protein share structural similarity with
CC mammalian metabolite or organic cation transporters, multi-drug
CC resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
CC other cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
CC manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
CC biological conditions.
XX
XX Sequence 3753 BP; 949 A; 937 C; 965 G; 901 T; 1 other;
SQ

Query Match 12.9%; Score 753.2; DB 22; Length 3753;
Best Local Similarity 52.9%; Pred. No. 7.1e-172;
Matches 1900; Conservative 0; Mismatches 1563; Indels 129; Gaps 8;

QY 421 ACCCAGTGGACAATGCTGGGCTTTTCTCTGTAUTGACTTTTTCGTGGCTTTCTTCTCTGG 480
Db 131 ACCCGTGGATGATGCGGGGCTACTCTCTTCGCCACATTTTCTTGGCTCAGCGCGTGA 190
QY 481 CCCGTGTGGCCACAAGAAGGGGAGCTCTCAATGGAAAGAGTGTGTCTCTGTCCAAGC 540
Db 191 TGGTGAAGGCTACCGGCAAG--GCTGACCGTAGACACCTGCCCCCTGTCGACAT 247
QY 541 ACAGATCTTCTGACGTGAACCTGCAGAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG 600
Db 248 ATGATCATCTGACACCAATGCCAAAGATTTCGAGTCTTTGGGATGAAGAGTAGCAA 307
QY 601 AAGTTGGCCAGAGCGCTGCTTCCCTGCGAAGGGTGTGTGGATCTTTCGCCGACACGCG 660
Db 308 GGGTGGTCTGAGAGGCCCTCTCTGAGCCACGTGGTGTGGAATTCAGAGGACACCGG 367
QY 561 TCATCTGTCTCATCGTGTGCTGATGATCAGCAGCTGGCTTTCAGTGGAGCAGGCT 720
Db 368 TGTGTGATGGACATCGTGCCCAACATCTCTGTCATCATGCGAGCCATAGGGCGGACAG 427
QY 721 TCATGGTGAACACCTCTTGGAGTATACCCAGGCAACAGAGCTTAACCTGCAGTACAGCT 780
Db 428 TTTCTATTTCACCAATCTCCAGCAGACTGAGAGGACCTCTGGGAAAGCTCTGGGTTGCA 487
QY 781 TGTGTTAGTCTGGGCTCTCTCTGACGGAATCGTGGCTTCTTGGTCGCTTGCACATGA 840
Db 488 TTGGACTGTGCATAGACCTTTTTCACCGAGTTTACCAAGTCTCTTTTGGGCCCTTG 547
QY 841 CTTGGGATTAATACCGAACCCTGCTGCTTTCGGGGGGCCATCTTAACCATGGCAT 900
Db 548 CTTGGGCTCACTACCTACCGCAGCCATCCGGTTGAAGTGGCGCTCTCCACCTTGGTTT 607
QY 901 TTAAGAGATCCITTAAGTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
Db 608 TTGAAGACCTAGTGTCTCTCAAGACATTTGACCCACATCTCTGTTGGCGAGGTGCTCAATA 667
QY 961 TTTGCTCCAAACGATGGGCGAGAGAAATGTTTGAAGCAGACAGCGCTTGGCAGCTGTGGCTG 1020
Db 668 TACTGTCAAGTGTAGTATTTCTTTGTTGAAGCTGCTTCTTGTCTTGTCCAGGCA 727
QY 1021 GAGGACCGGTTGTGGCCATCTTAGGCATGATTTATAATGTAATTTCTGGGACCAACAG 1080
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QY 1081 GCTTCTCCGGATCAGCTGTTTATCTCTTTTACCCAGCAATGATGTTTCTCATCAGCGC 1140
Db 788 CTCTCATCGGATATCAGTGTATGTCATATTCACCGCTCCAGTGTATGTCGCAAGC 847
QY 1141 TCACAGCATATTTACGAGAAATGCGTGGCCGCGGAGATGAACGTGTCCAGAGATGA 1200
Db 848 TCAATTCAGCTTTCCGAAGGTGAGCAATTTTGGTGACAGACAAGCGAGTTCAGACAATGA 907
QY 1201 ATGAAGTCTTACTTACATTAATTTTCAAAATGATGATGCTGGGTCAAGCATTTTCTC 1260
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QY 1261 AGAGTGTTCAAAATAATCCGCGAGGAGGCTGCGATTTGGAAGAAAGCCGGTACTTCC 1320
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QY 1321 AGGTATFACATGTGGGTGTGGCTCCCATTTGGTGGTGAATGCCAGGCTGGTGTACCTTCT 1380
Db 1028 AAAGTGAATACTGTCCCTGGCCCTCCATCGTGTCCACCATAGCCATCGTGTGACATAT 1087
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QY 1441 TCTTCAATTCATGACTTTTGTGCTTTGAAAGTAAACACCGTTTTCAGTAAAGCTCTCAGC 1500
Db 1148 TGTTTAAATGAAGTGTTCATTCGAATCTTGGCCCTCTCTCCATTAAGCAATGGCTG 1207
QY 1501 AAGCCTCAGTGGTGTGACAGATTTAAGAGTTTGTGTTTCTAATGAAGAGGTTTCACATGA 1560

[illegible]

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Qy	2610	-----CAGCTTGTGCAGCTGGAAGAGAAAGCGAGGTTCAGTGCCCTGGT	2655
Db	2270	AAATTCTTGAGCACCAGCTCATCCAGACTGAATCCCCCCAGGAAGAACGTCGACCTGGA	2329
Qy	2656	CAGTATATGGTGTACATATCCAGAGCTGTGGGGGCCCCCTTGGCATTCCTCGGTTATATNGG	2715
Db	2330	AAACATATCACAGTACATTAAGGCTTCCTGGAGGGTACCTCCCTTCTCTCTTCACTGTGT	2389
Qy	2716	CCCTTTTCATGCTGAATGTAGGCAGCACCGCCCTTCAGCACCTCGTGGTTTCAGTTACTGGGA	2775
Db	2390	TCCTCTCTCTCTGATGATTGGCAGGCTGCCTTTACAGAACTCGTGGCTGGGTCTCTGGT	2449
Qy	2776	TCAAGCAAGGAAGCGGGAAACACCACTGTGACTCGAGGGAACAGAGAC--TCGGTGAAGT	2832
Db	2450	TGGACAAGGCTCACGGATGACCTGTGGGCCCCAGGCAACAGGACCATGTGTGAGGTGC	2509
Qy	2833	ACAGCATGAAGACAATCTCATATGCATCTATATGCCAGCATCTACGCCCTCTCCATGG	2893
Db	2510	GGCGGCTGTGCAGACATCGGTTCAGCATGTGTACCACTGGGTGTACACTGCAAGCATGG	2569
Qy	2893	CAGTCATGCTGATCTGAAAGCCATTCGAGGAGTGTCTTTGTTCAGGGCACGCTGCGAG	2952
Db	2570	TGTTTCATGCTGGTGTGTGGCTGCACCAAGGCTTCGCTTCACCAAGACACACTGATGG	2629
Qy	2953	CTTCTCCCGGTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATCAAGTTTT	3012
Db	2630	CATCTCTCTCTGCATGACCGGTGTGTGATAAGATCTTAAGAGCCCAATGAGTTCT	2689
Qy	3013	TTGACAGACCCCCACAGGAGGATTCCTCAACAGTTTTTCCAAAGACATGGAAGTTG	3072
Db	2690	TTGACAGACTCCCACCTGCGAGCTTAATCAACCGTTTTTCCAAAGGATATGGACGAGCTG	2749
Qy	3073	ACGTGCGCTGCCGTTCAGGCCGAGATGTTTCATCAGAACGTTATCCTGGTGTCTTCT	3132
Db	2750	ATGTGAGCTGCCGTTTTCAGCAGAGAACTTTCGACGAGTTTTTTATGGTGGTGTGTTA	2809
Qy	3133	GTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGCCCTTGTCA	3192
Db	2810	TTCTCGTATCTTGGCTGCTGTGTTCCTGTCTCTTTTAGTCGTGGCCAGCCTTGCTG	2869
Qy	3193	TCCTCTTTTTCAGTCTGACATGTCTCCAGGCTCTGATTCGGGAGCTGAAGCCTCTGG	3252
Db	2870	TAGGCTTCTTCACTTCTTACGCAATTTTCCACAGAGGAGTCCAGGAGCTCAAGAAAGTGG	2929
Qy	3253	ACAATATCAGCAGTCACTTCTTCTCCACATCAGCTCCAGCATACAGGGCCTTGCCA	3312
Db	2930	AGAAGTTCAGCGGTCACCTCGTTTACCCACATCACTCCCTCCATTCGAGGGCTGGCA	2989
Qy	3313	CCATCCAGCCTTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAAGAGCTCTGGATG	3372
Db	2990	TCATTCAGCCTATGGCAAGAGGAGCTGCATCACTAGTTTAAAGCCTAAACGACG	3049
Qy	3373	ACAACAAGTCTCTTTTGTGTTTACGTGTGCGATCGGTGGGTGTGCGGCTGG	3432
Db	3050	AAAACTCAGTCACCTCTCTACTTTAACTGTGCTCTCAGGTGGTTTGGCCTCAGAAATGG	3109
Qy	3433	ACCTCATCAGATCGCCTCATCAACCACCGGGGTGATGATCTTCTTATCAGCGGC	3492
Db	3110	ATGTCTCTCATGAACATCTTACCTTCATCTGGCTTGTGGTGAACCTTGAGTTTCTCT	3169
Qy	3493	AGATTCCCCAGCCTATCGGGTCTCGCCATCTCTTATGCTGTCCAGTTTAAACGGGCTGT	3552
Db	3170	CCATCAGTACTTCACCAAGGCTGTCTATTGTCTATCATCTCCAGCTGAGCGGACTGC	3229
Qy	3553	TCCAGTTTACGCTCAGACTGGCATCTGAGACAGAAGCTCGATTCACTCGTGGAGAGGA	3612
Db	3230	TCCAAGTGTGTGCGAAGCGGAACAGAGACGCAAGCCAAATTCACCTCCGTGGAGCTGC	3289
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Db	3290	TCAGGGAATATTTTCGACTGTGTTCCTGTAATGACTCATCTCCCTTCAAGTGGGACCT	3349

Db 1000 GGTGGCTGAGCTACTGTGGTGGAGAGGGCTCGGGGACCAATAGACGCCGAGAGAGCAATG 1059
QY 2818 AGACC---TCGGGTGAGTGACAGCATGAAGACAACTCTCATATGACGTACTATGCCAGCA 2874
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QY 4375 ACAGAGTTCCTGATTCATGCCATTTTGTGTCTGTCG 4411
Db 2620 AGCCTGGGTCTATTGTCGACGCCCTCATGGCCACAGC 2656

RESULT 15

ABV26879
ID ABV26879 standard; cdna; 3055 BP.
XX AC ABV26879;
XX AC
XX AC
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cdna 26870.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
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PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of

prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer
 Claim 1; Page 5435-5436; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
 (a) assessing whether a patient is afflicted with prostate cancer;
 (b) monitoring the progression of prostate cancer in a patient;
 (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound;
 (g) determining whether prostate cancer has metastasized in a patient;
 (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 3055 BP; 731 A; 765 C; 845 G; 712 T; 2 other;

Query Match 12.5%; Score 727; DB 23; Length 3055;
 Best Local Similarity 55.8%; Pred. No. 1.4e-165;
 Matches 1428; Conservative 0; Mismatches 1120; Indels 9; Gaps 2;

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 166 GGATGGTGAAGACAGCTGTTCTAGCCATCTCGAGGAGATGACCTTGTCTCGAGGGCT 225
 1978 GCATTGCAATCAGTGAACCTTCCTGTTATGTGGCCAGCAGCCCTGATCTCAATGCTA 2037
 226 CGGTGGGGTGCAGGAAGACCTGGCTATGTCCTCCAGCAGCCCTGGATCGTCAGCGGA 285
 2038 CTCACAGACACATCTGTTGGAGGATATGATGAAGAGATACAACTCTGTGTC 2097
 286 ACATCAGGAGAACATCTCATGAGGAGCGCATATGACAGGCGCGATACCTCCAGGTGC 345
 2098 TGAACAGCTGCTGCTGAGGCTGACCTGGCCATTTCTCCAGCAGCAGCTGACGGAGA 2157
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 2158 TTGGAGAGGAGGAGCCAACTGAGCGGTGGCGAGCGCCAGAGATGACCTTGGCCGGG 2217
 406 TTGGAGAGCGGGCCCTCAACCTCTCTGGGGGCGAGAAACAGAGGATGACGCTTGGCCGGC 465
 2218 CTTCTAGTACAGGAGATCTACATCTCTGGAGAGCCCTCTAGTCCCTTAGATGCC 2277
 466 CGCTATCTCCAGCGTCAGATCTACCTGCTGGAGAGCCCTCTGCTGCTGGAGCGCC 525
 2278 ATGTGGGCAACACATCTTCAATAGTGTATCCGGAACATCTCAAGTCCAGAGAGTTC 2337
 526 ACGTGGGAAGACATTTTGGAGAGTCAATTAAGACACACTCAGGGGAGAGCGGTGC 585
 2338 TGTGTTGTTACCAACAGTACAGTACCTGTTGATGTGATGATGATGATGATGATGATG 2397
 586 TCTGTTGACCCAGCAGCTGAGTACTTGAATTTTGTGGCCAGATCATTTTGTGGAAA 645
 2398 AGGCTGTATTACGGAAGAGCCACCATGAGGACTGATGAATTAATGGTACTATG 2457
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 2458 CTACCATTTTAAATACCTGTTGCTGGGAGAGACACCCAGTGTGAGATCAATCAAAA 2517
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 QY 2818 AGACC---TCGGTGTAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCA 2874
 Db 1060 GAACCATGCGAGACCTGGGCAACATTCGAGACAACTCCTCACTGTCTCTTACCAAGCTGG 1119
 QY 2875 TCTACGCCCTCTCCATGGCAGTCACTGCTGATCTCTGAAAGCCATTCGAGGAGTTCCTTTG 2934
 Db 1120 TGTACGGGCTCAACGCCCTCTCTCATCTGTGTGGGGTCTCTCTCTCAGGATTTTCA 1179
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 Db 1240 GTCGCCCTGAGTCTTCTTGTACACCATCCCAATAGGCGGCTTTTGAACCTGCTCGAG 1299
 QY 3055 AAGACATGGATGAAGTGTGACGTGCGGCTGCGCTTCCAGGCGGAGATGTTTCATCCAGAACG 3114
 Db 1300 GGGACTTGAACAGCTGGAGCAGCTTGGCCATCTTTTCAGAGCAGTCTCCTGCTCTGT 1359
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	5838	100.0	5838	9	AF104942 Homo sapi
2	5754	98.6	5881	9	AF146074 Homo sapi
3	5715.8	97.9	5728	9	AB019002 Homo sapi
4	5671	97.1	5826	9	U83661 Homo sapien
5	4792.6	82.1	4847	6	AR099619 Sequence
6	4724.2	80.9	4781	6	AR091520 Sequence
7	4724.2	80.9	4781	6	AR136853 Sequence
8	4691.6	80.4	4939	9	AB005659 Homo sapi
9	4019.4	68.8	5744	10	AB020209 Rattus no
10	3786.6	64.9	5400	10	AB019003 Mus muscu
11	1936.4	33.2	2167	6	A64696 Sequence 62
12	1676	28.7	1761	6	A64695 Sequence 61
c 13	1467.8	25.1	159070	2	AC131160 Homo sapi
c 14	1467.8	25.1	178688	9	AC068644 Homo sapi
15	925.8	15.9	4101	6	AX210135 Sequence
16	921.4	15.8	4127	9	AF411577 Homo sapi
17	874.4	15.0	5168	9	AY040220 Homo sapi
18	804.6	13.8	4048	9	AF411578 Homo sapi
19	790.6	13.5	4008	6	AX210141 Sequence
20	787.8	13.5	4034	9	AF395908 Homo sapi
21	772.8	13.2	4492	9	AF352582 Homo sapi
22	766.4	13.1	4149	6	AX135184 Sequence
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26	757.8	13.0	4074	6	AX411822 Sequence
27	753.2	12.9	3753	6	AX210139 Sequence
28	723.8	12.4	3189	6	AX135172 Sequence
29	723.8	12.4	4083	6	AX468402 Sequence
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33	625	10.7	1076	10	AF213387 Mus muscu
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ALIGNMENTS

RESULT 1
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LOCUS AF104942 5838 bp mRNA linear PRI 12-JAN-1999
DEFINITION Homo sapiens ABC transporter MOAT-C (MOAT-C) mRNA, complete cds.
ACCESSION AF104942
VERSION AF104942.1 GI:4140697
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5838)
REFERENCE Belinsky,M.G., Bain,L.J., Balsara,B.B., Testa,J.R. and Kruh,G.D.
AUTHORS Characterization of MOAT-C and MOAT-D, new members of the MRP/CMOAT
TITLE subfamily of transporter proteins

J. Natl. Cancer Inst. 90 (22), 1735-1741 (1998)
99043202
PUBMED
9827529
REFERENCE
2 (bases 1 to 5838)
Belinsky, M.G., Bain, L.J. and Kruh, G.D.
Direct Submission
TITLE
Submitted (04-NOV-1998) Medical Oncology, Fox Chase Cancer Center,
7701 Burholme Avenue, Philadelphia, PA 19111, USA
JOURNAL
Location/Qualifiers
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FEATURES

source

gene

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LLVLGLLLEIVRSWLSALTWALNRTGVRURGALLTMAFKLLKLNKIKESLGE
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BASE COUNT 1422 a 1432 c 1509 g 1475 t

ORIGIN

Query Match 100.0%; Score 5838; DB 9; Length 5838;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AF146074

LOCUS AF146074 5881 bp mRNA linear PRI 10-AUG-1999

DEFINITION Homo sapiens ABC protein mRNA, complete cds.

ACCESSION AF146074

VERSION AF146074.1 GI:5006890

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 5881)

AUTHORS McAleer, M.A., Breen, M., White, N.L. and Matthews, N.

TITLE pABC11 (also known as MOAT-C and MRP5), a member of the ABC family of proteins, has anion transporter activity but does not confer multidrug resistance when overexpressed in human embryonic kidney 293 cells

J. Biol. Chem. 274 (33), 23541-23548 (1999)

99367488

10438534

REFERENCE 2 (bases 1 to 5881)

AUTHORS McAleer, M.A., Breen, M., White, N. and Matthews, N.

TITLE Direct Submission

JOURNAL Submitted (27-Apr-1999) Yamanouchi Research Institute, Armstrong Road, Oxford OX4 4SX, UK

FEATURES

source

1. 5881

Location/Qualifiers

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BASE COUNT 1414 a 1448 c 1531 g 1488 t

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Matches 5782; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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SOURCE	Homo sapiens	cDNA to mRNA.	
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Suzuki,T., Sasaki,H., Kuh,H.J., Agui,M., Tatsumi,Y., Tanabe,S., Terada,M., Saijo,N. and Nishio,K.		
TITLE	Detailed structural analysis on both human MRP5 and mouse mrp5 transcripts		
JOURNAL	Gene 242 (1-2), 167-173 (2000)		
MEDLINE	20184734		
REFERENCE			
AUTHORS	Suzuki,T., Kuh,H. and Nishio,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-OCT-1998) Toshihiro Suzuki, National Cancer Center Research Institute, Pharmacology Division; Tsukiji 5-1-1, Chuo-ku, Tokyo 104-0045, Japan (E-mail:tsuzuki@ncc.res.ncc.go.jp, Tel:81-3-3542-2511(ex.4451), Fax:81-3-3542-1886)		
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				Gaps	0;
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DEFINITION	HSU83661	5826 bp mRNA. linear PRI 21-JUN-2000	
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VERSION	U83661.2	GI:5685863	
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9270026	2 (bases 1 to 5826)	Wijnholds,J., Mol,C.A., van Deemter,L., de Haas,M., Scheffer,G.L., Baas,F., Beijnen,J.H., Scheper,R.J., Hatse,S., De Clercq,E., Balzarini,J. and Borst,P.
JOURNAL	Multidrug-resistance protein 5 is a multispecific organic anion transporter able to transport nucleotide analogs	
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (13), 7476-7481 (2000)	
PUBMED	20319051	
REFERENCE	10840050	
AUTHORS	3 (bases 3765 to 5822)	Kool,M., Wijnholds,J., de Haas,M., Mol,C.A.A.M., Ponne,N.J., Baas,F. and Borst,P.
TITLE	Direct Submission	
JOURNAL	Submitted (03-JAN-1997)	Molecular Biology, Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
REFERENCE	4 (bases 1 to 5826)	Wijnholds,J., Mol,C.A.A.M., Ponne,N.J., Baas,F. and Borst,P.
AUTHORS	Direct Submission	
TITLE	Submitted (03-AUG-1999)	Molecular Biology, Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
JOURNAL	Sequence update by submitter	
REMARK	On Aug 3, 1999 this sequence version replaced gi:2439973.	
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LOCUS AR091520 4781 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5994130.
ACCESSION AR091520
VERSION AR091520.1 GI:10018275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4781)
AUTHORS Shyjan,A.
TITLE Multidrug resistance-associated polypeptide
JOURNAL Patent: US 5994130-A 1 30-NOV-1999;
FEATURES
Location/Qualifiers
1. 4781
Source /organism="unknown"
BASE COUNT 1217 a 1161 c 1232 g 1165 t 6 others
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Db 2701 CAAGAAGGAAGCGGAACACCACTGTACTCGAGGAACAGACCTCCGCTGAGTGACAG 2760
QY 2837 CATGAGGACAATCTCATATGACGACTATGCGCAGCATCTACGCGCTCTCCATGGCAGT 2896
Db 2761 CATGAGGACAATCTCATATGACGACTATGCGCAGCATCTACGCGCTCTCCATGGCAGT 2820

QY 2897 CATGCTGATCCTGAAAGCCATTCAGGAGTTGTCTTTGTCAAGGCGCAGCTGCGAGCTTC 2956
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QY 2957 CTCCCGGCTGCATCAGCAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 3016
Db 2881 CTCCCGGCTGCATCAGCAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 2940
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QY 3137 GGAATGATCGCAGGAGTCTTCCGCTGTTTCTTGTGCGAGTGGGCCCTTGTGCATCCT 3196
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QY 3437 CATCAGCATCGCCCTCATCACCACCGGCGCTGATGATCGTCTTATGACGCGGCGAGAT 3496
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QY	4037	GAGACACACATGAAGAATGTATTGCTAGCTACCTCTGAACTTGAATCTGAAGTAT	4096
Db	3961	GAGACACACATGAAGAATGTATTGCTAGCTACCTCTGAACTTGAATCTGAAGTAT	4020
QY	4097	GGAAATGGGATCAACTCTCAGTGGGGAGCGCAGCTCTTGTCATAGTAGGCCCT	4156
Db	4021	GGAAATGGGATCAACTCTCAGTGGGGAGCGCAGCTCTTGTCATAGTAGGCCCT	4080
QY	4157	GCTCCGCACTGTAAGATCTTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC	4216
Db	4081	GCTCCGCACTGTAAGATCTTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC	4140
QY	4217	AGACTTATTGATTCAGAGACACATCCAGAGACATTTGACAGCTGTACCATGCTGACCAT	4276
Db	4141	AGACTTATTGATTCAGAGACACATCCAGAGACATTTGACAGCTGTACCATGCTGACCAT	4200
QY	4277	TGCCATCGCTGCACACAGGTTCTAGGCTCGGATAGGATTTAGTGTGGCCCGAGGACA	4336
Db	4201	TGCCATCGCTGCACACAGGTTCTAGGCTCGGATAGGATTTAGTGTGGCCCGAGGACA	4260
QY	4337	GGTGGTGGAGTTTGACACCCCATCGGCTCTCTGTCACACACAGTTCCCGATTCTATGC	4396
Db	4261	GGTGGTGGAGTTTGACACCCCATCGGCTCTCTGTCACACACAGTTCCCGATTCTATGC	4320
QY	4397	CATGTTTGTCTGTCAGAGAACAGGTCGCTGTCAAGGGCTGACTCCCTCCCTGTTGACGA	4456
Db	4321	CATGTTTGTCTGTCAGAGAACAGGTCGCTGTCAAGGGCTGACTCCCTCCCTGTTGACGA	4380
QY	4457	AGTCTCTTTTCTTTAGAGCATTTGCCATTCCTGCTGGGGGGGGCCCG-TCATCGCGTCC	4515
Db	4381	AGTCTCTTTTCTTTAGAGCATTTGCCATTCCTGCTGGGGGGGGCCCGTTCATCGCGTCC	4440
QY	4516	TCCTACCGAAACCTTGCTTTCTCGATTTATCTTTCGACAGCAGTTCCGGATTTGGCTT	4575
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QY	4636	AAACAAATTTAGTTTTTGTCTTAATTTGCATCTAAAGGTTTCAGGAACCGTTATAT	4695
Db	4561	AAACAAATTTAGTTTTTGTCTTAATTTGCATCTAAAGGTTTCAGGAACCGTTATAT	4620
QY	4696	AATTGTATCAGAGGCTTAAATGAAGCTTTATAGCTGTAGCTATATCTATATAATTTCT	4755
Db	4621	AATTGTATCAGAGGCTTAAATGAAGCTTTATAGCTGTAGCTATATCTATATAATTTCT	4680
QY	4756	GTACATAGCCTATATTTACAGTGAAGTGTATTTATTTATTTATTTAAATTAAGCAC	4815
Db	4681	GTACATAGCCTATATTTACAGTGAAGTGTATTTATTTATTTATTTAAATTAAGCAC	4740
QY	4816	TGTGCTTAATAACA	4828
Db	4741	TGTGCTTAATAAAA	4753
RESULT 7			
LOCUS	AR136853	4781 bp	DNA
DEFINITION	Sequence 1 from patent US 6162616.		linear
ACCESSION	AR136853		
VERSION	AR136853.1	GI:14478103	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 4781)		
AUTHORS	Shyjan, A.		

TITLE	Multidrug resistance-associated polypeptide									
JOURNAL	Patent: US 6162616-A 1 19-DEC-2000;									
FEATURES	Location/Qualifiers									
source	1..4781									
BASE COUNT	1217 a	1161 c	1232 g	1165 t	6 others					
ORIGIN										
Query Match	80.9%; Score 4724.2; DB 6; Length 4781;									
Best Local Similarity	99.7%; Pred. No. 0;									
Matches 4737; Conservative	6; Mismatches	9; Indels	1; Gaps	1;						
QY	77	TGATGTGAAACTAAACAGTCTGTGAGCCCTGGAACTCCGCTCAGAGAAATGAAGGATAT	136							
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QY	137	CGACATAGGAAAGAGTATATCATCCCACTCTGGGTATAGAAGTGTGAGGGAGAGAAC	196							
Db	61	CGACATAGGAAAGAGTATATCATCCCACTCTGGGTATAGAAGTGTGAGGGAGAGAAC	120							
QY	197	CAGCACTTCTGGGAGCACAGACCGCTGAAGATTCCAAAGTTCAGGAGAACTCGACCGTT	256							
Db	121	CAGCACTTCTGGGAGCACAGACCGCTGAAGATTCCAAAGTTCAGGAGAACTCGACCGTT	180							
QY	257	GGAATGCCAAGATGCTTGGAAACAGACGCCGAGCGGAGGGCCTCTCTCTTGATGCCCTC	316							
Db	181	GGAATGCCAAGATGCTTGGAAACAGACGCCGAGCGGAGGGCCTCTCTCTTGATGCCCTC	240							
QY	317	CATGCAATCTCAGCTCAGAAATCTGGATGAGGAGCATCCCAAGGAAAGTACCATCATGG	376							
Db	241	CATGCAATCTCAGCTCAGAAATCTGGATGAGGAGCATCCCAAGGAAAGTACCATCATGG	300							
QY	377	CTTGAGTCTCTGAAGCCCATCCGAGCTACTTCCAAACACACAGCACCAGCTGGACAATGC	436							
Db	301	CTTGAGTCTCTGAAGCCCATCCGAGCTACTTCCAAACACACAGCACCAGCTGGACAATGC	360							
QY	437	TGGCTTTTTCCTGATGACTTTTTCGTGGCTTTCTCTCTGCGCCGCTGTGCGCCACAA	496							
Db	361	TGGCTTTTTCCTGATGACTTTTTCGTGGCTTTCTCTCTGCGCCGCTGTGCGCCACAA	420							
QY	497	GAAGGGGAGCTCTCAATGGAAGAGCTGTGTCTCTGTCCAAAGCAGAGCTTCTGACGT	556							
Db	421	GAAGGGGAGCTCTCAATGGAAGAGCTGTGTCTCTGTCCAAAGCAGAGCTTCTGACGT	480							
QY	557	GAATGCAAGAGACTAGAGAGACTGTGGCAAGAGAGCTGAATGAAGTTGGGCCAGACGC	616							
Db	481	GAATGCAAGAGACTAGAGAGACTGTGGCAAGAGAGCTGAATGAAGTTGGGCCAGACGC	540							
QY	617	TGCTTCCCTCGAAGGTTGTGTGATCTTCTGCGCCAGCAGGCTCATCTCTGCCATCGT	676							
Db	541	TGCTTCCCTCGAAGGTTGTGTGATCTTCTGCGCCAGCAGGCTCATCTCTGCCATCGT	600							
QY	677	GTGCTGATGATCAGCAGCTGGCTTCAAGTGGAGCAGGCTTCAATGGTGAACACCT	736							
Db	601	GTGCTGATGATCAGCAGCTGGCTTCAAGTGGAGCAGGCTTCAATGGTGAACACCT	660							
QY	737	CTTGAGTATACCCAGGCAACAGAGTCTAACTGCACTACAGCTTGTGTTAGTGTGGG	796							
Db	661	CTTGAGTATACCCAGGCAACAGAGTCTAACTGCACTACAGCTTGTGTTAGTGTGGG	720							
QY	797	CCTCCTCTGACGAAATCGTGGGCTTGTGCTGCTTGCATCTGACTTGGGCATTGAATTA	856							
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QY	857	CCGAACCGGTGTCGGTTCGGGGGGCCATCTCAACCATGGCATTTAAGAAATTCCTTAA	916							
Db	781	CCGAACCGGTGTCGGTTCGGGGGGCCATCTCAACCATGGCATTTAAGAAATTCCTTAA	840							
QY	917	GTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCAACGATGG	976							
Db	841	GTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCAACGATGG	900							
QY	977	GCAGAGAAATCTTTGAGGCGACGACCGCTTGGCAGCCTGCTGGCTGGAGGACCGCTTGTC	1036							

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QY 1037 CATCTTAGGCATGATTATTAATGTAATTTATCTGGGACCAACAGGCTTCTGGGATCAGC 1096
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Db 1141 CATTAATTTATCAAAATGATGCTGGTCAAGCATTTTCACAGAGTGTCCAAAAT 1200
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QY 1937 CATTTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGCGACCATTCAGTGGAC 1996
Db 1861 CATTTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGCGACCATTCAGTGGAC 1920
QY 1997 CTTTCGCTTATGCGCCACGAGCGCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 2056
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AUTHORS Suzuki, K., Nishio, K., Sasaki, H., Kurokawa, H., Saito-Ohara, F.,
Ikeuchi, T., Tanabe, S., Terada, M. and Saijo, N.
TITLE cDNA cloning of a short type of multidrug resistance protein
homologue, SMRP, from a human lung cancer cell line
JOURNAL Biochem. Biophys. Res. Commun. 238 (3), 790-794 (1997)
MEDLINE 97472289
REFERENCE 2 (bases 1 to 4939)
AUTHORS Suzuki, T.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1997) Toshihiro Suzuki, National Cancer Center
Research Institute, Pharmacology Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104, Japan (E-mail:tsuzuki@ncc.res.ncc.go.jp,
Tel:03-3542-2511, Fax:03-3542-1886)
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 ORGANISM unidentified.
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 AUTHORS Oude,E.R., Paulusma,C.C., Bosma,P.J., Borst,P., Evers,R., Kool and Marcel.
 TITLE A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING

JOURNAL THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM
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 COMMENT INTRIGENE BV (NL)
 FEATURES Other publication AU 1736697 19970910.
 Location/Qualifiers
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BASE COUNT 494 a 511 c 626 t 25 others
 ORIGIN

Query Match 33.2%; Score 1936.4; DB 6; Length 2167;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 2069; Conservative 9; Mismatches 47; Indels 14; Gaps 10;

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HTG: HTGS_PHASE1.
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Karlsone, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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Weinstock, G., and Gibbs, R.

TITLE
JOURNAL
Direct Submission
REFERENCE
2 (bases 1 to 159070)
Unpublished
Worley, K.C.
Direct Submission
AUTHORS
Submitted (17-AUG-2002) Human Genome Sequencing Center, Department
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: HEMN
Center clone name: RP11-449K6
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 150858 bases at least Q40
Consensus quality: 152515 bases at least Q30
Consensus quality: 153446 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 17399 24864: contig of 7466 bp in length
* 24865 24964: gap of unknown length
* 24965 34874: contig of 9910 bp in length
* 34875 34974: gap of unknown length
* 34975 45070: contig of 10096 bp in length
* 45071 45170: gap of unknown length
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FEATURES

Source

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COMMENT
Gibbs,R.
Direct Submission
Unpublished
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Worley,K.C.
Direct Submission
Submitted (06-MAY-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178688)
Worley,K.C.
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Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 178688)
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Direct Submission
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of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 14, 2002 this sequence version replaced gi:21490042.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.
ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.
SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.
QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Turner,C.A., Mathur,B., Wang,X., Abuin,A., Friedrich,G.B.,
Zambrowicz,B. and Sands,A.T.
TITLE Human transporter proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0157214-A 43 09-AUG-2001;
Lexicon Genetics Incorporated (US)
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QY 901 TTAAGAAGATCCTTTAAGTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
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Db 908 ATGAGTTTCTGACCTGCATCAGGCTGATCAAAATGATGCTGGGAGAAATCTTTTACCA 967
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Db 968 ACATATCCAAGATATTAAGAGAGGAGGAAAGAAATTTACTGGAAGAAAGCTGGATTTGTC 1027
QY 1321 AGGTATCTAGTGGGTGTGGCTCCCTCCATTTGGTGGTGAATTCGCCAGCGTGGTGTCTCT 1380
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QY 1381 CTGTTTCATATGACCTTGGCTTTCATCTGACAGCAGCAGGCTTTCACATGTTGGTACAG 1440
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:25 ; Search time 4307.47 Seconds
(without alignments)
19096.316 Million cell updates/sec

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Perfect score: 5079
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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18: em_gss_hum:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	872.4	17.2	920	14	BQ941613	BQ941613 AGENCOURT
3	843.6	16.6	1098	14	BM924812	BM924812 AGENCOURT
4	821.2	16.2	860	14	BQ227366	BQ227366 AGENCOURT
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	10	691	13.6	776	13	BI907445	BI907445 603063536
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	19	642	12.6	773	12	BG285613	BG285613 602380619
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ALIGNMENTS

RESULT 1

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DEFINITION
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VERSION U66674.1 GI:1906559
KEYWORDS HTC.
SOURCE
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1977)
AUTHORS Allikmets,R., Gerrard,B., Hutchinson,A. and Dean,M.
TITLE Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database
JOURNAL Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
MEDLINE 97049974
PUBMED 8894702

REFERENCE 2 (bases 1 to 1977)
AUTHORS Allikmets,R., Gerrard,B. and Dean,M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES
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Location/Qualifiers
1..1977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="EST90757"
/note="similar to ATP-binding cassette transporter"

BASE COUNT 450 a 537 c 513 g 469 t 8 others

Query Match 34.48; Score 1749.4; DB 11; Length 1977;
Best Local Similarity 96.78; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;

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DB 1 TTGCACAGGACCTGCTGCACAAAGATAGCTGCACAGTCTCTTTTGACACCACA 60
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DB 1914 TAAAAATGGGAGTACTGATGAAATAAAACTACA 1946

RESULT 2
BQ941613
LOCUS
DEFINITION
ACCESSION

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2596 row: m column: 06
High quality sequence stop: 742.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6421421"
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 188 a 259 c 264 g 208 t 1 others
ORIGIN
Query Match 17.2%; Score 872.4; DB 14; Length 920;
Best Local Similarity 99.08; Pred. No. 3.7e-184;
Matches 898; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY 2710 GTTTATGAGACAGCTGAGTGCCCTGTCTCTCAGATGGGGAGGACAGGTCGGCGCTGTACC 2769
DB 1 GTTTATGAGACA-CTGAGTGCCCTGTCTCTCAGATGGGGAGGACAGGTCGGCGCTGTACC 59
QY 2770 CCGGAGGCACCTGGGTCCATCAGAGAAGGTGCAGGTGCAGAGCGCGAAGGCAGATGGGC 2829
DB 60 CCGGAGGCACCTGGGTCCATCAGAGAAGGTGCAGGTGCAGAGCGCGAAGGCAGATGGGC 119
QY 2830 ACTGACCCAGGAGAGAAACAGCCATTGGCACTGTGGAGCTCAGTGTCTTGGGATTA 2889
DB 120 ACTGACCCAGGAGAGAAACAGCCATTGGCACTGTGGAGCTCAGTGTCTTGGGATTA 179
QY 2890 TGCCAAGCCGTGGGGCTCTGTACCAAGCTGGCCATCTGTCTCTGTATGTGGGTCAAAG 2949
DB 180 TGCCAAGCCGTGGGGCTCTGTACCAAGCTGGCCATCTGTCTCTGTATGTGGGTCAAAG 239
QY 2950 TCGGGCTGCCATTGGAGCCCAATGTGGGCTCAGTGGCTGCAGCAAAATGATGCCATGGCAG 3009
DB 240 TCGGGCTGCCATTGGAGCCCAATGTGGGCTCAGTGGCTGGACAAATGATGCCATGGCAG 299
QY 3010 CAGTAGACAGAAACAACACTTCCCTGAGGCTGGCGCTATGTCTCTGTATGTGGGTCAAAG 3069
DB 300 CAGTAGACAGAAACAACACTTCCCTGAGGCTGGCGGCTATGTCTCTGTATGTGGGTCAAAG 359
QY 3070 AGGGTCTTTGGTGATGCTGCGACGCCATGGCCATGGCAGCGGGTGGGCATCCAGGCTCCCG 3129
DB 360 AGGGTCTTTGGTGATGCTGCGACGCCATGGCCATGGCAGCGGGTGGGCATCCAGGCTCCCG 419
QY 3130 TGTGTTGACCAAGGCACTGCTGCACAACAAGATACGCTGCCACAGCTCTCTTTGACAC 3189

female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT	178 a	365 c	293 g	262 t
ORIGIN				
Query Match	16.6%; Score 843.6; DB 14; Length 1098;			
Best Local Similarity	94.9%; Pred. No. 1.1e-177;			
Matches	905; Conservative	0; Mismatches	44; Indels	5; Gaps
3;				
Qy	1	CCCATGACGCCCTGTCGGTTCGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAACT	60	
Db	25	CCCCATGACGCCCTGTCGGTTCGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAACT	84	
Qy	61	GTCTGTGCACACAGAAACCGGACCTCACCTCCCTGCTTCCAGAACTCCCTGCTGGCTG	120	
Db	85	GTCTGTGCACACAGAAACCGGACCTCACCTCCCTGCTTCCAGAACTCCCTGCTGGCTG	144	
Qy	121	GCTGCCCTGCATCTACCTGTGGTGGCGCCCTGCTGCTTCTGCTTACCTGCGGCACCA	180	
Db	145	GCTGCCCTGCATCTACCTGTGGTGGCGCCCTGCTGCTTCTGCTTACCTGCGGCACCA	204	
Qy	181	TTGTGCGGCTACATCAATCTCTCCACCTGCTCAAGCTCAAGATGTCGTCGGTGTCT	240	
Db	205	TTGTGCGGCTACATCAATCTCTCCACCTGCTCAAGCTCAAGATGTCGTCGGTGTCT	264	
Qy	241	GCTGTGGTGGCTCTCTGGGGGACCTTTTCTTACTCTTCCATGCTGCTGCTGCTGCGG	300	
Db	265	GCTGTGGTGGCTCTCTGGGGGACCTTTTCTTACTCTTCCATGCTGCTGCTGCTGCGG	324	
Qy	301	GGCCCCCTGCCCTCTTTTCTTGTTCACCCCTTGGTGGTGGGCTCACATGCTGCTGGC	360	
Db	325	GGCCCCCTGCCCTCTTTTCTTGTTCACCCCTTGGTGGTGGGCTCACATGCTGCTGGC	384	
Qy	361	CACCTGCTGATACAGTATGAGCGGCTGCAGGGGTACAGTCTTCGGGGGTCTCATTTAT	420	
Db	385	CACCTGCTGATACAGTATGAGCGGCTGCAGGGGTACAGTCTTCGGGGGTCTCATTTAT	444	
Qy	421	CTTCTGTTCTCTGTGTGGTCTCGGCATGCTCCATTCGCTCCCAAGATCCTTTTAGC	480	
Db	445	CTTCTGTTCTCTGTGTGGTCTCGGCATGCTCCATTCGCTCCCAAGATCCTTTTAGC	504	
Qy	481	CAAGGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTACCACCTTCTACATCCACTTTGC	540	
Db	505	CAAGGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTACCACCTTCTACATCCACTTTGC	564	
Qy	541	CCTGGTACTCTGCGCTCATCTTGGGCTGTTTCAGGAGAAACCTCCATTTTTCGCGC	600	
Db	565	CCTGGTACTCTGCGCTCATCTTGGGCTGTTTCAGGAGAAACCTCCATTTTTCGCGC	624	
Qy	601	AAAGAATGTGACCCCTAACCCCTACCTGAGACCGGCTGGCTTTCTCTCCCGCTGTT	660	
Db	625	AAAGAATGTGACCCCTAACCCCTACCTGAGACCGGCTGGCTTTCTCTCCCGCTGTT	684	
Qy	661	TTTCTGGTGGTTTCAAAAGATGGCCATCTATGGCTACCGGCTACCCCTGGAGGAGGA	720	
Db	685	TTTCTGGGTTTCAAAAGATGGCCATCTATGGCTACCGGCTACCCCTGGAGGAGGA	744	
Qy	721	CCTCTGTCCTTAAAGGAGGAGACAGATCCAGATGGTGTGAGAGCTGTGAGGCT	780	
Db	745	CCTCTGTCCTTAAAGGAGGAGACAGATCCAGATGGTGTGAGAGCTGTGAGGCT	804	
Qy	781	ATGAGAGACAGAAAGCAGACCGGACACACAAGCTTCACGACCACTGGGAAAAA	840	
Db	805	TTGGAAGACAGAAAGCAGACCGGACACACAAGCTTCAGCAGAACCTGGGGGAAAT	864	
Qy	841	TGCTCTCGGCGGAGGACGAGTGTCTGTGGTGTG - CCCGCCCCAGGCCCGGAAGCCC - TC	897	

Db	865	GGCTCCCGCAGGACGAGTCTGCTGGGGGGCCCGCCAGGCCCGCGAAGCCCTCC	924
Qy	898	CTTCTGAAGCCCTGCTGGCCACCTT--CGGCTCCAGCTTCTCTCATCATGTC	949
Db	925	TTCTGTAAAGCCCTGTTGGCACCTTTCGGGTTCAGTTCTCTCATTAAGGCG	978
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LOCUS	BQ227366	860 bp	mRNA linear EST 02-MAY-2002
DEFINITION	AGENCOURT_7574821 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060072		
ACCESSION	BQ227366	5', mRNA sequence.	
VERSION	BQ227366.1	GI:20408766	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLMI3327 row: m column: 01 High quality sequence stop: 577.		
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BASE COUNT	146 a	288 c	215 g 211 t
ORIGIN			
Query Match	16.2%; Score 821.2; DB 14; Length 860;		
Best Local Similarity	98.7%; Pred. No. 1e-172;		
Matches	849; Conservative	0; Mismatches	8; Indels 3; Gaps 2;
QY	148	CCTGCGCTGCTACTTGTCTTACCTCGGGCACCATGTGCTGGCTACATCATCTCTCCCA	207
Db	1	CCTGCGCTGCTACTTGTCTTACCTCGGGCACCATGTGCTGGCTACATCATCTCTCCCA	60
QY	208	CCTGTCCAAGCTCAAGATGGTCTGGGTGTCTGCTGTGGTGGCTCTCTGGCGGACCT	267
Db	61	CCTGTCCAAGCTCAAGATGGTCTGGGTGTCTGCTGTGGTGGCTCTCTGGCGGACCT	120
QY	268	TTTTTACTCTTCATGGCCTGGTCCATGGCGGGCCCTGCCCCCTGTTTCTTCTGAC	327
Db	121	TTTTTACTCTTCATGGCCTGGTCCATGGCGGGCCCTGCCCCCTGTTTCTTCTGAC	180
QY	328	CCCTTGTGGTGGGGTCCACCATGCTGCTGGCCACCTGCTGTATACAGTATGAGCGGCT	387
Db	181	CCCTTGTGGTGGGGTCCACCATGCTGCTGGCCACCTGCTGTATACAGTATGAGCGGCT	240
QY	388	GCAGGGCTACAGTCTTCGGGGGTCTCTCATTTCTTCTGGTCTCTGTGTGCTGCGC	447
Db	241	GCAGGGCTACAGTCTTCGGGGGTCTCTCATTTCTTCTGGTCTCTGTGTGCTGCGC	300

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QY 448 CATCGTCCCATTCGGCTCCCAAGATCCCTTTTAGCAAGCAGAGGCTGAGATCTCAGACCC 507
Db 301 CATCGTCCCATTCGGCTCCCAAGATCCCTTTTAGCAAGCAGAGGCTGAGATCTCAGACCC 360
QY 508 CTTCGGCTTACACACCTTCTACATCCTTTGCGCTGGTACTCTCTGCGCTCATCTTGGC 567
Db 361 CTTCGGCTTACACACCTTCTACATCCTTTGCGCTGGTACTCTCTGCGCTCATCTTGGC 420
QY 568 CTGCTTTCAGGAGAAACCTCCATTTTCTCCGAAAGAAATGCGACCTTAACCCCTACCC 627
Db 421 CTGCTTTCAGGAGAAACCTCCATTTTCTCCGAAAGAAATGCGACCTTAACCCCTACCC 480
QY 628 TGAGACAGCGCTGGGCTTCTCTCCGCGCTGTTTTTCTGCTGGTTTACAAAGATGGCCAT 687
Db 481 TGAGACAGCGCTGGGCTTCTCTCCGCGCTGTTTTTCTGCTGGTTTACAAAGATGGCCAT 540
QY 688 CTATGCTTACCGCATCCCTCGAGAGAGAGACCTCTGCTCCCTTAAGGAAGAGGACAG 747
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QY 748 ATCCAGATGGTGTGTCAGCAGCTGCTGGAGGCATGAGGAAGCAGGAAGCAGACGGC 807
Db 601 ATCCAGATGGTGTGTCAGCAGCTGCTGGAGGCATGAGGAAGCAGGAAGCAGACGGC 660
QY 808 AGACACAAGGCTTACAGCAGCACTCGGAAATGCTCCGGGAGAGCAGAGTGTCTGCT 867
Db 661 AGACACAAGGCTTACAGCAGCACTCGGAAATGCTCCGGGAGAGCAGAGTGTCTGCT 720
QY 868 GGGTCCCGCCAGCCCGGAGCCCTCTCTCTGAGG-CCCTGCTGGCCACCTTCG 926
Db 721 GGGTCCCGCCAGCCCGGAGCCCTCTCTCTGAGG-CCCTGCTGGCCACCTTCG 780
QY 927 GCTCAGCTTCTCTCAGTGTCTGCTTCAAGC--TTATCCAGGACCTGCTCTCTCTCAT 984
Db 781 GCTCAGCTTCTCTCAGTGTCTGCTTCAAGC--TTATCCAGGACCTGCTCTCTCTCAT 840
QY 985 CAATCCACAGCTGCTCAGCA 1004
Db 841 CAATCCACAGCTGCTCAGCA 860

RESULT 5
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LOCUS
DEFINITION 602755456F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4891237 5',
            mRNA sequence.
ACCESSION BI196662
VERSION BI196662.1 GI:14651682
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 849)
REFERENCE NIH-MGC http://mhc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaaps-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM769 row: o column: 14
            High quality sequence stop: 799.
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site:1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 175 a 241 c 243 g 190 t
ORIGIN

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Query Match 15.8%; Score 800.8; DB 13; Length 849;
Best Local Similarity 98.8%; Pred. No. 3.7e-168;
Matches 838; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 2709 AGTTTATGAGACAGCTGAGTCCCTGCTCAGATGGGAGGAGGAGGCTGGCTGTAC 2768
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QY 2769 CCGGAGGACCTGGGTCCATCAGAGAAGTGCAGGTGCAGAGCGGAGGAGGAGGAGG 2828
Db 62 CCGGAGGACCTGGGTCCATCAGAGAAGTGCAGGTGCAGAGCGGAGGAGGAGGAGG 121
QY 2829 CACTGACCCAGGAGGAGAAAGCAGCCATGTCAGTGTGGAGCTCAGTGTGGGATT 2888
Db 122 CACTGACCCAGGAGGAGAAAGCAGCCATGTCAGTGTGGAGCTCAGTGTGGGATT 181
QY 2889 ATGCAAGGCGTGGGCTGTACCAAGCTGGCCATCTGCTCTCTATGTGGTCAAA 2948
Db 182 ATGCAAGGCGTGGGCTGTACCAAGCTGGCCATCTGCTCTCTATGTGGTCAAA 241
QY 2949 GTGCGGTGCTATGGAGCCAAATGTGGCTCAGTGTGGAGCAATCATGCCATGGCAG 3008
Db 242 GTGCGGTGCTATGGAGCCAAATGTGGCTCAGTGTGGAGCAATCATGCCATGGCAG 301
QY 3009 ACAGTAGACAGACACACTTCCCTGAGGCTGGGCGTCTATGCTCTTTAGGAATCTGC 3068
Db 302 ACAGTAGACAGACACACTTCCCTGAGGCTGGGCGTCTATGCTCTTTAGGAATCTGC 361
QY 3069 AAGGGTTCTTGGTGTATGCTGGCAGCCATGGCCATGGCAGGGGTGGCATCGGCTGCC 3128
Db 362 AAGGGTTCTTGGTGTATGCTGGCAGCCATGGCCATGGCAGGGGTGGCATCGGCTGCC 421
QY 3129 GTGTGTGACACGAGCAGTCTGCACAAAGATACCTCGCCACAGTCTCTTTTGGACA 3188
Db 422 GTGTGTGACACGAGCAGTCTGCACAAAGATACCTCGCCACAGTCTCTTTTGGACA 481
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QY 3489 -GGGCTTACAACCGCAGCGGGATTTTGTGATCATCATGATGATATAA--GGTGTGATCCAA 3546
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QY 3547 CCAGAGAA 3554
Db 841 CCAGAGAA 848

RESULT 6
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DEFINITION 603048767F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188984 5',
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ACCESSION BI761935
VERSION BI761935.1 GI:15753513
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cygabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11472 row: e column: 17
High quality sequence stop: 832.
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/clone_lib="NIH_MGC_116"
/lab_host="PHI0B"
/note="Organ: pooled colon, kidney, stomach; Vector:
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source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 159 a 325 c 254 g 221 t
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Query Match 15.4%; Score 784.4; DB 13; Length 959;
Best Local Similarity 94.5%; Pred. No. 1.8e-164;
Matches 835; Conservative 0; Mismatches 46; Indels 3; Gaps 2;
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Db 65 CCCATGGAGCGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCGTGGACTCCAACCT 124
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Db 185 GGTGCGCTGTACATCACTGTGGGTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
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/clone_lib="NIH_MGC_116"
/lab_host="PHI0B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 159 a 325 c 254 g 221 t
ORIGIN
Query Match 15.4%; Score 784.4; DB 13; Length 959;
Best Local Similarity 94.5%; Pred. No. 1.8e-164;
Matches 835; Conservative 0; Mismatches 46; Indels 3; Gaps 2;
QY 1 CCCATGGAGCGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCGTGGACTCCAACCT 60
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QY 181 TTGTGCTGGTGTACATCACTGCTCCCACTGTGCTCAAGCTCAAGATGGTCTGCTGGGTGCTCT 240
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/clone="IMAGE:6481379"

/clone_lib="NIH_MGC_40"

/tissue_type="carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT

241 a 245 c 261 g 220 t

2 others

ORIGIN

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Best Local Similarity 98.3%; Pred. No. 2.6e-163;

Matches 798; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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4267

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Db

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QY

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QY

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4445

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4446

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Db

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QY

4506

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Db

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QY

4566

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4625

Db

512

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453

QY

4626

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4685

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393

QY

4686

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QY

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4805

Db

332

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273

QY

4806

GCAGTTAGACTAGTCCCGGCTCCCGATTCCCACTGAGTGTATTTCACACTGCAC

4865

Db

272

GCAGTTAGACTAGTCCCGGCTCCCGATTCCCACTGAGTGTATTTCACACTGCAC

213

QY

4866

TGTTTTCAATAACGATTTTATGAAATGACCTCTGCTCCCTCTGATTTTTCATATTTT

4925

Db

212

TGTTTTCAATAACGATTTTATGAAATGACCTCTGCTCCCTCTGATTTTTCATATTTT

153

QY

4926

CTAAAGTTTCGTTCTGTTTTTAAATAAAGCTTTTCTCTCGAACAAGACAGCT

4985

Db

152

CTAAAGTTTCGTTCTGTTTTTAAATAAAGCTTTTCTCTCGAACAAGACAGCT

93

QY

4986

GCTGGGTGAGGCCACCCCTAGGAACTCAGTCTGCTGCTGGGGTGTGCTGCTGAATCCAT

5045

Db

92

GCTGGGTGAGGCCACCCCTAGGAACTCAGTCTGCTGCTGGGGTGTGCTGCTGAATCCAT

33

QY

5046

TAAAAATGGAGTACTGATGAAATAAACTAC

5077

Db

32

TAAAAATGGAGTCTGATGAAATAAACTAC

1

RESULT 8

BQ687464 888 bp mRNA linear EST 15-JUL-2002

LOCUS

DEFINITION AGENCOURT_8058516 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206756 5', mRNA sequence.

ACCESSION BQ687464

VERSION BQ687464.1 GI:21812780

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 888)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCM2361 row: 1 column: 21

High quality sequence stop: 707.

FEATURES

source

1..888

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6206756"

/clone_lib="NIH_MGC_110"

/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 178 a 263 c 260 g 186 t

ORIGIN

Query Match 15.2%; Score 773; DB 14; Length 888;

Best Local Similarity 95.6%; Pred. No. 6.2e-162;

Matches 839; Conservative 0; Mismatches 31; Indels 8; Gaps 4;

Db	241	GCATCTGAGGCGGCAAGGTTGAATCCGATGATGGCTCAATGTGGCAGACATCG	300	
Qy	4077	GCCTCATGACCTGGCTCTCAGCTGACCATCATCCGAGGAGCCCATCTGTTCTCGG	4136	
Db	301	GCCTCATGACCTGGCTCTCAGCTGACCATCATCCGAGGAGCCCATCTGTTCTCGG	360	
Qy	4137	GGACCTGGCATGAACCTTGAGCCCTTCGGGAGCTACTCAGAGGAGACATTTGTTGGG	4196	
Db	361	GGACCTGGCATGAACCTTGAGCCCTTCGGGAGCTACTCAGAGGAGGACATTTGTTGGG	420	
Qy	4197	CTTTGGAGCTGCTCCACCTGCACACGTTTGTGAGCTCCAGCGGCGAGCTTCC	4256	
Db	421	TTTTGGAGCTGCTCCACCTGCACACGTTTGTGAGCTCCAGCGGCGAGCTTCC	480	
Qy	4257	ACTGCTCAGAGCGGGGAGAACTCTCAGCTGGGCGAGAGGAGCTGCTGCTGGCC	4316	
Db	481	AGTGTCTAGAGCGGGGAGAACTCTCAGCTGGGCGAGAGGAGCTGCTGCTGGCC	540	
Qy	4317	GAGCCCTGCTCGGCAAGAGCCGATCTCTGGTTTTAGACGAGGCGACATCGACC	4376	
Db	541	GAGCCCTGCTCGGCAAGAGCCGATCTCTGGTTTTAGACGAGGCGACATCGACC	600	
Qy	4377	TGGAGACTGACAACTCATCAGGCTACCATCCGACCCAGTTTGTATCTGCACTGTC	4436	
Db	601	TGGAGACTGACAACTCATCAGGCTACCATCCGACCCAGTTTGTATCTGCACTGTC	660	
Qy	4437	TGACCATCGCACACCGGCTTAACACTATCATGACTACACAGGCTCTGCTGGACA	4496	
Db	661	TGACCATCGCACACCGGCTTAACACTATCATGACTACACAGGCTCTGCTGGACA	720	
Qy	4497	AAGGAGTAGTAGTGAATTTGATTTCCAGGCAACCTCATTCAGCTAGAGCATCTT	4554	
Db	721	AAGGAGTAGTAGTGAATTTGATTTCCAGGCAACCTCATTCAGCTAGAGCATCTT	779	
Qy	4555	CTACGGAGTGGCAGAGATGCTGG--ACTTGCTTAAATATATCTCTGAGA--TTTCT	4609	
Db	780	TACCGAATGGCCAGAGATGCTGGAGCTTGGCTTAAATATTTTTCCTGAGATTCCCT	839	
Qy	4610	CCTGCTCTTCTGTTTTCATCAGGAAGAAATGACA	4647	
Db	840	CCTGCTCTTCTGTTTTCATCAGGAAGAAATGACA	877	
RESULT 9				
BQ690370				
LOCUS				
DEFINITION BQ690370.1 898 bp mRNA linear EST 15-JUL-2002				
5', mRNA sequence.				
ACCESSION BQ690370				
VERSION BQ690370.1 GI:21815686				
KEYWORDS EST.				
SOURCE human.				
ORGANISM Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 898)				
NIH-MGC http://mgi.nci.nih.gov/.				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs-remail.nih.gov				
Tissue Procurement: ATCC				
CDNA Library Preparation: Rubin Laboratory				
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Agencourt Bioscience Corporation				
Clone distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
Plate: LLCM2397 row: j column: 05				
High quality sequence start: 7				
High quality sequence stop: 708.				
Location/Qualifiers				

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	/clone_lib="NIH_MGC_110"				
	/tissue_type="ductal carcinoma, cell line"				
	/lab_host="DH10B (phage-resistant)"				
	/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
BASE COUNT	176 a	264 c	268 g	190 t	
ORIGIN					
Query Match	13.9%; Score 708.2; DB 14; Length 898;				
Best Local Similarity	98.8%; Pred. No. 1.9e-147;				
Matches 724; Conservative	0; Mismatches	8; Indels	1; Gaps	1;	
Qy	3777	AGAGGTCAGGAGTACTCAAGACAGACAGAGGCGCCCTGGGTGGTGAAGGACGCC	3836		
Db	1	AGAGGTCAGGAGTACTCAAGACAGACAGAGGCGCCCTGGGTGGTGAAGGACGCC	60		
Qy	3837	GCCTCCCGAAGGTTGGCCCGCCACGTGGGGAGGTGGGAATTTCTGTGCGCT	3896		
Db	61	GCCTCCCGAAGGTTGGCCCGCCACGTGGGGAGGTGGGAATTTCTGTGCGCT	120		
Qy	3897	ACCGCGGGGCTTAGACCTGGTCTGAGAGACCTGAGTCTGCATGTGCAGGTGGCGAGA	3956		
Db	121	ACCGCGGGGCTTAGACCTGGTCTGAGAGACCTGAGTCTGCATGTGCAGGTGGCGAGA	180		
Qy	3957	AGGTGGGATCGTGGCGCGACTGGGCTGGCAAGTCTTCATGACCCCTTGGCTGTTC	4016		
Db	181	AGGTGGGATCGTGGCGCGACTGGGCTGGCAAGTCTTCATGACCCCTTGGCTGTTC	240		
Qy	4017	GCATCTTGAGGCGGCAAGGTTGAATTCGCATTTGATGGCTCAATGTGCACACATCG	4076		
Db	241	GCATCTTGAGGCGGCAAGGTTGAATTCGCATTTGATGGCTCAATGTGCACACATCG	300		
Qy	4077	GCCTCCATGACCTGGCGCTCTCAGCTGACCATCATCCGCGAGGAGCCCATCTGTTCTCGG	4136		
Db	301	GCCTCCATGACCTGGCGCTCTCAGCTGACCATCATCCGCGAGGAGCCCATCTGTTCTCGG	360		
Qy	4137	GGACCTGGCATGAACCTTGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGG	4196		
Db	361	GGACCTGGCATGAACCTTGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGG	420		
Qy	4197	CTTTGGAGCTGTCCACCTGTCACACGTTTGTGAGCTCCAGCGCGAGGCTGGACTTCC	4256		
Db	421	TTTTGGAGCTGTCCACCTGTCACACGTTTGTGAGCTCCAGCGCGAGGCTGGACTTCC	480		
Qy	4257	AGTGTCTAGAGGCGGGGAGAAATCTCAGCGTGGGCCACAGAGGACGCTCGTGTGCTGGCCC	4316		
Db	481	AGTGTCTAGAGGCGGGGAGAAATCTCAGCGTGGGCCACAGAGGACGCTCGTGTGCTGGCCC	540		
Qy	4317	GAGCCCTGCTCGCAAGAGCGCGCATCCTGGTTTTTAGACGAGGCCACAGCTGCCATCGACC	4376		
Db	541	GAGCCCTGCTCGCAAGAGCGCGCATCCTGGTTTTTAGACGAGGCCACAGCTGCCATCGACC	600		
Qy	4377	TGGAGACTGACAACTCATCCAGGCTACCATCCGACCCAGTTTGATACCTGCACTGTCC	4436		
Db	601	TGGAGACTGACAACTCATCCAGGCTACCATCCGACCCAGTTTGATACCTGCACTGTCC	660		
Qy	4437	TGACCATCGCACACCGGCTTAACACTATCATGGAAGTGTGCATGTGCAGGTGGCGAG	4495		
Db	661	TGACCATCGCACACCGGCTTAACACTATCATGGAAGTGTGCATGTGCAGGTGGCGAG	720		
Qy	4496	AAAGGAGTAGTAG	4508		
Db	721	CAAAGGAGGTAG	733		

ORIGIN

Query Match 13.5%; Score 688.2; DB 14; Length 956;
Best Local Similarity 99.3%; Pred. No. 5.8e-143;
Matches 701; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 4027 GCGCGCAAGGGTGAATCCGATTCATGCGCTCAATGTGGCAGACATCGGCTCCATGA 4086
Db 1 GCGCGCAAGGGTGAATCCGATTCATGCGCTCAATGTGGCAGACATCGGCTCCATGA 60

QY 4087 CTTGGGCTCTAGCTGACCATCATCCCGCAGGACCCCATCTCTTCTCGGGACCCCTGGC 4146
Db 61 CTTGGGCTCTAGCTGACCATCATCCCGCAGGACCCCATCTCTTCTCGGGACCCCTGGC 120

QY 4147 CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGCATTTGGTGGCTTTGGAGCT 4206
Db 121 CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGCATTTGGTGGCTTTGGAGCT 180

QY 4207 GTCCACCTGACACAGTGTGTGAGCTCCCGCAGGACCCCATCTCTTCTCGGGACCCCTGGC 4266
Db 181 GTCCACCTGACACAGTGTGTGAGCTCCCGCAGGACCCCATCTCTTCTCGGGACCCCTGGC 240

QY 4267 GGGCGGGAGAACTCAGCGTGGCGCAGAGGAGCTCGTGTGCTGGCCGCGGAGCCCTGCT 4326
Db 241 GGGCGGGAGAACTCAGCGTGGCGCAGAGGAGCTCGTGTGCTGGCCGCGGAGCCCTGCT 300

QY 4327 CGCAAGAGCCGATCTCTGCTTTTGTAGAGAGGCCACAGCTGCCATCGACCTGGAGACTGA 4386
Db 301 CGCAAGAGCCGATCTCTGCTTTTGTAGAGAGGCCACAGCTGCCATCGACCTGGAGACTGA 360

QY 4387 CAACCTCATCCAGGCTACCATCCGACCCAGTTTCATACCTGCTGCTGCTGCTGCTGCTGCT 4446
Db 361 CAACCTCATCCAGGCTACCATCCGACCCAGTTTCATACCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 4447 ACACCGGCTTAACACTATCATGAGCTACACAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4506
Db 421 ACACCGGCTTAACACTATCATGAGCTACACAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

QY 4507 AGCTGAATTTGATTCAGCGCAACCTCATTCGACCTAGAGGCTCTTCTACGGGATGGC 4566
Db 481 AGCTGAATTTGATTCAGCGCAACCTCATTCGACCTAGAGGCTCTTCTACGGGATGGC 540

QY 4567 CAGAGATCTGAGCTTGCTTAAATATATCTGAGATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 4626
Db 541 CAGAGATCTGAGCTTGCTTAAATATATCTGAGATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 599

QY 4627 TTCATCAGGAAGAAATGACACCAATATGTCCGAGAAATGGACTGTGATAGCAACACTG 4686
Db 600 TTCATCAGGAAGAAATGACACCAATATGTCCGAGAAATGGACTGTGATAGCAACACTG 659

QY 4687 GGGGACCTTAAGATTTTGGACCTGTAAGTGCCTTACAGGGTAA 4732
Db 660 GGGGACCTTAAGATTTTGGACCTGTAAGTGCCTTACAGGGTAA 705

RESULT 12
BQ009190/c

LOCUS BQ009190 717 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-ED1-axx-m-22-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5835069 3', mRNA sequence.
ACCESSION BQ009190
VERSION BQ009190.1 GI:19734091
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of IowaClone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

Location/Qualifiers

1. .717

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/clone="IMAGE:5835069"

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/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Left Public Bone; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to Bonaldo
Lennon and Soares, Genome Research, 6:791-806, 1996.First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an Ecor I adaptor, digested with Not I, and
cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dfr)18 tail. The
sequence tag for this library is GCTCAAGGCT.

TAG_LIB=UI-H-ED1

TAG_TISSUE=Chondrosarcoma

TAG_SEQ=CGTCAAGGCT"

BASE COUNT 195 a 148 c 171 g 201 t

ORIGIN 2 others

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Best Local Similarity 99.7%; Pred. No. 1.7e-142;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4391 CTCATCCAGGCTACCATCCGACCCAGTTTGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4450
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QY 4451 CGGCTTAAACACTATCATGAGCTACACAGGCTCCTGGTCTCGACAAAGGAGTAGTAGCT 4510
Db 657 CGGCTTAAACACTATCATGAGCTACACAGGCTCCTGGTCTCGACAAAGGAGTAGTAGCT 598

QY 4511 GAATTTGATTTCTCCAGCCCAACCTCATTTGAGGCTAGAGGCTCTTCTACGGGATGGCCAGA 4570
Db 597 GAATTTGATTTCTCCAGCCCAACCTCATTTGAGGCTAGAGGCTCTTCTACGGGATGGCCAGA 538

QY 4571 GATGCTGGACTTGCCTAAAATATATATTCCTGAGATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 4630
Db 537 GATGCTGGACTTGCCTAAAATATATATTCCTGAGATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 478

QY 4631 TCAGGAAGGAAATGACACCAAAATATGTCGCGAGAATGGACTTGTAGCAAAACACTGCGGG 4690
Db 477 TCAGGAAGGAAATGACACCAAAATATGTCGCGAGAATGGACTTGTAGCAAAACACTGCGGG 418

QY 4691 CACCTTAAGATTTTGCACCTGTAAGTGCCTTACAGGGTAACCTGCTGCTGAATCTTTAGA 4750
Db 417 CACCTTAAGATTTTGCACCTGTAAGTGCCTTACAGGGTAACCTGCTGCTGAATCTTTAGA 358

QY 4751 TCAGGAATGATCCCAAGTGGTGAATGACACCCCTTAAGTCACTAGTTTGGAGCCAG 4810
Db 357 TCAGGAATGATCCCAAGTGGTGAATGACACCCCTTAAGTCACTAGTTTGGAGCCAG 298

QY 4811 TTAGACTAGTCCCGGCTCTCCGATTCCCAACTGAGTGTTATTGTCACACTGCACGTGTTT 4870
Db 297 TTAGACTAGTCCCGGCTCTCCGATTCCCAACTGAGTGTTATTGTCACACTGCACGTGTTT 238

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QY 4871 TCAATAACGATTTTATGAATGACCTCTCTCCTCCCTCTGATTTTCATATTTCTAAA 4930
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QY 4931 GTTCTCTTTCTGTTTTTAAATAAAGCTTTTCCCTCTGGAACAGACAGCTGCTGG 4990
Db 177 GTTCTCTTTCTGTTTTTAAATAAAGCTTTTCCCTCTGGAACAGACAGCTGCTGG 118
QY 4991 GTGAGCCACCCCTAGAACTAGTCTCTGACTCTGGGGTGGCTGCTGAATCATTAATA 5050
Db 117 GTGAGCCACCCCTAGAACTAGTCTCTGACTCTGGGGTGGCTGCTGAATCATTAATA 58
QY 5051 ATGGGAGTACTGATGAATAAATAACTACA 5078
Db 57 ATGGGAGTACTGATGAATAAATAACTACA 30

RESULT 13
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DEFINITION 602707348F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844026 5',
mRNA sequence.
ACCESSION BG750831
VERSION BG750831.1 GI:14061484
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1680 row: p column: 11
High quality sequence stop: 677.
FEATURES
source
Location/Qualifiers
1..680
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/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCACAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
BASE COUNT 131 a 182 c 219 g 148 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e-140;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3465 CAGTGACTGGTCCAGTGTATCCGGGCTACAAACCCGAGCGGGGATTTGAGATCATCA 3524
Db 2 CAGTGACTGGTCCAGTGTATCCGGGCTACAAACCCGAGCGGGGATTTGAGATCATCA 61
QY 3525 GTGATACTAAGTGGATGCCAACCAGAGAGCTGCTACCCCTACATCATCTCCACCGGT 3584

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Db 62 GTGATCTAAGGTGGATGCCAACAGAGAAAGTGTACCCCTACATCATCTCCACCGGT 121
QY 3585 GGCTGAGCATCGGAGTTCGCTGGGAACTCGGTGGTGTCTTTGCTGCTGACATATTG 3644
Db 122 GGCTGAGCATCGGAGTTCGCTGGGAACTCGGTGGTGTCTTTGCTGCTGACATATTG 181
QY 3645 CCCTCATCGGAGAGAGAGCCTGAACCCGGGGCTGGTGGGCTTTCTGTGCTCTACTCT 3704
Db 182 CCCTCATCGGAGAGAGAGCCTGAACCCGGGGCTGGTGGGCTTTCTGTGCTCTACTCT 241
QY 3705 TGCAGGTGACATTTGCTGTAACCTGGAATACGAATCATGTGAGATTTGGAATCAACA 3764
Db 242 TGCAGGTGACATTTGCTGTAACCTGGAATACGAATCATGTGAGATTTGGAATCAACA 301
QY 3765 TCCTGGCTGTGGAGAGGGTCAAGAGTACTCCAAAGACAGACAGAGCGCCCTGGGTGG 3824
Db 302 TCCTGGCTGTGGAGAGGGTCAAGAGTACTCCAAAGACAGACAGAGCGCCCTGGGTGG 361
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Db 362 TGAAGGACAGCGCCCTCCCGAAGTTGGCCCCACGTGGGGAGGTGGAGTTCCGGAATT 421
QY 3885 ATTCTGTGCGCTACCGCGCGGCTAGACCTGTGCTGTGAGAGAGCTGAGTGTGCATGTC 3944
Db 422 ATTCTGTGCGCTACCGCGCGGCTAGACCTGTGCTGTGAGAGAGCTGAGTGTGCATGTC 481
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Db 482 ACGTGCGGAGAGAGTGGGATCGTGGCGGCTGCGGCTGGCAAGTCTTCCATGACCC 541
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QY 4065 TGCAGACATCGGCTCCATGACCTGCGGCTCTCAGCTGACCATCATCCCGAGGACCCCA 4124
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Db 662 TCCTGTTCCTCGGGACCC 679

RESULT 14
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DEFINITION 602726915F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4866603 5',
mRNA sequence.
ACCESSION BG823723
VERSION BG823723.1 GI:14171310
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1733 row: m column: 04
High quality sequence stop: 712.
FEATURES
source
Location/Qualifiers
1..1047

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QY	4170	GCTACTCAGAGGAGGACATTTTGGTGGCTTTGGAGCTGTCCACCTGCACACGTTTGTGA	4229
Db	772	AGTATCCAGAGGAGGACA-TTGGAGGCTTTGGAGCTGTCCACTGGAAAGTACTGAGAG	830
QY	4230	GCTCCAGCGGCGAGGCTGGACTTC-----CAGTGTCTCAGAGGCGGGGAGAAATCTCAGC	4285
Db	831	TCACAGAGCGGAGGCTGGGAATCCACAGTGTGTACAGAGGCGGGGACAACTTCAAGC	890
QY	4286	GTGGGCGGAGGAGGAGCTGCTGTGCTGGCC--CAGCCCTCTCTCCGCAAGAGCGGATCC	4343
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QY	4344	TGTTTTAGAGGAGGCGACAGCTGCCATCGACCTGGAGACTGACAACTCATCCAGCTA	4403
Db	951	GGGTAAACGAAGCGCCAAAGAGGCAATCGACCTGAGGACATGAGACCCACATCAAGGA	1010
QY	4404	CCATCCGCGACCCAGTTTGATAC	4425
Db	1011	CACACGAGCAAGTTGGTAAC	1032
<p>RESULT 15 BI524575/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT</p>			
<p>BI524575 793 bp mRNA linear EST 29-AUG-2001 603051980T1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201898 3', mRNA sequence. BI524575 BI524575.1 GI:15349367 EST. human, Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NIH-MGC http://mgi.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11505 row: 0 column: 19 High quality sequence start: 10 High quality sequence stop: 783.</p>			
<p>FEATURES source 1..793 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5201898" /clone_lib="NIH_MGC_122" /lab_host="DH10B" /note="Organ: pooled lung and spleen; Vector: PCMV-SPORT6; Site_1: Noti; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library." BASE COUNT 183 a 208 c 220 g 182 t ORIGIN</p>			
<p>Query Match 13.1%; Score 663.2; DB 13; Length 793; Best Local Similarity 95.8%; Pred. No. 2.1e-137; Matches 757; Conservative 0; Mismatches 23; Indels 10; Gaps 7;</p>			
QY	3391	TGCAGCCACATCAGCGCAACTGAAGCGGCTGGAATCAGTCAGCGCTCACTATCTACTC	3450
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Job time : 4358.72 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:49:35 ; Search time 122.989 Seconds
(without alignments)
16388.716 Million cell updates/sec

Title: US-09-647-140A-5

Perfect score: 5079

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:**
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749.4	34.4	1977	10	US-09-954-456-804
2	1749.4	34.4	1977	10	US-09-880-107-3407
3	1749.4	34.4	1977	10	US-09-967-768A-190
4	1408.6	27.7	1448	10	US-09-925-299-157
5	1094.8	21.6	5300	10	US-09-880-107-3373
6	1034	20.4	4918	10	US-09-917-800A-1578
7	1030.2	20.3	5728	10	US-09-917-800A-479
8	982	19.3	1019	10	US-09-925-297-247
9	407	8.2	418	10	US-09-998-598-2049
10	407	8.0	419	10	US-09-998-598-175
11	386	7.6	1936	10	US-09-880-107-3832
12	354	7.0	4551	9	US-09-938-842A-1674
13	335.2	6.6	418	9	US-10-042-125A-32
14	326	6.4	4872	9	US-09-938-842A-436
15	311	6.1	329	10	US-09-864-761-16892
16	297.2	5.9	4545	9	US-09-938-842A-55
17	280	5.5	496	10	US-09-864-761-51
18	279.4	5.5	3786	9	US-10-012-896-1006
19	279.4	5.5	4395	9	US-10-012-896-1007

20	279.4	5.5	6140	9	US-10-012-896-536	Sequence 536, App
21	279.4	5.5	6140	10	US-09-759-143-536	Sequence 536, App
22	279.4	5.5	6140	10	US-09-780-669-536	Sequence 536, App
23	279.4	5.5	6140	10	US-09-822-827-536	Sequence 536, App
24	279.2	5.5	4869	9	US-09-938-842A-1392	Sequence 1392, Ap
25	269	5.3	6082	9	US-10-012-896-535	Sequence 535, App
26	269	5.3	6082	10	US-09-759-143-535	Sequence 535, App
27	269	5.3	6082	10	US-09-780-669-535	Sequence 535, App
28	269	5.3	6082	10	US-09-822-827-535	Sequence 535, App
29	259	5.1	259	9	US-10-046-935-964	Sequence 964, App
30	259	5.1	259	9	US-09-878-178-964	Sequence 964, App
31	220.6	4.3	460	10	US-09-864-761-30348	Sequence 30348, A
32	211.8	4.2	478	10	US-09-864-761-5895	Sequence 5895, Ap
33	210	4.1	221	10	US-09-864-761-22655	Sequence 22655, A
34	164	3.2	467	10	US-09-864-761-13775	Sequence 13775, A
35	139	2.7	88421	9	US-09-976-059-1	Sequence 1, Appli
36	130.4	2.6	163	10	US-09-954-456-1571	Sequence 1571, Ap
37	128.4	2.5	1812	10	US-09-815-242-4147	Sequence 4147, Ap
38	127	2.5	1074	9	US-10-012-896-824	Sequence 824, App
39	127	2.5	1074	10	US-09-759-143-824	Sequence 824, App
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43	121.6	2.4	4425	10	US-09-769-097-3	Sequence 3, Appli
44	118.4	2.3	473	10	US-09-560-863-603	Sequence 603, App
45	118.4	2.3	3912	10	US-09-917-800A-1560	Sequence 1560, Ap

ALIGNMENTS

RESULT 1
US-09-954-456-804
; Sequence 804, Application US/09954456
; Patent No. US200201115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 804
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-804

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Best Local Similarity	96.7%	Pred. No. 0		
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QY 3311	GTATCATATGCGCAGACGCGCG---CTCTTCTCACTGTGTCTATCTGCTGCGCTGCTGTC 3367			
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QY 3368	-TACACTTATGTCACGGCTTCTATCGACGCCACATCAGCGCAACTGAAGCGGTGGAATC 3426			
DB 241	TTACACTTATGTCACGGCTTCTATCGACGCCACATCAGCGCAACTGAAGCGGTGGAATC 3426			
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QY 3487	CGGGGCTTACACCGACGCGGGATTTTGAGATCATCAGTGTACTAAGGTGGATGCCAA 3546			
DB 360	CGGGGCTTACACCGACGCGGGATTTTGAGATCATCAGTGTACTAAGGTGGATGCCAA 3546			
QY 3547	CCAGAGAAGCTGCTACCCCTACATCATCTCCAAACGGTGGCTGAGCATCGGAGTGGAGTT 3606			
DB 420	CCAGAGAAGCTGCTACCCCTACATCATCTCCAAACGGTGGCTGAGCATCGGAGTGGAGTT 3606			
QY 3607	CGTGGGAACCTCGCTGGTGTCTTTGCTGCACTATTTCGCTCATCGGGAGGAGCAGCCT 3666			
DB 480	CGTGGGAACCTCGCTGGTGTCTTTGCTGCACTATTTCGCTCATCGGGAGGAGCAGCCT 3666			
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DB 659	GGAGTACTCAAGACACAGACAGAGGCGCCTGGTGGTGGAGGAGCGCCCTCCCGA 3846			
QY 3847	AGGTTGGCCCCACGTGGGGAGGTGGAGTTCCGGAATTAATCTGTGCGCTACCGCGCGG 3906			
DB 717	AGGTTGG-CCCCACGTGGGGAGGTGGAGTTCCGGAATTAATCTGTGCGCTACCGCGCGG 3906			
QY 3907	CCTAGACCTGGTGTCTAGAGACCTGAGTCTGATGTGCACGTGTGCGAGAGGTGGGAT 3966			
DB 776	CCTAGACCTGGTGTCTAGAGACCTGAGTCTGATGTGCACGTGTGCGAGAGAGGTGGGAT 3966			
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QY 4087	CCTGGCTCTCAGCTGACCATCATCCCGCAGGACCCCATCTGTTCTCGGGACCCCTGCG 4146			
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RESULT 5

US-09-880-107-3373

; Sequence 3373, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3373

; LENGTH: 5300

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U49248

US-09-880-107-3373

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Db	1920	AGTGTCTCCACAGAGCGGCTAGAGAAGTACTTCTGGAGGGATGACTTGGACATC - --T	1976
QY	1850	GTGGAAGAAGACCATCTCCCGAGGCTATGCCATCACCATACACAGTGGCACCCTTCCAC	1909
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QY	1910	TGGGCCAGGACTGCCCCCACTCTGCAACAGCTAGACATCCAGTCCCGAAAGGGCA	1969
Db	2037	TGGGAACATGATTCGGAAGCCACAGTCCAGATGTGAACCTGGACATATGGCAGGCCAA	2096
QY	1970	CTGGTGGCGGTGTGGGGCTGTGGCTGTGGGAAGTCTCCCTGGTGTCTGCCCCGTGTG	2029
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QY	2270	CGGACGGGTGAGTCTGGCTCGAGCTGTTTACAGTGTATGCCGATATTTCTTGTCTGGAT	2329
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RESULT 6
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Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
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NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1578
LENGTH: 4918
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012833
US-09-917-800A-1578
Query Match 20.4%; Score 1034; DB 10; Length 4918;
Best Local Similarity 55.8%; Pred. No. 5.5e-250;
Matches 2067; Conservative 0; Mismatches 1615; Indels 24; Gaps 4;
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Db 4589 AAGATAATGGTCTTAGACAACGGGAAGATTGTCTGAGTATGGCAGTCTCTCAAGAACTGCTG 4648

Db 601 TGAACGGCATCAAGGTGCTGAAGCTGTACGCTGGGAGCCAGCTTCTCTGAACAGGTGG 660
QY 1548 AGGCGATCAGGCGAGGTGAGCTCCAGCTGTGCGCAGCGGGGCTACCTCCACACCACAA 1607
Db 661 AGGCGATCAGGCGAGGTGAGCTCCAGCTGTGCGCAGCGGGGCTACCTCCACACCACAA 720
QY 1608 CCACCTTCACCTGGATGTGAGCGCCCTTCTGCTGACCCCTGATCACCCTCTGGGTGACG 1667
Db 721 CCACCTTCACCTGGATGTGAGCGCCCTTCTGCTGACCCCTGATCACCCTCTGGGTGACG 780
QY 1668 TGTACGTGACCCAAACAATGTGCTGGACCGCGAGAGGCGCTTGTGTCTGTCTCTCTGT 1727
Db 781 TGTACGTGACCCAAACAATGTGCTGGACCGCGAGAGGCGCTTGTGTCTGTCTCTCTGT 840
QY 1728 TTAATATCTTAAGACTTCCCTCAACATGCTGCCCGCCAGTTAATCAGCAACCTGACTCAG 1787
Db 841 TTAATATCTTAAGACTTCCCTCAACATGCTGCCCGCCAGTTAATCAGCAACCTGACTCAG 900
QY 1788 CCAGTGTGTCTCTGAACGGATCCAGCAATTCCTGAGCCAGAGGAACCTTGACCCCGAGA 1847
Db 901 CCAGTGTGTCTCTGAACGGATCCAGCAATTCCTGAGCCAGAGGAACCTTGACCCCGAGA 960
QY 1848 GTGTGGAAGAAGAACCATCTCCCGAGGCTATGCCATCACCATACACAGTGGCACCCTTCA 1907
Db 961 GTGTGGAAGAAGA-CATCTTCCAGGCTATGC--ATACCATACACAGTGGNACCTTTA 1017
QY 1908 CC 1909
Db 1018 CC 1019

RESULT 9
US-09-998-598-2049/c
; Sequence 2049, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 2049
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-2049

Query Match 8.2%; Score 418; DB 10; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4566 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCCTGGT 4625
Db 418 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCCTGGT 359
QY 4626 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACAAACACT 4685
Db 358 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACAAACACT 299
QY 4686 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGTAACCTGTGCTGAATGCT 4745
Db 298 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGTAACCTGTGCTGAATGCT 239
QY 4746 TTAGATGAGGAATGATCCCAAGTGGTGAATGACAGCCCTAAGGTACACAGCTAGTTTGA 4805
Db 238 TTAGATGAGGAATGATCCCAAGTGGTGAATGACAGCCCTAAGGTACACAGCTAGTTTGA 179

QY 4806 GCCAGTTAGACTAGTCCCGGTCTCCGATTTCCCAACTGAGTGTATTGTCACACTGCAC 4865
Db 178 GCCAGTTAGACTAGTCCCGGTCTCCGATTTCCCAACTGAGTGTATTGTCACACTGCAC 119
QY 4866 TGTTCCTCAATAACAGATTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTTT 4925
Db 118 TGTTCCTCAATAACAGATTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTTT 59
QY 4926 CTAAGTTTCCTGCTTTTCTTTTAAATAAAGCTTTTTCCTCTGGAACAGACAG 4983
Db 58 CTAAGTTTCCTGCTTTTCTTTTAAATAAAGCTTTTTCCTCTGGAACAGACAG 1

RESULT 10
US-09-998-598-175
; Sequence 175, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 175
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-175

Query Match 8.0%; Score 407; DB 10; Length 419;
Best Local Similarity 99.8%; Pred. No. 8.2e-93;
Matches 418; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4566 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCCTGGT 4625
Db 1 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCCTGGT 60
QY 4626 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACAAACACT 4685
Db 61 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACAAACACT 120
QY 4686 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGTAACCTGTGCTGAATGC 4744
Db 121 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGTAACCTGTGCTGAATGC 180
QY 4745 TTTAGATGAGGAATGATCCCAAGTGGTGAATGACAGCCCTAAGGTACAGCTAGTTTG 4804
Db 181 TTTAGATGAGGAATGATCCCAAGTGGTGAATGACAGCCCTAAGGTACAGCTAGTTTG 240
QY 4805 AGCCAGTTAGACTAGTCCCGGTCTCCGATTTCCCAACTGAGTGTATTGTCACACTGCA 4864
Db 241 AGCCAGTTAGACTAGTCCCGGTCTCCGATTTCCCAACTGAGTGTATTGTCACACTGCA 300
QY 4865 CTGTTTCCTCAATAACAGATTTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTT 4924
Db 301 CTGTTTCCTCAATAACAGATTTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTT 360
QY 4925 TCTAAAGTTTCCTGCTTTTCTTTTAAATAAAGCTTTTTCCTCTGGAACAGACAG 4983
Db 361 TCTAAAGTTTCCTGCTTTTCTTTTAAATAAAGCTTTTTCCTCTGGAACAGACAG 419

RESULT 11
US-09-980-107-3832
; Sequence 3832, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:

APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Iwe
APPLICANT: Gene Logic, Inc.
FILE OF INVENTION: Gene Expression Profiles in Liver Cancer
TITLE OF INVENTION: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3832
LENGTH: 1936
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X95715
US-09-880-107-3832

Query Match 7.6%; Score 386; DB 10; Length 1936;
Best Local Similarity 60.3%; Pred. No. 3.8e-87;
Matches 638; Conservative 0; Mismatches 420; Indels 0; Gaps 0;

Qy 3556 CTGCTACCCCTACATATCTCCAAACGGTGGCTGAGCATCGGAGTGGAGTTCTGTTGGGAA 3615
Db 445 CTGTTTCTCTCTACGCTGGGTTTTCAGGTGGCTTGGCGCAATGTGGAGTCTCTGGGAA 504
Qy 3616 CTGGTGTGCTCTTCTGCTGACATTTTGGCGTATCGGAGGAGGAGCCCTGAACCCGG 3675
Db 505 TGGCTGTGTTTGCACATGCGACGTGCTGCTGCTGAGCAAAAGCCACCTCATGTGCG 564
Qy 3676 GCTGGTGGGCTTCTGTGCTCTACTCTTGCAGGTGACATTTCTGCTGAAGTGGATGAT 3735
Db 565 CTTGTTGGCTTCTCTCTCTGCTGCTCCAGTCCAGGTGACCCAGACATGCTGAGTGGTGT 624
Qy 3736 AGAATGATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3795
Db 625 TCGAAGTGGACAGACATGAGAAACAGCATGCTGCTAGTGGAGGAGTGCAGGACTATGC 684
Qy 3796 CAACAGAGACAGAGCGGCTGGTGGTGGAGGAGGAGCGCCCTCCGAAGTGGCC 3855
Db 685 CTGAGCCCAAGAGGCTCCCTGGAGGCTGCCACATGTGACGCTCAACCCCTGGCC 744
Qy 3856 CCCAGTGGGAGGTGGAGTTCCGGAATTTCTGCTGCTACCGGCGGCGCTAGACCT 3915
Db 745 TCAGGGCGGCAGATCAGTTCCGGACTTTGGCTAAGATACCGACTGAGCTCCGCT. 804
Qy 3916 GGTGCTGAGAGACCTGAGTCTGCATGTGCAGGTGGCGAGAGGTGGGATGCTGGGCGG 3975
Db 805 GGCTGTGAGGGCTGTGCTTCAAGATCCAGGAGGAGAGGTTGGGCTGCTGGGCTGAG 864
Qy 3976 CACTGGGCTGGCAAGTCTCCATGACCTTTCCTCTTCCGATCTCCGAGCGGCAAA 4035
Db 865 GACCGGGCAGGAGTCTCCCTGGCCAGTGGGCTGCTGGGCTCCAGGAGGAGCTGA 924
Qy 4036 GGTGAAATCCGATTTGATGGCTCTCAATGTGGCAGACATCGGCTCCATGACCTGCGCTC 4095
Db 925 GGTGGATCTGGATCAGCGGGTCCCATTTGCCACGTGGGCTGCACACATGCGCTC 984
Qy 4096 TCAGTGAACATATCCGAGGAGACCCATCTCTGTTCTGGGAGACCTCGCATGACCT 4155
Db 985 CAGGATCAGATCATCCCGAGGAGCCATCTCTGCTGGGCTCCAGGAGGAGCTGA 1044
Qy 4156 GGACCCCTTGGCAGCTACTCAGAGGAGACATTTGTTGGCTTTGAGCTGTCCACCT 4215
Db 1045 CGACCTCTGCAGGAGACACTCGGAGGAGGTATCTGGGAGCCCTCGGAGCGGTGACCT 1104
Qy 4216 GCACAGCTTTGTAGCTCCCGAGCGGAGGCTGAGCTTCCAGTGTCTCAGAGGCGGGA 4275
Db 1105 CAAGCCCTTGGTGGCTTGGCTGGCCCGCCAGCTGCAGTACAGTGTCTGACCGAGCGGA 1164

Qy 4276 GAATCTAGCGTGGCCAGAGGAGCACTCGTGTGCTGCGCCGAGCCCTGCTCCGCAAGAG 4335
Db 1165 GGACCTGAGCGTGGCCAGAAACAACTCTGTGTGGCAGCTCCCTTCTCCGGAAGAC 1224
Qy 4336 CGCATCTGCTGTTTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4395
Db 1225 CCAGATCTCTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1284
Qy 4396 CCAGCTTACCATCCGACCCAGGTTTGTATACCTGCTGCTGACCATGCTGACCATGCTG 4455
Db 1285 GCAGGCAATGCTCGGAGGAGTGTGTCACAGTGTGCTGCTGCTGCTGCTGCTGCTG 1344
Qy 4456 TAACACTATCATGAGTACACAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4515
Db 1345 CGCTTCCGTGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
Qy 4516 TGATTTCTCCAGCCACCTCATTTGACGCTAGAGGATCTTCTACGGGATGGCCAGAGTGC 4575
Db 1405 CGGAGCGCCGCGCCAGCTGCTGGCCAGAGAGGCTGTTTACAGACTGGCCCGAGGATC 1464
Qy 4576 TGGACTTGCCTAAATATATATTCCTGAGATTTCTCTCTCTG 4613
Db 1465 AGGCTGTCTGAGCCAGGACCTCAACCGTACCCAG 1502

RESULT 12

US-09-938-842A-1674
Sequence 1674, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1674
LENGTH: 4551
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1674

Query Match 7.0%; Score 354; DB 9; Length 4551;
Best Local Similarity 45.9%; Pred. No. 6.9e-79;
Matches 1671; Conservative 0; Mismatches 1865; Indels 108; Gaps 9;

Qy 893 CCCTCTCTTGAAGGCGCTGCTGCGCCACCTTTCGGCTCCAGCTTCCATCATGCTGCTGC 952
Db 934 CACCTATCCGTACGACTCTACTCCGATGTTCTTGGAGGAGAGATCCTCTTACCCGAT 993
Qy 953 TTCAAGCTTATTCAGGAGCTGCTCTCTTTCATCAATCCACAGCTGCTCAGCATCTGATC 1012
Db 994 CTAGCCATCGTCCGCTCGGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1053
Qy 1013 AGGTTTATCTCCACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
Db 1054 GATTTCACCTCCGCAAGAGATCTCCCGGTGGCAAGGTTATTACCTGCTCTCATCTC 1113
Qy 1073 TTCTGTGCTCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1132
Db 1114 CTGTTGCCAANTTCGTGAGGTCTTGACAGCGCATCATGTTCAATTTCCGATTCCAGAAG 1173

[illegible]

Qy	4424	ACCTGCACTCTCTGACCAATCGGACACCGCGTTACACTATCATGAGATACACCAAGGTC	4483
Db <td>4375 <td>TCGTGCAACCATCATACAGATTCGCCACCGGATTCCTACAGTATGAGCGGCATCGAGTC <td>4434</td> </td></td>	4375 <td>TCGTGCAACCATCATACAGATTCGCCACCGGATTCCTACAGTATGAGCGGCATCGAGTC <td>4434</td> </td>	TCGTGCAACCATCATACAGATTCGCCACCGGATTCCTACAGTATGAGCGGCATCGAGTC <td>4434</td>	4434
Qy <td>4484 <td>CTGTCTCTGGACAAAGAGTAGTAGTGAATTTGATTTCTTCAGC <td>4527</td> </td></td>	4484 <td>CTGTCTCTGGACAAAGAGTAGTAGTGAATTTGATTTCTTCAGC <td>4527</td> </td>	CTGTCTCTGGACAAAGAGTAGTAGTGAATTTGATTTCTTCAGC <td>4527</td>	4527
Db <td>4435 <td>CTTGTCTATTGATGCTGGGAAAGCGAAAGAGTTTCGATAGCCGGC <td>4478</td> </td></td>	4435 <td>CTTGTCTATTGATGCTGGGAAAGCGAAAGAGTTTCGATAGCCGGC <td>4478</td> </td>	CTTGTCTATTGATGCTGGGAAAGCGAAAGAGTTTCGATAGCCGGC <td>4478</td>	4478

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RESULT 13
US-10-042-125A-32
; Sequence 32, Application US/10042125A
; Patent No. US20020164345A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.557
; CURRENT APPLICATION NUMBER: US/10/042,125A
; CURRENT FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 4, 352
; OTHER INFORMATION: n = A,T,C or G
US-10-042-125A-32

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RESULT 14
US-09-938-842A-436
; Sequence 436, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED
; TITLE OF INVENTION: SAME, AND METHOD

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; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 436
; LENGTH: 4872
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-436

Query Match          6.4%; Score 326; DB 9; Length 4872;
Best Local Similarity 46.6%; Pred. No. 8e-72;
Matches 1653; Conservative 0; Mismatches 1740; Indels 153; Gaps 13;

QY 1034 GCCCCCTCCTGGTGGGGTTCCTGGTGGCTGGCTGGCTGATGTTTCTGCTGCCATGATGCAG 1093
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1000 GCGCCAGCTTCGGATGGGTACATCATCGCTTCTCAATCTTTGTTGGAGTGGTTCGGG 1059

QY 1094 TCGGTGATCTTTACAACTATTATACCACATACATCTTTTGTGACTGGGGTGAAGTTTCGTACT 1153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1060 GTGCTATGTGAAGCTCAATAATTTCCAGAATGTCATCGCTGTTGGTTACCGACTGAGATCT 1119

QY 1154 GGGATCATGGGTGTCATCTACAGAAAGCTCTGGTTATCACCACTCAGTCAAAAGTGGC 1213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1120 GCTCTGATGCTGCTGTGTTCCCGAAATFCGTTGAGGTTAACTAATGAAGGTCGTAGAAG 1179

QY 1214 TCCACTGTGGGGGAAATGTCAACCTCATGTCAGTGGATGCCAGCGCTTTCATGACCTT 1273
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1180 TTTCAACAGGAAGATACCAACTTAATGAGACTGATGCCGATCTCTTCAGCAATA 1239

QY 1274 GCCCCTTCCTCAATGCTGTGTGTCAGCACCCCTGCAGATCATCTCGGGGATCTACTTC 1333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1240 TCGCAATCACATTACATACCATGTTGTCGGCTCCATTCGTATAAATATAGCACTGATTC 1299

QY 1334 CTCTGGCAGAACCTAGGTCCTCTGCTCGCTCGAGTCGCTTTTCATGGTCTTCTGCTGATT 1393
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1300 CTCTATCAGCAATTGGGTGTTGCCCTCGCTCATGTTGGTGCATGTTGGTCCCTTATGPTC 1359

QY 1394 CCACTCAACGGAGCTGTGGCGGTGAAGATCGCGCTTCCAGTAAAGCAATGAAATG 1453
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1360 CTTTACAGACTGTTATTATAAGCAAAATGAGAAGCTGACAAGGAAGGCTTCGACGGT 1419

QY 1454 AAGCACTCGCCATCAAGCTGATGAGTGATCTGTAACGGCATCAAGGTGCTGAAAGTG 1513
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1420 ACTGACAGAGAATTGGCCTTATGAATGAAGTTTTAGCTCAATGGATACAGTAAAGTGT 1479

QY 1514 TACGCTGGGAGCCAGCTTCCTCAAGCAGGTGAGGGCATCAGCGAGGTGAGCTCCAG 1573
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1480 TATGCTTGGGAAAACAGTTTCCAGTCCAAGGTCCAAACTGTTCTGTGATGATGAATATCT 1539

QY 1574 CTGCTGGCGACGGCGGCTTACTCCACACCAACCACTTCCACTGGATGTGCGACGCC 1633
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1540 TGGTTCGGAAATCACAGCTCCTGGGAGCTTGAATATGTTTCATCTGAATAGCATTCCT 1599

QY 1634 TTCCTGGTGACCCGTATCAACCTCTGGGTGACGTGTACGTGGACCCCAACAATGTGCTG 1693
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1600 GTTCTTGTGACTATTGTTTCATTTGGTGTGTTACATTTACTTGGAGGAGAC-----CTG 1653

QY 1694 GACGCCGAGAAGGCTTTGTGCTGTCTGCTGTTGTTTAAATATCTTAAGACITCCCTCAAC 1753
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1654 ACCCCTGCAAGAGCATTTACGTCACTCTCTCTCTTGTGCTGCTTTTCCCTCTCTTC 1713

QY 1754 ATGCTGCCCAAGTTAATCAGCAACCTGACTCAGSCCAGTGTGTCCTCTCTGTAACGATCCAG 1813
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1714 ATGCTTCCAAACATTAATCACTCAGTGGTAAATGCTAATGATATCTTAACACGCTTCGAG 1773

QY 1814 CAATTCTGAGCCAAAGAGAACTTTGACCCCCAGAGTGTGGAAAGAAAGACCATCTCCCA 1873

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Db 2740 GCACCTGGAGGGGCGATGGGTAGTGATGATGCTCTCTTTTATGTTACGCTCTTAACAGAACTA 2799
QY 2948 AGTGGCGCTGCCATTTGAGGCAATGTGTGCTCAGTCCCTGGGACAAATGATGCCATGGCA 3007
Db 2800 TTTGGGTTACTA-----GCAGCACGTGGTTGAGTGGAGTGGATGATGAGGAACCTCA 2853
QY 3008 GACAGTAGACAGAACACACTTCCCTGAGCTGGCGCTCTATGCTCTTTAGGAATCTG 3067
Db 2854 AAGAGT-----CATGGACCCCTTTCTACAATCTCAATATGACACTCTCTCTGTTTGGGA 2907
QY 3068 CAAGGGTTCTTGGTGTGCTGGAGCCATGGCCATGGCAGCGGGTGGCATCCAGCGTGC 3127
Db 2908 CAGGTTTGGTGACATTTGACCAATTCATATGTTGATTTATGTCACAGTCTTTATGACGT 2967
QY 3128 CGTGTGTGACAGGACGTGTGCGACAAAGATAGCTCGGCCACAGTCTCTTTTGGAC 3187
Db 2968 AAGAAGTTACACGACAAATATGCTTCAATTCATATGAGGGCCCGATGCTCTTCTTCAT 3027
QY 3188 ACCACACCATCAGCGCGCATCTGAACTGCTCTCCAAAGACATCTATGCTGTGATGAG 3247
Db 3028 ACCAATCCGTAGACGGATAATCAATCGATTTCGAAAGATCTGGGTGATATGATCGGA 3087
QY 3248 GTTCTGGCCCTGTCACTCTCTGCTGCTCAATTCCTTCTTCAACGCCATCTCCACTCTT 3307
Db 3088 ACTGTGGCGCTCTTTGTAACATGTTTATGGGTCAAGTCTCACAGCTCTTTCAACTGTA 3147
QY 3308 GTGGTCAATATGCGCAGCGCGCTCTTCACTGTGTGTATCTCTGCGCCCTGGGTGCTC 3367
Db 3148 GTGTGATTTGGCAATTTGAAGCACTTTTGTCTTGTGGGCCATCATGCCCTCTCTGCTTG 3207
QY 3368 TACACCTTAGTCAGCGCTCTATGAGCCACATCAGGCAACTGAGCGCTGGATCA 3427
Db 3208 TTTTATGGAGCTATCTTTATATAGACAGCCCGGTGAGGTAAAGCTGATGGATCA 3267
QY 3428 GTCAGCGCTCACTATCTACTCCACTTTTTCGAGACAGTGTGTCGACAGTGTATC 3487
Db 3268 ATTTCAAGATCGCTGTTTATGACAGATTTTGAGAGGCAATGATGCTTATCAACTATC 3327
QY 3488 CGGCGCTACAAACCGAGCGGGATTTTGTAGATCATAGTGTATAGTGGATGCCAAC 3547
Db 3328 CGTGTCTTACAAAGCATATGATCGTATGGCTGATATCAACGGAAGATCAATGGATAAATAC 3387
QY 3548 CACAGAGGTGCTACCCCTACATCATCTCAACCGGTGGCTGAGCATCGAGTGGAGTTC. 3607
Db 3388 ATCAGATTCACCTTGTCAACATGGGTGCAATCGGTGGCTTGGAAATCCCTTTAGAACT 3447
QY 3608 GTGGGAACGTGCTGTGCTCTTTGTGTGCTATTTGCCGTCTATCGGGGAGGAGCGCTG 3667
Db 3448 CTGGGTGCTTATGATATGGCTGACAGCATCGTTGCTGTCATGCAGATGGAAGAGCG 3507
QY 3668 AACCCGGGGTGG-----TGGGCTTTCTGTGTCTTACTCTCTTGCAGGTG 3712
Db 3508 GAGAACCAACAGGCAATTTGCATCATCAATGGGTGTTGCTTCTCAGTTATGCTTAAATAT 3567
QY 3713 ACATTTGCTGTGAACGTGATGATACCAATGATGTCAGATTTTGAATCTAATCGTGGCT 3772
Db 3568 ACTAGCTTTTAAACAGTGTCTGAGACTTGGAGTTTGGCTGAGAAATAGCTTAAACGG 3627
QY 3773 GTGAGAGGCTCAAGAGTACTTCAAGACAGACAGAGAGCGCCCTGGGTGGTGAAGGC 3832
Db 3628 GTCGAGCGTGTGGCAATATATAGAGATTCGCCAGAGGCTCCGCTGTCTTATGAGAAC 3687
QY 3833 AGCCGCCCTCCGAAGTTGGGCCCGACGTGGGGAGGTGAGTTCGGGAATATTTCTGTG 3892
Db 3688 AACCGTCCACCTCTCTGGATGGCCATCATCTGGATCCATAAAGTTTGAGGATGTTGTTCTC 3747
QY 3893 CGCTACCGCGCGGCTAGACCTGGTGTCTGAGAGACCTGAGTGTGATGTCGACGCTGGC 3952
Db 3748 CGTTACCGCCCTCAGTTACCGCTGTGCTTCAATGCGGTTCTTCTTCATPTCAATCAACA 3807
QY 3953 GAGAAGGTGGGATCGTGGCGCGACTGGGCTGGCAAGTCTTCCATGACCCCTTTGCCTG 4012
Db 3808 GATAAGGTGGGATTTTGAAGGACTGTGTCTGGAAGTCAAGCCCTGTTGAATGATG 3867

QY 4013 TTCGCATCTCTGGAGCGGCAAAAGGTTGAAATCCGCATTTGATGGCTCAATGTGCAGAC 4072
Db 3868 TTTAGAATTTGGAGGTGGAAAAGAGGATCTTAATCGATGATTTGTGACCTTGGAAAG 3927
QY 4073 ATCGGCTCCATACCTCGGCTCTCAGCTGACCATCATCCCGCAGAGCCCATCTGTTTC 4132
Db 3928 TTTGACTGATGGACCTACGTAAAGTGTCTCGAATCATTCACACAGTCCCGGTTCTTTTC 3987
QY 4133 TCGGGGACCCCTCGCATGAACCTTGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGG 4192
Db 3988 TCAGAACTGTGAGGTTCAATCTTGATCCATTGTTGTAACACAATGATGCTGATCTTTGG 4047
QY 4193 TGGCTTTGGAGCTGTCCCACTCTGCACAGTGTGTGAGCTCCCGAGCGGAGGCTGAC 4252
Db 4048 GAATCTCTAGAGAGGACACTTTGAAGGATACCATCCCGCAGAAATCTCTTTGGTCTTGT 4107
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QY 4553 TTTCTAC 4558
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RESULT 15
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; Sequence 16892, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16892
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 19
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; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
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; OTHER INFORMATION: SWISSPROT HIT: O15438, EVALUE 7.00e-44
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Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 CCTTAGTGAG 311

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Job time : 203.989 secs

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:05:00 ; Search time 101.285 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1737.8	34.2	5011	2	US-08-460-907B-1
5	1737.8	34.2	5011	3	US-08-463-179A-1
6	1737.8	34.2	5011	3	US-08-461-384B-1
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31 351.4 6.9 4877 3 US-08-488-546A-8 Sequence 8, Appli
32 351 6.9 2294 2 US-08-404-531B-30 Sequence 30, Appl
33 351 6.9 2294 3 US-08-476-900A-30 Sequence 30, Appl
34 351 6.9 2294 3 US-08-488-546A-30 Sequence 30, Appl
35 333.4 6.6 5110 2 US-08-404-531B-5 Sequence 4, Appli
36 333.4 6.6 5110 2 US-08-404-531B-5 Sequence 5, Appli
37 333.4 6.6 5110 3 US-08-476-900A-4 Sequence 4, Appli
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43 318.6 6.3 1308 2 US-08-404-531B-2 Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-08-141-893-1
; Sequence 1, Application US/08141893
; Patent No. 5489519
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,893
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923; 08/029,340
; FILING DATE: 27-OCT-1992; 8-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Decont, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5149
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-141-893-1

Query Match 34.2%; Score 1737.8; DB 1; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

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 ; Sequence 1, Application US/08462109A
 ; Patent No. 5882875
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; APPLICANT: Dealey, Roger G.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING
 ; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,109A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/966,923
 ; FILING DATE: 27-OCT-1992
 ; APPLICATION NUMBER: 08/029,340
 ; FILING DATE: 8-MAR-1993
 ; APPLICATION NUMBER: 08/141,893
 ; FILING DATE: 26-OCT-1993
 ; APPLICATION NUMBER: 08/407,207
 ; FILING DATE: 20-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeConti, Giulio A. Jr.
 ; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: P01-002CP4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

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; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5011 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 196..4788

; US-08-462-109A-1

Query Match 34.2%; Score 1737.8; DB 2; Length 5011;

Best Local Similarity 62.2%; Pred. No. 0;

Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

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QY 265 CTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324

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RESULT 4
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; Sequence 1, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340

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; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-460-907B-1

Query Match 34.2%; Score 1737.8; DB 2; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative. 0; Mismatches 1662; Indels 87; Gaps 6;

QY 25 CGGGAGGCTCGGCTCCAAAGTTCTGGGACTCAACCTGTCTGTGCACACAGAAACCCGA 84
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QY 2977 GCTCAGTGCCTGGCAAAATGATGCCATGGCAGACAGTAGACAGAAACAACACTTCCCTGAG 3036
DB 3180 GCTCAGCCTCTGACTGATGATGACCCCATCTCAACGGGACTCAGGAGCACAACGAACTCCG 3239
QY 3037 GCTGGCGCTCTATGTGTCTTATAGGAATCTGCAAGGGTTCTTGGTGATGCTGCGACGCCAT 3096
DB 3240 GCTGAGCGTCTATGGAGCCCTGGCATTTTCAAAAGGATCGCGTCTTTTGGCTACTCCAT 3299
QY 3097 GSCCATGGCAGCGGTGGCATCCAGGCTCGCCGTGTGTGGCAGGCACTGCTGACAAA 3156
DB 3300 GCGCGTGTCTATCGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGAGCTGCTGTCACAG 3359
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DB 3360 CATCTCGGTCACCATCAGCTTCTTTCAGCGGACCCCGAGTGGGAACTGCTGGAACCG 3419
QY 3217 CTCTCCAAAGGACATCTATGTGTGTAGTGAAGTCTTGGGCCCTGTCTCATCTCATGCTGT 3276
DB 3420 CTCTCCAAAGGAGCTGGACACAGTGGACTTCCATGTATCCCGGAGGTCATCAAGATTTCA 3479
QY 3277 CAATTCCTTCTTCAAGCCATCTCCACTCTTGTGTGTATCATGCGCAGCAGCCGCTCTT 3336
DB 3480 GGGCTCCCTGTCAAGCTCATTTGGTGCCTGTCTTATCTCTGTGGCCACGCCCATCGC 3539
QY 3337 CACTGTGTGTATCTTCCCTCGCTGTCTTACACTTGTAGTGCAGCGCTTCTATGCGAC 3396
DB 3540 GCGCATCATCATCCCGCCCTTGGCCCTCATCTACTTCTTCCGACAGGTTCTACGTGCG 3599
QY 3397 CACATCAGGCAACTGAAGCGGCTGGAATCAGTCAAGCCGCTCACTATCTTCTCCACTT 3456
DB 3600 TTCTTCCCGGAGCTGAAGCGCTCGAGTGGTCAAGCCGCTCCCGGCTCTATTTCCCATTT 3659
QY 3457 TTCGAGAGACGTGACTGGTGGCAGTGTATCCGGCGCTACACCCGAGCCGCGGATTTGA 3516
DB 3660 CAACGAGACCTTGTGGGGTTCAGCGTCTATTCAGCCTTTCGAGGAGCAGGAGCGCTTCA 3719
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DB 3720 CCACCAGAGTGACCTGAAGGTGGACGAGAACCAAGAGGCTTATACCCAGCATCGTGC 3779
QY 3577 CAACCGTGGCTGAGCATCGGAGTGGAGTTCGTGGGAACTCGGTGGTCTCTTGTCTGTC 3636
DB 3780 CAACAGGTGGTGGCGCTGCGGCTGGAGTGTGTGGCAACTGCATCTCTTCTTGTCTGTC 3839
QY 3637 ACTATTTCCCTCATCGGAGGAGCAGCTGAACCCGGGCTGGTGGGCTTCTTGTCTGTC 3696
DB 3840 CCGTGTGGGTGATCTCCAGGCACAGCCTCAGTGTGGTGGGCTCTCAGTGTCTGTC 3899
QY 3697 CTACTCTCTTGCAGGTGACATTTGCTCTGAACGTGATGATACGAATGATGTCTAGATTTGA 3756
DB 3900 TTACTCATTTGAGGTTCACACGCTTGAACCTGGCTGGTTCGATGTCTCTGAATGGA 3959
QY 3757 ATCTAACATCTGCTGTGGAGAGGCTCAAGGAGTACTCCAAAGACAGACAGAGCGGCC 3816

Db 3960 AACCAACATCGTGGCGCTGAGAGGCTCAAGGAGTATTACAGACTCAGAGAGGCGGCC 4019
QY 3817 CTGGGTGGTGAAGGAGCGCGCCCTCCGAAAGTGTGGCCCGGAGGTGGGAGGTGGAGTT 3876
Db 4020 CTGGCAAAATCCAGGAGACAGCTCGGCCAGCAGCTGGCCCGGAGGTGGGAGT 4079
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Db 4080 CCGAACTACTGCTCGCTACCGGAGAGACCTGGAGTCTGCTCAGGACACATATGT 4139
QY 3937 GCATGTGCAGGCTGGCGAGAGGAGTGGGAGTCTGCGCGGAGTGGGCTGGCAAGTCTTC 3996
Db 4140 CAGATCAATGGGGAGAGAGTGGGCTGCTGGGGGAGCGGAGTGGGAGTGGTCTC 4199
QY 3997 CATGACCTTTGCTCTGTCGCTACCGCGGCGGCAAGGAGTGAATCCGATTTGATGG 4056
Db 4200 CTGACCTCTGGGCTTTATTCGGATCAACGAGTCTGCGGAGGAGAGATCATCATGATG 4259
QY 4057 CCTCAATGTGGCAGACATGGGCTCTCATGACCTGGGCTCTCAGCTGACCATCATCCGCA 4116
Db 4260 CATCAACATCGGCAAGATCGGCTGACGACCTCCGCTTCAAGATCACCATCATCCGCCA 4319
QY 4117 GGACCCATCTCTTCTCGGGAGCCTGCGCATGAACTGGACCCCTTGGGAGTACTC 4176
Db 4320 GGACCTGTGTTGTTTGGGTTCCCTCGAATGAACCTGGACCCATCAGCCAGTACTC 4379
QY 4177 AGAGGAGGACATTTGCTGGGCTTTGAGCTGTGCCACCTGACACGCTTTGTGAGCTCCCA 4236
Db 4380 GGATGAAGAAGTCTGACGCTCCCTGGAGCTGGCCACCTGAAGGACTCTGCTGTCAGCCCT 4439
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Db 4560 GCGCAGCGGAGCGTGGAGCTGGAACGAGCAGCCTCATCCAGTCCACCATCGGACACA 4619
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Db 4620 GTTCGAGGACTGACCGCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4679
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Db 4740 GCAGCAGAGAGGCTTCTTACAGATGCGCAAGAGCGCGGCTGCTGCTGAGCGGCCAGA 4799
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Db 4800 GCTGGCATATC 4810

RESULT 6

US-08-461-384B-1
; Sequence 1, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deele, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario

COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-461-384B-1

Query Match 34.2%; Score 1737.8; DB 3; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;
QY 25 CGGGGAGCTCGGCTCCAGTTCCTGGGACTCCAACTCTCTGTGTGCACACAGAAACCCGGA 84
Db 219 CGCGGAGTGGCTCGGACCGCTCTGGGACTGGAATGTACGTGGAAATACACAGCAACCCGGA 278
QY 85 CCTCACTCCCTGCTCCAGAACTCCCTGCTGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 144
Db 279 CTTCAACCAAGTCTTTTCAAGAACACAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 338
QY 145 CGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
Db 339 CTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 398
QY 205 CCACCTGTCCAACTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 264
Db 399 ACCTCTCAACAAACCAAACTGCTTGGGATTTTCTGCTGGATCTGCTGCTGCTGCTGCTGCTGCTGCT 458
QY 265 CPTTTTACTCCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
Db 459 CPTTCTTACTCTTCTTGGGAAAGAAAGTCTGGGCAATATCTCTGCGCCCAAGTGTCTGCTGCTGCT 518
QY 325 CACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
Db 519 CAGCCCAACTCTCTTGGGATCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
QY 385 GCTGAGGGGCTTACAGTCTTGGGGTTCCTCAATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444
Db 579 GAGGAAGGGAGTTCAGTCTTCAAGGATCATGCTCACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
QY 445 CGCCATCGTCCCAATTCGCTTCCAGATCTTTTAGCCAAAGCAGGAGGCTGAGATCTCAGA 504
Db 639 TGCCCTAGCCATCTCTGAGATCCAAATTTATGACAGCCTTAAAGAGGATGCCAGGTTGA 698

QY 505 CCCCTTCGGCTTACACCCTTCTACATCCACTTTGGCCCTGGTACTCTCTGCCCTCATCTT 564
DB 699 CCTGTTTCGTGACATCACTTTTCTACGTCTACTTTTCTCTTACTCACTACGTCTCTT 758
QY 565 GGCCTGCTTACAGGAGAAACCTCCATTCTTCGCGAAGAAATGTCGACCTCAACCCCTA 624
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QY 625 CCTGAGACCAAGCCTGGCTTCTCTCCCGCTGTTTCTGTTGGTGTTCACAAAGATGGC 684
DB 819 CCCAGATCCAGCGCTTCTTCTCTGTCGAGGATCACTTCTGTTGGTATCAACAGGTTGAT 878
QY 685 CATCTATGGCTACCGGATCCCTTGGAGGAGAAAGACCTCTGGTCCCTAAAGAAAGAGA 744
DB 879 TGTCCGGGGCTACCGCAGCCCTCGAGGCGAGTGACCTCTGGTCTTAAACAAGAGGA 938
QY 745 CAGATCCAGATGTTGTCAGCAGCTGCTGGAGGCATGGAGGA----- 788
DB 939 CACGTCGGACAAAGTCGTGCTGTTTGGTAAAGAACTGGGAAGAGGAATCGGCCAAGAC 998
QY 789 -----AGCAGAAAAGCAGACGCGACGACACAAAGGCTTTCAGCAGCACCTGGGAAAAA 840
DB 999 TAGGAACAGCGCGTGAAGTTGTGTACTCTCTCAAGGATCCTGCCAGCCGAAGAGAG 1058
QY 841 TGCCTCCGGGAGGACGAGGTGCTGCTGGTG-----CCCCGCCACAGGCC 885
DB 1059 TTCCAAGGTGGATCGGAATGAGGAGTGGAGGCTTTGATCGTCAAGTCCCAACAAGGA 1118
QY 886 CCGGAAGCCCTCTCTCTGAAGCCCTGCTGGCCACCTTCCGCTCCAGCTTCTCTCATCAG 945
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DB 1179 CTCTCTTCAAGCCATCACGACCTGATGATGTTTCCGGGCCGAGATCTTAAAGTT 1238
QY 1006 CTTGATCAGGTTTATCTCAACCCCATGGCCCCCTCTGTTGGGCTTCTCTGGTGGTGG 1065
DB 1239 GCTCATCAAGTTCGTGAATGACACGAAGGCCCAAGACTGGCAGGGCTACTTCTACCCGT 1298
QY 1066 GCTGATGTTCTGCTCCATGATGACAGTGCCTGATCTTACAACACTTATACACTACAT 1125
DB 1299 GCTGCTGTTTGTCACTGCCCTGCTGAGACCCCTGCTGCTGCACAGTACTTCCACATCTG 1358
QY 1126 CTTTGTGACTGGGTAAGTTTCGTATGGGATCATGGGTGCTATCTACAGGAAGGCTCT 1185
DB 1359 CTTGCTAGTGGCATGAGGATCAAGACCGCTGTCATTGGGGCTGCTATCGGAAGGCCCT 1418
QY 1186 GGTATACCAACTCAGTCAAACTGCGTCCACTGTGGGGAATGTTCACCTCATGTC 1245
DB 1419 GGTGATCACCATAATCAGCCAGAAAATCCTCCAGCTCGGGGAGATGTTCACACCTCATGTC 1478
QY 1246 AGTGGATGCCAGCGCTTCATGACCTTGGCCCCCTTCTCAATCTGCTGTTGGTTCAGCAC 1305
DB 1479 TGTGAGCGCTCAGAGGTTCAAGCTTGGCCACGATTAACATGATGCTGGTCAGCCCC 1538
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QY 1366 TGGAGTCCCTTTCATGCTGTTGATTCACCTCAACGAGGCTGTGGCGGTGAAGATGCG 1425
DB 1599 TGGAGTGGCGGTGATGCTCTCATGTTGGTGGCCCTCAATGCTGATGGCGATGAAGACAA 1658
QY 1426 CGCTTCCAGGTAAGCAATGAATGAAGGACTCCGCGATCAAGCTGATGATGATGAT 1485
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QY 1486 CTTCAAGCGCATCAAGTGTCTGAAGTGTATCGCTGGGAGCCCAAGCTTCTCTGAAGCAGGT 1545
DB 1719 TCTCAATGGGATCAAGTGTCTGAAGCTTTATGCTGGGAGCTGGCATTCAGGACAGGT 1778

QY 1546 GGAGGSCATCAGCAGGGTGAAGTCCAGTGTGCGCACGGCGCTTACTCTCCACACCAC 1605
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DB 1839 GGGCACCCTTTCACCTGGGTGTCGACGCCCTTCTGTTGGCTTGTGACACATTTGCCCTCTA 1898
QY 1666 CGGTACGTGGAGCCCAACAATGTGTCGACGCCGAGAGGCTTGTGCTGTGTCCTT 1725
DB 1899 CGTGACCATTTAGAGCAACAACATCTGTGATGCCAGACAGCTTCTGTTTGGCCCTT 1958
QY 1726 GTTTAATATTTAAGACTTCCCTTCAACATGCTGCCCTTAACTTAATCAGCAACCTGACTCA 1785
DB 1959 GTTCAACATCTCCGCTTCCCTTGAACATCTTCCCTTGGTATCATCAGCAGCATCTGTCGA 2018
QY 1786 GGCAGTGTCTCTGTAACAGGATCCAGCAATCTCTGAGCCCAAGAGGAATCTTGACCCCCA 1845
DB 2019 GGCAGTGTCTCTTCAACAGCTTGAAGATCTTCTCTCCATGAGGAGCTGGAACCTGA 2078
QY 1846 GAGTGTGGAAGAAAGACCATCTCCCCAGSC-----TATGCCATCACCATACACAG 1896
DB 2079 CAGCATGAGCGACGCGCTGTCAAGACGCGCGGGGCGACGAACAGCATCACGTTGAGGA 2138
QY 1897 TGGCACCTTACCTTGGGCCAGGACCTGCCCTCCCTCTCTGCACAGCTTACAGATCCAGGT 1956
DB 2139 TGGCACATTCACCTGGCCAGGAGCGACCTCCACACTGAATGATGATCACCCTTCTCCAT 2198
QY 1957 CCGGAAAGGGGACATGTTGGCGCTGTTGGGCTGTGGGCTGTGGGAGTCTCTCCCTGTG 2016
DB 2199 CCCCCAAGGTGCTTGTGGCTGTGGGCGAGGTGGGCTGCGGAAAGTGTGCTCCCTGTG 2258
QY 2017 GTCTCCCTGCTGGGAGATGAGGAAGCTAGAACCAAGTGCACATCAAGGGTCCCT 2076
DB 2259 CTACGCCCTTGTGGCTGAGATGGACAAAGTGGAGGGGCGACGTGATCAAGGGTCCCT 2318
QY 2077 GGCTTATGTGCCCCAGCAGGACATGATCCAGAACTGCATCTTTCAGAAAGCTGCTTTT 2136
DB 2319 GGCTTATGTGCCACAGCAGCGCTGGATTCAGATGATTTCTCTCCGAGAAACATCTTTT 2378
QY 2137 CGGCAAGCCCTGAACCCCAAGCGGTACAGCAGACTCTGGAGGCTGTGGCTGTGCTAGC 2196
DB 2379 TGGATGTGAGTGGAGGAACCATATTTACAGGTCCCTGTATACAGGCTGTGCCCTCTCC 2438
QY 2197 TGACCTGAGATGCTGCTGTTGGGATCAGACAGAGATTGGAGAGAGGCTATTAACCT 2256
DB 2439 AGACCTGGAATCTTCCCGAGTGGGATCGGACAGAGATTGGGAGAGGGGCTGATCCT 2498
QY 2257 GTCTGGGGCCAGCGGCTGAGTGTGCTGAGCTGTGAGCTGTTTACAGTGTATGCCGATAT 2316
DB 2499 GTCTGGGGCAGAGCAGCGCTGAGCTTGGCCGGGCGGTACTTCCACGCTGACAT 2558
QY 2317 TTTCTGCTGATGATCCACTGTCGCGGTGACTCTCATGTGGGCCAAGCAGCATCTTTGA 2376
DB 2559 TTACCTTCTGATGATCCCTCTCAGCAGTGGATGCCATGTGGAAAAACATCTTTGA 2618
QY 2377 CCAGCTCATCGGGCAGAGGCTGCTGCGAGGCAAGAGCGAGTCTGCTGCGAGCACCG 2436
DB 2619 AATGTGATTGGCCCAAGGGATGCTGAGAACAAAGACCGCGATCTTGGTCAGGCACAG 2678
QY 2437 CATTAGCTTCTGCCCCAGACAGACTTCAATGTTGCTAGCTGATGAGAGGCTGTCTGA 2496
DB 2679 CATGAGTACTTGGCGAGGTGAGCTCATCATCTCATGATGCTGCGGCGCAAGATCTCTGA 2738
QY 2497 GATGGCCGTACCCAGCCCTGCTGCGAGGCAAGGCTCTTTGGCAACTTCTCTGCNA 2556
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QY 2617 AGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCTAGCAACACCACAGGATCTGACAGA 2676

ADDRESSEE: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1512
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS
LOCATION: 196..4788
US-08-407-207A-1

Query Match 34.2%; Score 1737.8; DB 3; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

QY 25 CGGGAGCTGGCTCCAAAGTTCTGGGACTCCAACTGTCTGTGCACACAGAAAAACCGGA 84
DB 219 CGCGATGGCTCCGACCCGCTCTGGGACTGGAATGTCAGTGGATACCGACACCCCGA 278

QY 85 CTTCACTCCCTGCTTCAGAACTCCCTGCTGGGCTGGGCTGGGCTGCTACCTACCTGTTGGT 144
DB 279 CTTCAACAAGTCTTTTCAGAACACGGTCTCTGCTGGGCTGGGCTGCTTTTACCTCTGGC 338

QY 145 CGCCCTCCCTGCTACTGCTTACCTACCTGCGGCACCAATGCTGCTGCTGCTGCTGCTGCTC 204
DB 339 CTGTTTCCCTTCTACTTCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGAC 398

QY 205 CCACCTGTCACAGCTCAAGATGGTCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
DB 399 ACCTCTCAACAAAACCAAACTGCTTTGGGATTTTCTGCTGGATGCTGCTGCTGCTGCTGCTG 458

QY 265 CTTTCTTCT 324
DB 459 CTTCTTCT 518

QY 325 CACCCCTTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384
DB 519 CAGCCCAACTCTCTTGGGATCACCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578

QY 385 GCTGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
DB 579 GAGGAAGGAGTTCAGTCTTCAGGATCATGCTCAGCTTTCTGGCTGCTAGCCCTAGTGTG 638

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DB 639 TGCCTTAGCCATCCTGAGATCCAAAATTTATGACAGCCTTTAAAGAGAGATGCCCGAGTGA 698

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QY 745 CAGATCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
DB 939 CAGTCTGGAACAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998

QY 789 -----AGCAGAGAAAGCAGACGCGCACACAGGCTTCAGACAGACCTGGGAAAAA 840
DB 999 TAGGAAGCAGCGGTGAAGTTGTGTACTCTCTCAAGGATCTGCGCCAGCGGAGAGAG 1058

QY 841 TGCCTCCGGCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
DB 1059 TTCCAAGGTGGATGCGAATGAGGAGTGGAGGCTTTGTGTAAGAACTGGAAGAGGAATG 1118

QY 886 CGGAAGCCCTCTCTCTGCTGAAGCCCTGCTGCGCAGCTTCTGCTGCTGCTGCTGCTGCTGCT 945
DB 1119 GTGGAACCCCTCTCTGTTTAAAGTGTATACAGACCTTTTGGGCGCTTCTCTCTATGAG 1178

QY 946 TGCTCTTCAAGCTTATCCAGGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1005
DB 1179 CTTCTCTTCAAGGCCATCCACGACCTGATGATGTTTTCGGGCGCGCAGATCTTAAAGTT 1238

QY 1006 CTTGATCAGGTTTATCTCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1065
DB 1239 GCTCATCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1298

QY 1066 GCTGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
DB 1299 GCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1358

QY 1126 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
DB 1359 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418

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DB 1419 GGTATATCAACAACTCAGTCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1478

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DB 1479 TGTGAGCTCAGAGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1538

QY 1306 CTTGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1365
DB 1539 CTTGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1598

QY 1366 TGGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1425
DB 1599 TGGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1658

QY 1426 CGCTTCCAGTAAAGCAATGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 1485
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Db 1719 TCTCAATGGGATCAAGTCTAAAGCTTTATGCTGGAGCTGGCATTCAGACAGGT 1778
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Db 1839 GGGCAGCTTCACCTGGGTGTGCACGCCCTTCTCTGGTGGCCCTTGTCACATTTGCCCTCTA 1898
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QY 1726 GTTAAATATCTTAAGACTTCCCTCTCAACATGTGCCCCAGTTAATCAGCAACCTGACTCA 1785
Db 1959 GTTCAACATCTCCGCTTCCCTCTCAACATCTTCTCTCCCATGAGGAGCTGGAACCTGA 2018
QY 1786 GGCCAGTGTCTCTGAAGGATCCAGCAATTCCTGAGCCAAAGAGAACTTGACCCCCA 1845
Db 2019 GGGAGTGTCTCCCTCAACAGCCCTGAGGATCTTCTCTCCCATGAGGAGCTGGAACCTGA 2078
QY 1846 GAGTGTGGAAGAAAGACCATCTCCCGAGCG-----TATGCCATCACCATACACAG 1896
Db 2079 CAGCATCAGAGCAGCGCTCTCAAGACGGCGGGGCCAGACAGCATCACCCTGAGGAA 2138
QY 1897 TGGCAGCTTACCTGGGCCAGGACCTGCCCCACTCTGACAGCTGAGACATCCAGGT 1956
Db 2139 TGGCAGATTACCTGGGCCAGGAGCGACCTCCACACTGAATGGCATCACCTTCCAT 2198
QY 1957 CCGGAAAGGGGACTGGTGGCGGTGTGGGGCTGTGGGCTGTGGGAAGTCTCCCTGGT 2016
Db 2199 CCGGAAAGTGTGTGGTGGCGGTGTGGGCGGAGGTGGGCTGCGGAAAGTGTGCCCTGCT 2258
QY 2017 GTCTGCCCTGTGGGAGAGATGGAGAACTAGAAAGCAAGTGCACATGAAGGGCTCCGT 2076
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QY 2077 GGCCTATGTGCCCCAGCAGGCTGGATGCAGAACTGCATCTCTCAGGAAAGCTGTTTT 2136
Db 2319 GGCCTATGTGCCACAGCAGCGCTGGATTGAGAAATCTCTCCGAGAAACATCCTTTT 2378
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QY 2197 TGACCTGGAGATGCTGCTGTGGGATCAGACAGAGATTGGAGAGGCGGATTAACCT 2256
Db 2439 AGACCTGGAATCCTGCCAGTGGGATCGGACAGAGATTGGCAGAGGGCGTGAACCT 2498
QY 2257 GTCTGGGGCCAGCGGCTGAGTGTGGCTGAGGTGTTTACAGTGTATGCCGATAT 2316
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QY 2317 TTTCTTGTGTGATGACCCACTGTCCGCTGGACTCTCATGTGGCCAAAGCAGCATCTTGA 2376
Db 2559 TTACCTTCTGATGATTCCTCTCAGCAGTGGATGCCCATGTGGGAAACACATCTTTGA 2618
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QY 2437 CATTAGCTTCTGCCCGCAGACAGACTTCATCATTTGTGTAGCTGTATGAGCAGGTCTGA 2496
Db 2679 CATGAGCTACTTCTGCGCAGGTGGAGCTCATCATCTGATGATGAGTGGCGGCAAGATCTCTGA 2738
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Db 2739 GATGGGCTCCTACAGAGAGCTGCTGGCTCGACAGCGCGCTTGGCTGAGTTCTCGGTAC 2798
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QY 2677 CAATGATCCAGTCACTATGTGTGTCAGAGCAGTATTTATGAGACAGTGTGCTGCTGTGTC 2736
Db 2895 -----GCTGTGACGACAGTGCAGGGAAGCAACTCAGAGCAGCTCAGCAGCTCCTC 2948
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Db 2949 CTCCTATAGTGGGACA-----TCAGCAGGACCACCAACAGCAGCCGAGAACTGCAGAAA- 3003
QY 2797 GGTGCAGGTGACAGAGCGGAGGACAGATGGGACATGACCAGGAGGAGAGAGCAGCCAT 2856
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QY 2857 TGGCAGTGTGGAGCTCAGTGTGTCTGGGATTTATGCCAAGCGCTGGGCTCTGTATCCAC 2916
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QY 2917 GCTGGCCATCTCTCCTGTATGTGGGTCAAAGTGGCGCTGCCATTTGAGCCAAATGTGTG 2976
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Db 1839 GGGCACCTTCCACTGGGTCTGACGCCCTTCTTGGTGGCTTGTGACATTTGCCGCTA 1898
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Db 1899 CTTGACCATTTGAGAGAACAAACATCTTGGATGCCAGACGCTTCTGTCTTGTGGCCTT 1958
QY 1726 GTTATAATCTTAAAGACTTCCCTCAACGTCTGCCACGTTAATCAGACCTGACTCA 1785
Db 1959 GTTCAACATCTCCGCTTCCCTGAACATTTCCCCATGGTCTATCAGCAGCATCTGTGCA 2018
QY 1786 GGCAGTGTCTCTGAAACGGATCCAGCAATCTCTGAGCAAGAGGAACCTTGAACCCCA 1845
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QY 1846 GAGTGTGGAAGAAGAACCATCTCCCGAGC-----TATGCCATCACCATACACAG 1896
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QY 1897 TGCACCTTCCACTGGGCCAGGACCTTCCCGCTCTCTCACAGCCTAGACATFCCAGGT 1956
Db 2139 TGCCACATCTACCTTGGCCAGGAGCGACCTCCCACTGAATGGCATCACCCTTCTCAT 2198
QY 1957 CCGAAAGGGCACTGTGTGGCCGTGTGGGCTGTGGGCTGTGGGAAGTCTCCCTCGT 2016
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QY 2137 CGCAAGCCCTGAAACCCCAAGCCTACACAGCAGCTCTGGAGGCTGTGCCCTGTGCTAGC 2196
Db 2379 TGGATCTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCTGTGCCCTCCCTCC 2438
QY 2197 TGACCTTGGAGATGCTGCCGTGGGGATCAGACAGAGATTGGAGAGGCGCATTAACCT 2256
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QY 2317 TTTCTTGTGATGACCCCACTGTCCCGGTGTGACTCTCATGTGGCCCAAGCACATCTTTGA 2376
Db 2559 TTACCTTCTCGATGATCCCTCTCTCAGCAGTGGATGCCCATGTGGGAAACACATCTTTGA 2618
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QY 4597 CTTGAGATTTC 4607
 Db 4800 GCTGGCATATC 4810

RESULT 9
 US-08-462-109A-3
 ; Sequence 3, Application US/08462109A
 ; Patent No. 5882875
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; APPLICANT: Delevy, Roger G.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING
 ; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,109A
 ; FILING DATE:
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/966,923
 ; FILING DATE: 27-OCT-1992
 ; APPLICATION NUMBER: 08/029,340
 ; FILING DATE: 8-MAR-1993
 ; APPLICATION NUMBER: 08/141,893
 ; FILING DATE: 26-OCT-1993
 ; APPLICATION NUMBER: 08/407,207
 ; FILING DATE: 20-MAR-1995

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 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5011 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 196..4788
 ; US-08-462-109A-3

Query Match 34.2%; Score 1736.2; DB 2; Length 5011;
 Best Local Similarity 62.2%; Pred. No. 0;
 Matches 2881; Conservative 0; Mismatches 1663; Indels 87; Gaps 6;

QY 25 CGGGAGCTCGGCTCCAAAGTTCTGGACTCCAACTGTGTGACACAGAAAACCCGGA 84
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QY 85 CTTCACTCCCTGTTCCAGAACTCCCTGCTGGCGTGGGTGCGCTGACTACTGTTGGGT 144
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 Db 399 ACCTCTCAACAAACCAAACTGCTTGGGATTTTCTGTGGATCTGTCTGGCGGAGA 458
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 Db 999 TAGGAAGACAGCGGTGAAGGTTGTACTCTCCAAAGGATCTTCCCGAGCGGAAAGAG 1058
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Qy	1366	TGGAGTGCCTTTTCATGCTCTGCTGATTCACCTCAACGGAGCTGTGGCCGTGAAGATGGC	1425
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Qy	1426	CGCCTCCAGGTAAAGCAAAATGAATTTAAGGACTCGCGCATCAAGCTCAAGCTGATGAGTGA	1485
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Qy	1606	AACCACCTTCACCTGTGATGTGCAGGCCCTTCTGCTGTGACCTGATCACCTCTGGGTGA	1665
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Qy	1786	GGCAGTGTCTCTCTGAACGGATCCAGCAATTCCTGAGCCAAGAGAACTTGACCCCCA	1845
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Qy	1897	TGSCACCTTCACCTGGGCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGT	1956
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Qy	2197	TGACCTGGAGATGCTGCCTTGTGGGATCAGACAGATTGGAGGAAGGGCATTTAACTT	2256
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Qy	2257	GTCTGGGGCCAGCGCAGCGGCTCAGTCTGGCTCGAGCTGTTTACAGTGAATGCCGNAT	2316
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Db 2739 GATGGGCTCTACCCAGGAGCTGTGCTCGAGACGCGCTTCTGCTGAGTTCCTGCGTAC 2798
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Db 2799 CTATGCGACAGACAGGAGGAGGAGGATGTCAGAGAGAGACGGGTGTCACGGGCTCAGCGG 2858
QY 2617 AGAGGTAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACACACGCGATCTGACAGA 2676
Db 2859 TCCAGGAGGAGCAAGCAAAATGAGATGGCAT----- 2894
QY 2677 CAATGATCCAGTCACTATGTGTGTCAGAGACAGTATTATGAGACAGCTGAGTCCCTGTC 2736
Db 2895 -----GCTGGTGACGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTC 2948
QY 2737 CTCAGATGGGAGGACAGGCTGGCTGTACCCCGAGGCACTGGTGGTCCATCAGAGAA 2796
Db 2949 CTCCTATGTGGGGACA----TCAGCAGGCAACCAACAGCACCAGCAGAACTCGAGAA- 3003
QY 2797 GGTGAGGTGACAGAGCGGAAGGACAGATGGGCACTGACCCAGGAGGAGAAAGCAGCCAT 2856
Db 3004 ----GCTGAGGCCAAGAGGAGGAGACCTGGAGCTGATGGAGGCTGACNAGGCGGAGAC 3059
QY 2857 TGGCACTGTGGAGCTCAGTGTGTTCTGGGATATGCCAAGCGCGTGGGCTCTGTACCAC 2916
Db 3060 AGGCGAGGTCAAGCTTTCGGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119
QY 2917 GCTGGCCATCTGCTCTCTATGTGGGTCAAGTGGCGTGGCTGCCATTTGGAGCCAAATGTGTG 2976
Db 3120 CTTCCTCAGCATCTTCTTTTCATGTGAACCATTTGTCGGGCTGGCTTCCAACTATTG 3179
QY 2977 GCTCAGTGGCTGACAAATGATGCCATGCGACAGACTAGACAGAAACAACTTCCCTGAG 3036
Db 3180 GCTCAGCTCTGAGCTGATGACCCCATGCTCAACGGGACTCAGGACACACGAAAGTCCG 3239
QY 3037 GCTGGCGCTTATGTGCTTTTAGGAATTCGCAAGGGTTCTTTGGTGATGCTGGCAGCCAT 3096
Db 3240 GCTGAGCGCTATGAGCGCTGGGCAATTCACAAAGGATGCGCGTCTTTGGCTACTCCAT 3299
QY 3097 GGCATGAGGAGCGGTTGGATCCAGCTGCCCTGTGTTGACACCGCACTGCTGCACAA 3156
Db 3300 GGCCTGTCCATGTGGGGGATCTTTGGCTTCCGCTGTCTGCAAGTGGACCTGCTGCACAG 3359
QY 3157 CAAGATACGCTGCCACAGTCTCTTTTTCACACACACACACAGCGCGCATCTGAAGTGTG 3216
Db 3360 CATCTTGGGTCACCCATGAGCTTCTTTGAGGAGGACCCCAAGTGGAAACCTGGTGAACCG 3419

QY 3217 CTTCTCCAAGSACATCTATGTGTTGATGAGGTTCTTGCCCTCTGTCACTCCATCCTGCT 3276
Db 3420 CTTCTCAAGSAGCTGGACACAGTGGACTCCATCATCCGAGGCTCATCAAGATGTTTCA 3479
QY 3277 CAATTCCTTTTCAAGCGATCTCCACTCTTGTGTGATCATATGCGCCAGCAGCGCTCTT 3336
Db 3480 GGGCTCCTGTTCACGCTCATTTGGTGTGCTGATCGTTCCTGTGGCCACGCCATCGC 3539
QY 3337 CACTGTGTCTCATCTCCCTTGGCTGTCTACACCTTAGTGTGAGCGCTCTATGACG 3396
Db 3540 CGCATCATCATCCCGCCCTTGGCTCATCTCTTCTGTCAGAGGTTCTACGTGGC 3599
QY 3397 CACATCAGCGCACTGAAGCGGCTGGAATCAGTCAGCGGCTCACTATCTACTCCCACT 3456
Db 3600 TTTCTCCCGCAGCTGAAGCGCTCGAGTCGGTCAGCGCTCCCGGCTCTATTCCCATTT 3659
QY 3457 TTCGGAGACAGTACTGTGTCAGCTGTATCCCGGCTTACAAACCGCAGCGGATTTGA 3516
Db 3660 CAACGAGACCTTGTGGGGTTCAGCTCATTCGAGCCTTCGAGGAGGAGGAGCGCTTCA 3719
QY 3517 GATCATCAGTGTACTAAGGTGGATGCCAACCCAGAGAAGTGTACCCCTACATCATCTC 3576
Db 3720 CCACGAGTGAACCTGAAGGTGGAGAGAACCAAGAGGCTTATACCCAGCATCTGGC 3779
QY 3577 CAACCGTGTGCTGAGCATCGAGTGGAGTTCGTGGGAACTGCGTGGTGTCTTTGTGTC 3636
Db 3780 CAACAGTGTGCTGGCGTGGCTGGAGTGTGGGCACTGATCTCTCTGTTTGTGTC 3839
QY 3637 ACTATTTTCGCTCATCCGAGGAGCAGCTGAAACCCGGGCTGTGGGCTCTTGTGTGTC 3696
Db 3840 CTTGTTTGGGCTGATCTCCAGGCAAGCTCAGTGTCTGGCTTGTGGGCTCTCAGTGTG 3899
QY 3697 CTACTCTTCCAGTGTACTTGTCTGAACTGATATGATGATGATGATGATGATGATGATG 3756
Db 3900 TTACTATTGCAAGTCAACAGTACTTGAACCTGGTGGTGGATGATGATGATGATGATG 3959
QY 3757 ATCTAACATCTGTGGCTGTGGAGAGGTCAGAGGATCTCCAAAGACAGACAGAGGCGC 3816
Db 3960 AACCAACATCTGTGGCGTGGAGAGGTCAGAGGATTCAGAGACTCAGAGAGGAGCGC 4019
QY 3817 CTGGTGTGGAAGGACGCGCTCCGAGAGTGTGGCCCGCAGCTGGGAGGAGTGGAGTT 3876
Db 4020 CTGGCAAACTCCAGGAGACAGCTCCGCGCAGCAGCTGGCGCCAGGTGGGCGGAGT 4079
QY 3877 CCGGAATATTCTGTGGCTACCGCGCGCTAGACCTGTGTCTGAGAGACCTGAGTCT 3936
Db 4080 CCGAAGTACTGCTGCGCTACCGAGAGGACCTGGACTTCTCTCAGGACATCAATGT 4139
QY 3937 GCATGTGCAGGCTGGGAGAGGTTGGGATCTGTGGCGGCACTGGGCTGGCAAGTCTTC 3996
Db 4140 CAGCATCAATGGGGAGAAAGTTCGSCATCTGTGGGCGGAGCGGAGCTGGGAAGTCTC 4199
QY 3997 CATGACCTTTGCTGTTCGCTATCTGGAGCGGCAAGAGGTGAATTCGCAATGTATGG 4056
Db 4200 CTTGACCTTGGGCTTATTTCCGATCAACAGTCTGCCAAAGAGAGATCATCATCGATGG 4259
QY 4057 CTTCAATGTGGCAGACATCGGCTTCCATGACCTGCTCTCAGCTGACCATCATCCCGCA 4116
Db 4260 CATCAACATCGCCAAAGTTCGCGCTGACAGACCTTCCAGTCAACATCACTATCCCA 4319
QY 4117 GGACCCCATCTCTTCTCGGGGACCTTGGCATGAACCTGGACCCCTTTCGGCAGTACTC 4176
Db 4320 GGACCTGTTTCTTTTTCGGGTTCCCTCCGAATGAACCTGGACCCATTCAGCCAGTACTC 4379
QY 4177 AGAGGAGGACATTTGGTGGCTTTGGAGCTGTCCACCTGCACACGTTTGTAGCTCCCA 4236
Db 4380 GGATGAAGAAGTCTGGACGCTCCCTGGAGCTGGCCCACTGAAGGACCTTCTGTGACGCT 4439
QY 4237 GCGGCGAGGCTGAGCTTCCAGTGTCTCAGAGGCGGGGAGAACTTCAAGCTGGGCGCAG 4296
Db 4440 TCTGACAGCTAGACCAATGATGTCGAAGGCGGGGAGAACTTCAAGTGTGCGGCGAGC 4499

Qy	946	TGCTGCTTCAGCTTATCCAGGACCTGCTCTCTTCATCAATCCACAGTCTCAGCAT	1005
Db	1179	CTTCTCTCAAGGCCATCCAGACCTGATGATGTTTTCGGGGCGGAGATCTTTAAAGTT	1238
Qy	1006	CTTGATCAGGTTTATCTCCAACCCCATGSCCCCTCTCTGTTGGGGCTTCTTGTTGGCTGG	1065
Db	1239	GCTCATCAGTTGCGTAATGACAGGAAGGCCAGACTGGCAGGGCTACTTCTACACCGT	1398
Qy	1066	GCTGATGTTTCTGTGCTCCATGATCAGTTCGCTGATCTTCAACACACTATTACCACTACAT	1125
Db	1299	GCTGCTGTTGTCACTGCTGCTCGACAGCCCTCGTCTGCACCACTACTTCCACATCTG	1358
Qy	1126	CTTTGTGACTGGGGTGAAGTTTCTGACTGGGATCATGGGTGTCAATCACAGGAAGGCTCT	1185
Db	1359	CTTTCGTCACTGAGGATCAAGACCGCTGTCAATGGGGCTGTCTATCGGAAGGCCCT	1418
Qy	1186	GGTTATCACCACACTCAGTCAAACTGTCGCTCCACTGTGGGGGAAATTTGTCAACCTCATGTC	1245
Db	1419	GGTGATCACCATAATTCAGCCAGAAAATCTCCACGGTGGGGAGATTTGTCAACCTCATGTC	1478
Qy	1246	AGTGGATGCCACGCGTTCATGACCTTTGCCCTTCCCTAACTCTGCTGTGGTCAAGCAAC	1305
Db	1479	TGTGGACGCTCAGAGTTCACTGGACTTGCCACGCTACATTTAAACATGATCTGGTCAGCCCC	1538
Qy	1306	CTCTCAGATCATCTCGCGGATCTACTTCTCTGCGAGAACCTAGGTCCCTCTGTCTCTGGC	1365
Db	1539	CTTGAAGTCACTCTTGCTCTACTCTCTGTGGCTGAATCTGGGCCCTTCCCGTCTCTGGC	1598
Qy	1366	TGAGTTCGCTTTCATGGCTTCTCTGATTTCCACTCAACGGAGCTCTGGCGGTGAAGATGCG	1425
Db	1599	TGGAGTGGCGGTGATGGTCCCTCATGGTCCCGCTCAATGCTGTGATGGCGATGAAGACAA	1658
Qy	1426	CGCTTCCAGGTAAAGCAATGAAGTATCGCGCATCAAGCTGAAGCTGATGAGTGAGAT	1485
Db	1659	GAGTATCAGGTGGCCCATCAAGAGCAAGACATCGGATCAAGCTGATGAACGAAT	1718
Qy	1486	CTGAAACGGGATCAAGGTGCTGAAGCTGTAGCGCTGGGAGCCCCAGCTTCTGTAAGCAGGT	1545
Db	1719	TCCTAATGGGATCAAGTGCTAAAGCTTTATGCTTGGGAGCTGGCATTCAGGACACAAGT	1778
Qy	1546	GGAGGCATCAGCAGGTGAGCTCCAGTCTGCGCACGCGGCCCTACCTCCACACCAC	1605
Db	1779	GCTGGGCCATCAGCAGGAGGAGCTGAAGGTGCTGAAGAAGTCTGCCCTACCTGTACGCCGT	1838
Qy	1606	AACCACTTTCACCTTGATGTGAGCCCTTCTGTGTACCTGATCAACCTCTGGGTGTA	1665
Db	1839	GGCACCTTTCACCTGGGTCTGCACGCCCTTCTGTGGCCCTTGTGCACATTTGCCGTCTA	1898
Qy	1666	CGTGTACGTGGACCAACAATGTGCTGGAGCGCGAGAAGGCCPTTGTGTGTGTCTCT	1725
Db	1899	CGTGACCATTGACGAGAACATCTCGATGCCAGACAGCCCTCTGTTCTTTGGCCCT	1958
Qy	1726	GTTTATATCTTAAGCTTCCCTCAACATGCTGCCCCAGTTATACAGAACCTGACTCA	1785
Db	1959	GTTCAACATCTCCCGTTTCCCTGAACATTTCTCCCATGGTCTACAGACGATCTGTGCA	2018
Qy	1786	GGCCAGTGTCTCTGAACGGATCCAGCAATTCCTGAGCCAGAGAGAACTTGACCCCCA	1845
Db	2019	GGCGAGTGTCTCCCTCAACGCGTGAAGATCTTTCTCTCCATGAGGAGCTGGAACCTGA	2078
Qy	1846	GAGTGTGGAAGAAAGAACCATCTCCCCAGC-----TATGCCATCACCATACACAG	1896
Db	2079	CAGCATCAGACGACGCGCTGTCAAGACGCGGGGGCAGCAACAGCATCACCTGAGGAA	2138
Qy	1897	TGCACTTTCACCTGGGGCCAGGACCTGCCCCCACTCTGCACAGCCTACAGATCCAGGT	1956
Db	2139	TGCCACATTTCACTCGGGCCAGGACGACCCCTCCACACTGAATGGCATCACTTCTCCAT	2198
Qy	1957	CCGGAAGGGGCACTGTTGGCGGTGTGGGCGCTGTGGGTGTGGGAAGTCTCTCCCTGGT	2016
Db	2199	CCCCGAAGGTGCTTTGGTGGCCGTGGTGGGCGAGCTGGGCTGCGGAAGTCTGTCCCTGCT	2258
Qy	2017	GTCTGCCCTCTCGGAGAGATGGGAAGCTAGAAGGCAAAAGTCACATGAAGGGCTCCGT	2076

Db	2259	CTCAGCCCTCTTGGCTAGATGGCAAAAGTGAGGGGCACGTGGCTATCAAGGGCTCCGT	2318
Qy	2077	GGCCTATGTCCCCAGCAGCAGCATGGATCCAGAACTGCACCTCTCTCAGGAAAAACGTGCTTTT	2136
Db	2319	GGCCTATGTGCCACAGCAGCGCTGGATTTCAGATGATTCTCTCCGAGAAAACATCCTTTT	2378
Qy	2137	CGGCAAAAGCCCTGAACCCCAAGCGCTACAGCAGACTCTGGAGGCGCTGTGCTTGTGCTAGC	2196
Db	2379	TGGATGTACGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCGCTGTGCCCTCTCC	2438
Qy	2197	TGACCTGGAGATGCTGCCGTGGGGATCAGACAGAGATTGGAGAGAAGGCATTAACCT	2256
Db	2439	AGACCTGGAAATCCTGCCAGTGGGGATCGGACAGAGATTGGCAGAGAAGCGGTCAACCT	2498
Qy	2257	GTCTGGGGCCAGCGCAGCGGTGAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT	2316
Db	2499	GTCTGGGGACAGAAGCAGGCGTGAGCTGGCCGGCGCGTGACTCCACAGCTGACAT	2558
Qy	2317	TTTCTTGTCTGGATGACCCACTCTCCGCGGTGGACTCTCATGTGGCCAAAGCACATCTTTGA	2376
Db	2559	TTACCTCTTCGATGATCCCTCTCAGCAGTGTGATGCCATGTGGGAAAAACACATCTTTGA	2618
Qy	2377	CCAGCTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGAGCGCAGG	2436
Db	2619	AAATGTGATTGGCCCCCAAGGGGATGCTGAAGAACAAAGACGCGGATCTTGGTCAGCGCAC	2678
Qy	2437	CATTAGCTTCTGCCCCAGACAGACTTCATCATTTCTGCTAGCTGATGGACAGGTTGCTGA	2496
Db	2679	CATGAGCTACTTCCCGCAGTGGACGTCACTCATCTCATGCTAGTGGCGCAAGTCTCTGA	2738
Qy	2497	GATGGGCCGTATCCCAAGCCCTGCTCGAGCGCAACGGCTCTTTGCCAACTTTCTCTGCAA	2556
Db	2739	GATGGGCTCTTACCAGGAGTCTGCTGCTCGAGACGGCGCTTCCGTGAGTTTCTCGGTAC	2798
Qy	2557	CTATGCCCGGATGAGGACCAAGGCGACCTGGAGACAGCTGGACCGCGTTGGAAAGTGCG	2616
Db	2799	CTATGCCCAGCACAGACGAGGACGAGATGCAAGAGAAACGGGGTCACGGCGCTCAGCGG	2858
Qy	2617	AGAGGATTAAGAGGGCACTGCTGATTGAAGACACACTCAGCAACACACGCGATCTGACAGA	2676
Db	2859	TCCAGGAAGAGCAAGCAAAATGGAGNATGGCAT-----	2894
Qy	2677	CAATGATCCAGTCCACTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC	2736
Db	2895	-----GCTGGTCAGGCAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTC	2948
Qy	2737	CTCAGATGGGAGGACAGGTCGGCCTGTACCCCGGAGGACCTGGGTCCATCAGAGAA	2796
Db	2949	CTCCTATAGTGGGGACA----TCACGACGACCAACACGACCGCAGAACTGCAGAAA-	3003
Qy	2797	GGTGCAGGTGACAGAGCGCAAGCGAGATGGGGCACTGACCCAGGAGAGAGAAGCAGCCAT	2856
Db	3004	----GCTGAGGCCAAGAGAGAGACACCTGGNAGCTGATGAGGCTGACAAAGGCCAGAC	3059
Qy	2857	TGGCACTGTGAGCTCAGTGTGTTCTGGGATTTATGCCAAGCCGCTGGGGCTCTGTACCA	2916
Db	3060	AGGCGAGGTCAAGCTTTCCGTGCTACTGGGACTTACATGAAGGCCATCGGACTTTCATCTC	3119
Qy	2917	GCTGGGCATCTGTCTCTGTATGTGGGTCAAAGTGGCGCTGCCATTTGGAGCCAAATGTGTG	2976
Db	3120	CTTCTCTCAGCATCTTCTTTTCATGTGAACCATGTGTCCGCGCTGGCTTCCAACTATTG	3179
Qy	2977	GCTCAGTGTCTGACAAATGATGCCATGGCAGACAGTAGACAGAACACTTCCCTGAG	3036
Db	3180	GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGAGACACAGAAAGTCCG	3239
Qy	3037	GCTGGGCGCTATGCTGCTTTTAGGAATTCTCAAGGGGTTCTTGGTGTGCTGTGGCAGCCAT	3096
Db	3240	GCTGAGGCTATGAGCCCTGGGCATTTCAAGAGGATGCCGTGTTTGGCTACTCCAT	3299
Qy	3097	GGCCATGGCAGGGGTGGCATCCAGGCTGCCCGTGTGTTGCCACGACATGCTGCACAA	3156

Db 3300 GCGGCTGTCCATCGGGGGGATCTTGGGCTTCCCGTGTGTGACGTGGACCTGCTGCAACAG 3359
Qy 3157 CAAGATAGCTTCGCCACAGTCTTCTTTTTCACACACACATCAGCCGCCATCTCTGAACCTG 3216
Db 3360 CATCTGGGTTCACCATGAGCTTCTTTGACGGAGCCCAAGTGGGAACCTGGTGAACCG 3419
Qy 3217 CTTCTCAAGACATCATGTCTGTGTGATGAGGTCTTGCCGCCCTGTCACTCTCATCTGCTGCT 3276
Db 3420 CTTCTCAAGAGCTGGACACAGTGGACTTCCATGATCCCGGAGGTCTATCAAGATGTTTCAT 3479
Qy 3277 CAATCTCTTCTTCAACGCCATCTCCACTCTTTGTGTGTATCATGTGCGACGACGCCGCTCTT 3336
Db 3480 GGGCTCCTGTTCAACGTCAATGTGTGCTGTGCTGTATCTGTGCGCCAGCCCATCGC 3539
Qy 3337 CACTGTGTGTCATCTGCGCCCTGCTGTCTACACCTTAGTGAGGCTTCTTATGACG 3396
Db 3540 CGCCATCATCATCCGCCCTTGGCCCTCATCTACTTCTGCTCCAGAGTTCTACGTGGC 3599
Qy 3397 CACATCAGGGAAGTGAAGCGGCTGGAATCAGTCAGCGGCTCACTATCTACTCTCCACTT 3456
Db 3600 TTTCTCCCGGAGCTGAAGCGCCTCGAGTCGCTCAGCGCTCCCGGCTCTATTCCTCCATTT 3659
Qy 3457 TTCCGAGACAGTACTGCTGCTGCTGCTCAGCGCTTACACCGCAGCGCGGATTTGA 3516
Db 3560 CAACGAGACCTTGTGTGGGTTCAGCGTCACTTCGAGCCTTCGAGGAGCAGGAGCGCTTCAT 3719
Qy 3517 GATCATCAGTACTAAGTGGATGCTCAACACGAGAGAGTGTCTACCCCTACATCATCTC 3576
Db 3720 CCACAGAGTCACTGAAGGTGGAGAGACCAAGAGCCCTATTACCCAGCATCTGGC 3779
Qy 3577 CAACCGTGTGCTGAGCATCGGAGTGGAGTGTCTGGGAACTGCTGTGTCTTTGTCTGTC 3636
Db 3780 CAACAGTGTGCTGCGGCTGGAGTGTGGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3839
Qy 3637 ACTATTTGCGTATCGGAGGAGCAGCTGAACCGCGGCTGTGGGCTTCTGCTGCTGCT 3696
Db 3840 CTTGTTTGGGTGATCTCCAGGACAGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3899
Qy 3697 CTACTCTTCCAGTGACATTTGCTCTGAATGATGATGATGATGATGATGATGATGATGATGAT 3756
Db 3900 TTACTCATTGACGTCAACAGTACTTGAATGATGATGATGATGATGATGATGATGATGATGAT 3959
Qy 3757 ATCTAATCCTGTGTGAGAGGTCAAGAGTACTCAAGACAGACAGAGAGGCGCC 3816
Db 3960 AACCAACATCTGTGCGGCTGGAGAGCTCAAGAGTATTCAGAGACTGAGAGAGGAGGCGCC 4019
Qy 3817 CTGGTGTGGAAGGAGCGCCCTCCCGAGGTTGCGCCCACTGGGGAGTGGAGTT 3876
Db 4020 CTGGCAATCCAGAGACAGCTCCGCGCCAGCAGCTGCGCCCACTGGGGAGTGGAGTT 4079
Qy 3877 CCGGAATTTCTGTGCGCTTACCGCGCGGCTAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3936
Db 4080 CCGGAATTTCTGTGCGCTTACCGCGCGGCTAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4139
Qy 3937 GCATGTCCAGGTGGGAGAGTGGGATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGGCTGCT 3996
Db 4140 CAGCATCAATGGGGAGAGAAAGTTCGCGCATCTGGGCGGAGCGGAGCTGGGAAAGTCTGTC 4199
Qy 3997 CATGACCTTTGCTGTTCCGCTCTTGGAGGCGGCAAGGTTGAATCCGCATTTGATGG 4056
Db 4200 CTTGACCTTGGGCTTATTTTCGATCAACGAGTCTGCGGAAGGAGAGATCATCATCTGATGG 4259
Qy 4057 CTTCAATGTGGCAGACATCGGCTTCCATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4116
Db 4260 CATCAACATCGCCAGATCGGCTGACAGACCTCCGCTTCAAGATCAACATCATCTCCCA 4319
Qy 4117 GGACCCCATCTGTTCTCGGGACCTTCGCGATGAACCTGGACCCCTTCGCGACGACTACT 4176
Db 4320 GGACCCCTGTTTGTGTTTTCGGTTCCTCCGAAATGAACCTGGACCCATTCAGCCAGTACTC 4379
Qy 4177 AGAGGAGGATTTGGTGGCTTTGGAGCTTCCACCTGCACAGCTTTGTGAGCTCCCA 4236
Db 4380 GGATGAAGAGTCTGGAGCTCCCTGGAGCTGGCCCACTGAAGGACTTCTGTGTCAGCCCT 4439

Qy 4237 GCGGCGAGGCTTGGACTTCCAGTGTCTCAGAGGGCGGGGAGAAATCTCAGCTGGGCGCAGAG 4296
Db 4440 TCCTGACAGCTAGACCATGAATGTCCAGAGGCGGGGAGAACTCAGTGTGGGCGAGCG 4499
Qy 4297 CGAGCTGTGTGCTGGGCGGAGCCTGTCTCCGAAAGAGCCGATCTCTGTTTGTAGACA 4356
Db 4500 CCAGCTTGTGTGCTAGCCGGGCGCTGTCTGAGGAAGAGAAATCTCTGTTGTGATGA 4559
Qy 4357 GSCCAGAGCTGCATCGAGCTGAGACTGACAACTCTATCCAGGCTACCATCGGACCCA 4416
Db 4560 GCCCAGGAGCGGTGGACCTGGAACGAGCAGCTATCCAGTCCACCATCGGACACA 4619
Qy 4417 GTTGTATACCTGCTGCTGACCATCGCACCGGCTTAACTATATCATGAGCTACAC 4476
Db 4620 GTTCAGGAGCTGACCGCTCTCACCATCGCCACCGGCTCAACACCATCATCGAGTACAC 4679
Qy 4477 CAGGCTCTGTCTGTGGACAAAGAGTAGTAGTGAATTTGATTTCCAGCCAACTCAT 4536
Db 4680 AAGGTGTATGCTTGTGGACAAAGAGAAATCCAGGAGTACGGCGGCCCATCGGACTCT 4739
Qy 4537 TCCACTGAGCGCATCTTCTACGGGATGCCAGAGATGCTGAGCTTGCCTAAATATAT 4596
Db 4740 GCAGCAGAGAGCTCTTCTTACAGCATGGCCAAAGACCGCGCTTGGTGTGAGCCCCAGA 4799
Qy 4597 CCTGAGATTTTC 4607
Db 4800 GCTGCCATATC 4810

RESULT 12
US-08-461-384B-3
; Sequence 3, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196...4788
US-08-461-384B-3

Query Match 34.2%; Score 1736.2; DB 3; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2881; Conservative 0; Mismatches 1663; Indels 87; Gaps 6;

QY 25 CGGGAGCTCGGCTCCCAAGTTCTGGAGCTCCAACTGCTGTGTGCACACAGAAACCCGGA 84
DB 219 CGCGATGGCTCCGACCCGCTCTGGGACTGGAATGTCACGTGGAATACCAAGCAACCCGA 278
QY 85 CTTCACTCCCTGCTCCAGAACTCCCTGCTGGCTGGTGGCTGGCTGGCTGGCTGGCTGGCT 144
DB 279 CTTCAACAAGTGTCTTCAGAAACAGGTCCTGCTGGTGGTGGCTGGTGGTGGCTGGTGG 338
QY 145 CGCCCTCGCCCTGCTACTGCTCTACCTCGGGCACCAATGTCGTGGCTACATCATCTCTC 204
DB 339 CTGTTTCCCTCTACTCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGAC 398
QY 205 CCACCTGTCCAGCTCAAGATGCTCTGGGTGCTGCTGCTGTGTGTGTGTGTGTGTGTGT 264
DB 399 ACCTCTCAACAAACAAACAACTGCCCTGGGATTTTGTGTGGATCGTCTGTGGGCGAGA 458
QY 265 CTTTCTTACTCTTCCATGGCTGTGTCCATGCGCGGGCCCTGCGCCGCTGTTTCTTGT 324
DB 459 CTTCTTCTACTCTTCTGGGAAAGAGTCTGGGCAATATCTGCGCCCAAGTGTGTCTGT 518
QY 325 CACCCCTTGGTGGTGGGCTCACTGCTGTGCGCACCTGCTGATACAGTATGAGCG 384
DB 519 CAGCCCACTCTCTGGGATCAGCAGCTGCTGTACTCTTTTAATTCAGCTGAGAG 578
QY 385 GCTGAGGGGTACAGTCTTGGGGTCTCTCATATCTCTGTGTGTGTGTGTGTGTGTGTGT 444
DB 579 GAGGAAGAGGTTCAGTCTTCAAGGATCATGCTCACTTCTGTGCTGTGTGTGTGTGTGT 638
QY 445 CGCATCTGCTCCATCCGCTCCAAAGATCTTTTAGCAAGGACGAGGTGAGATCTCAGA 504
DB 639 TGCCCTAGCATCTGAGATCCAAATTAAGCAGCCTTAAAGAGAGATGCCAGAGTGA 698
QY 505 CCCCCTCCGCTTCCACACCTTCTACATCCACTTTGCGCTGGTACTCTCTGCCCTCATCTT 564
DB 699 CCGTGTTCGTGATCAGTCTTCTACGCTACTTTTCCCTCTTACTTATTCAGCTCGTCT 758
QY 565 GGCCTGCTTCAGGAGAAACCTCCATTTTCTCCGCAAGAAATGTGACCCCTAACCCCTA 624
DB 759 GTCTGTTTCTCAGATCGCTCACCCCTGTCTGGAAGCAATCCACGAGCCCTAATCCCTG 818
QY 625 CCTGAGACAGCGCTGGCTTCTCTCCGCTCTGTTTCTGGTGTTCACAAGATGGC 684
DB 819 CCGAGAGTCCAGCGCTCTCTCTGTCGAGGATCAGCTTCTGTGTGATCACAGGTTGAT 878
QY 685 CATCTATGCTACCGCATCCCTCGGAGGAGAGGACCTCTGTCTCCCTTAAAGGAGAGGA 744
DB 879 TGTCCGGGGTACCGCCAGCCCTCGAGGAGAGTGAACCTCTGTCTCTTAAACAGGAGGA 938
QY 745 CAGATCCAGATGGTGGTGCAGCAGCTGTGTGAGGATGGAGGA-----788
DB 939 CAGCTCGGAACAGTCTGCTCTGTTTGGTAAAGAACTGGAAGAAATGCGCCCAAGAC 998
QY 789 -----AGCAGGAAACAGACGACACAGAGGCTTACAGCAGCAGCTGGGAAAAA 840
DB 999 TAGGAAGCAGCGGTGAAGGTGTGTACTCTCCAGGATCTGCGCCAGCGGAAAGAG 1058
QY 841 TGCTCCGCGGAGGAGGAGTGTGTGTGGGTG-----CGCGCCCAAGGCC 885
DB 1059 TTCCAGGTGGATGCCAATGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCGCACAGAGGA 1118

QY 886 CCGGAAGCCCTCTCTCTGAGGCGCCCTGTGGCCACACTTGGCTCCAGCTTCTCTCATCAG 945
DB 1119 GTGAACCCCTCTCTGTTAAGGTGTTATACAAGACCTTTGGGCCCTTCTCTCATCAG 1178
QY 946 TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTCTCATCAATCCAGAGCTGCTCAGCAT 1005
DB 1179 CTTCTTCTTCAAGGCCATCCACGACCTGATGATGTTTTCCGGGCCGAGATCTTAAAGTT 1238
QY 1006 CTTGATCAGGTTTATCTCCAAACCCATGGCCCTCTCTGTTGGGCTTCTCTGGTGGCTG 1065
DB 1239 GCTCATCAGGTTCTGATGACAGGAAGGCCAGACTGGCAGGGCTACTTCTACACCGT 1298
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RESULT 14

US-08-462-109A-5
; Sequence 5, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340

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Db 1909 CGATCAAGAGTGGAGAGGAATAGCATCACTGTGAAGAAATGCAACTTTCACATTGGGCCA 1968
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QY	4494	ACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCCAACCTCATTTGCAGCTAGAGGCATCT	4553
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RESULT 15

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US-08-460-907B-5
: Sequence 5, Application US/08460907B
: Patent No. 5891724
: GENERAL INFORMATION:
: APPLICANT: Deeley, Roger G.
: APPLICANT: Cole, Susan P.C.
: TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
: TITLE OF INVENTION: RESISTANCE ON A CELL
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
: STREET: Queen's University at Kingston
: CITY: Kingston
: STATE: Ontario
: COUNTRY: CANADA
: ZIP: K7L 3N6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460,907B
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923

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Search completed: December 18, 2002, 21:35:15
 Job time : 169.285 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:00:25 ; Search time 635.101 Seconds
(without alignments)
18009.573 Million cell updates/sec

Title: US-09-647-140A-5

Perfect score: 5079
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5079	100.0	5079	AAZ30080	CDNA encoding a hu
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3	4586.8	90.3	4762	18 AAT94052	Human multidrug re
4	1749.4	34.4	1977	24 ABN96910	Gene #3408 used to
5	1749.4	34.4	1977	24 ABL65494	Lung cancer relate
6	1749.4	34.4	1977	24 ABL67998	Ovary cancer relat
7	1737.8	34.2	5011	15 AAO65377	Multidrug resistan
8	1737.8	34.2	5011	17 AAT17173	CDNA encoding mult
9	1737.8	34.2	5011	19 AAV31497	Human multidrug re

10	1737.8	34.2	5011	20	AAZ19817	Human multidrug re
11	1737.8	34.2	5011	20	AAZ21976	Human multidrug re
12	1737.8	34.2	5011	21	AAZ60522	Multidrug resistan
13	1737.8	34.2	5011	21	AAZ94741	Human ATP binding
14	1737.8	34.2	5011	21	AAZ90192	Human multidrug re
15	1737.8	34.2	5011	21	AAZ39555	Human multidrug re
16	1737.8	34.2	5011	24	ABK92125	Prostate cancer-as
17	1736.2	34.2	5011	19	AAV31498	Human MRP variant
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19	1736.2	34.2	5011	20	AAZ19818	Human MDR variant
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25	1612.6	31.8	5889	21	AAZ21978	Mouse multidrug re
26	1612.6	31.8	5889	21	AAZ90194	Murine multidrug r
27	1559	30.7	4885	21	AAZ39557	Murine multidrug r
28	1502.6	29.6	4864	17	AAT14910	CDNA encoding mult
29	1473	29.0	4834	17	AAT14911	CDNA encoding mult
30	1439.2	28.3	4423	17	AAT14912	CDNA encoding mult
31	1408.6	27.7	1448	21	AAZ98147	Human colon cancer
32	1210.2	23.8	4669	17	AAT14913	CDNA encoding mult
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ALIGNMENTS

RESULT 1
AAZ30080
ID AAZ30080 standard; cDNA; 5079 BP.
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AC AAZ30080;
XX
DT 26-JAN-2000 (first entry)
XX
DE CDNA encoding a human MPR-related ABC transporter designated MOAT-D.
XX
KW Human: MPR-related ABC transporter; MOAT protein; MOAT-D;
KW MOAT mediated transport; anticancer drug sensitivity;
KW transporter mediated cellular efflux; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
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FT /transl_except= (pos: 638..640, aa: Val)
FT /note= "MPR-related ABC transporter"

PN WO9949735-A1.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06644.

XX 27-MAR-1998; 98US-0079759.

XX 03-AUG-1998; 98US-0095153.

(FOX-) FOX CHASE CANCER CENT.

Kruh G, Lee K, Belinsky M, Bain L;

WPI; 1999-610812/52.

P-PSDB; RAY43543.

New transporter gene useful for screening for anti-cancer drugs

Claim 23; Page 138-140; 153pp; English.

The present sequence encodes a human MPR-related ABC transporter (MOAT) protein, designated MOAT-D. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating MOAT proteins.

Sequence 5079 BP; 1040 A; 1476 C; 1388 G; 1175 T; 0 other;

Query Match 100.0%; Score 5079; DB 20; Length 5079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	GTCTGTGCACAGAAAACCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCGTG	120
QY	121	GGTGGCTGATACATGCTGGTGGGTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
DB	121	GGTGGCTGATACATGCTGGTGGGTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
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DB	181	TTGTCGTGGGTACATCTCTCCACCTGTCTCCAACTCAAGATGTCCTGGGTGTCCT	240
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QY	301	GGCCCTGCCCCCTGTTTCTTTGTCACCCCTTGGTGGTGGGTCACCATGCTGCTGGC	360
DB	301	GGCCCTGCCCCCTGTTTCTTTGTCACCCCTTGGTGGTGGGTCACCATGCTGCTGGC	360
QY	361	CACCTCTGATACAGTATGAGGGCTGCGAGGGCTACAGTCTTCGGGGTTCCTCATAT	420
DB	361	CACCTCTGATACAGTATGAGGGCTGCGAGGGCTACAGTCTTCGGGGTTCCTCATAT	420
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DB	421	CTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
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DB	541	CCTGGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
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DB	721	CCTCTGGTCCCTAAAGGAGGACAGATCCAGATGGTGGTGCAGCAGCTGCTGGAGGC	780
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DB	841	TGCTCTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	900
QY	901	CCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	960
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DB	961	TATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1020
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Db	4081	CCATGACTCGGCTCTCAGCTGACCATCATCCCAGAGACCCCATCTGTCTCGGGGAC	4140
Qy	4141	CCTGGCATGAACCTGGACCCCTTCGGAGCTACTCAGCAGGACACATTTGGTGGGCTTT	4200
Db	4141	CCTGGCATGAACCTGGACCCCTTCGGAGCTACTCAGCAGGACACATTTGGTGGGCTTT	4200
Qy	4201	GGAGCTGTCCCACCTGCACACCTTTGTGAGTTCOCAGCCGGCAGGCGCTTCCAGTG	4260
Db	4201	GGAGCTGTCCCACCTGCACACCTTTGTGAGTTCOCAGCCGGCAGGCGCTTCCAGTG	4260
Qy	4261	CTCAGAGGGCGGGAGAACTCAGCGTGGGCCAGAGGCAGCTGTGTGCCGCCGAGC	4320
Db	4261	CTCAGAGGGCGGGAGAACTCAGCGTGGGCCAGAGGCAGCTGTGTGCCGCCGAGC	4320
Qy	4321	CCTGCTCCGCAAGCGCGCATCCTGGTTTATAGCAGAGGCCACAGCTGCATCGACCTGGA	4380
Db	4321	CCTGCTCCGCAAGCGCGCATCCTGGTTTATAGCAGAGGCCACAGCTGCATCGACCTGGA	4380
Qy	4381	GACTGACACCTCATCCAGGCTACCATCCGACCCAGTTTGATACCTGCACCTGTCTGTAC	4440
Db	4381	GACTGACACCTCATCCAGGCTACCATCCGACCCAGTTTGATACCTGCACCTGTCTGTAC	4440
Qy	4441	CATCGCACACCGCTTAACACTATCATGCACTACACAGGGTCTGTGCTGGACAAAGG	4500
Db	4441	CATCGCACACCGCTTAACACTATCATGCACTACACAGGGTCTGTGCTGGACAAAGG	4500
Qy	4501	AGTAGTAGCTGAATTGATCTCCAGCCAACTCATTTGCAGCTAGAGGCATCTCTACGG	4560
Db	4501	AGTAGTAGCTGAATTGATCTCCAGCCAACTCATTTGCAGCTAGAGGCATCTCTACGG	4560
Qy	4561	GATGGCCAGAGATGCTGGACTTGCCTAAAATATATTCCTGAGATTCCTCCTGGCCTTTC	4620
Db	4561	GATGGCCAGAGATGCTGGACTTGCCTAAAATATATTCCTGAGATTCCTCCTGGCCTTTC	4620
Qy	4621	CTGGTTTTTCATCAGGAGGAATGACACCAATATGTGCCAGAACTGATAGCAA	4680
Db	4621	CTGGTTTTTCATCAGGAGGAATGACACCAATATGTGCCAGAACTGATAGCAA	4680
Qy	4681	ACACTGGGGCACCTTAAGATTTTCACCTCTAAAGTGCCTTACAGGGTAACCTGTCTGA	4740
Db	4681	ACACTGGGGCACCTTAAGATTTTCACCTCTAAAGTGCCTTACAGGGTAACCTGTCTGA	4740
Qy	4741	ATGCTTTAGATGAGGAATGATPCCCAAGTGGTGAATGACACGCTTAAGTCCACAGCTAG	4800
Db	4741	ATGCTTTAGATGAGGAATGATPCCCAAGTGGTGAATGACACGCTTAAGTCCACAGCTAG	4800
Qy	4801	TTTGGACCAAGTTAGACTAGTCCCGGCTCCCGATCCCAACTCCCAACTGAGTGTATTGACAC	4860
Db	4801	TTTGGACCAAGTTAGACTAGTCCCGGCTCCCGATCCCAACTCCCAACTGAGTGTATTGACAC	4860
Qy	4861	TGCACGTGTTTTCAAAATAACGATTTTATGAAATGACCTCTGTCTCCTCTGATTTTTCAT	4920
Db	4861	TGCACGTGTTTTCAAAATAACGATTTTATGAAATGACCTCTGTCTCCTCTGATTTTTCAT	4920
Qy	4921	ATTTTCTAAAGTTTCGTTCTGTTTTTATPAAAAAGCTTTTTTCCCTCGTGGAGCAAGA	4980
Db	4921	ATTTTCTAAAGTTTCGTTCTGTTTTTATPAAAAAGCTTTTTTCCCTCGTGGAGCAAGA	4980
Qy	4981	CAGCTGCTGGGTCAAGCCACCCCTAGGAACCTACGTCTCTGTACTCTCGGGTGCTGCCTGAA	5040
Db	4981	CAGCTGCTGGGTCAAGCCACCCCTAGGAACCTACGTCTCTGTACTCTCGGGTGCTGCCTGAA	5040

CC	present sequence encodes a NOVX protein.									
XX										
SQ	Sequence 5193 BP; 1083 A; 1511 C; 1410 G; 1189 T; 0 other;									
	Query Match 99.9%; Score 5071.6; DB 24; Length 5193;									
	Best Local Similarity 99.9%; Pred No. 0;									
	Matches 5074; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
QY	1	CCCCATGGACGCCCTGTGCGGTTCGGGGAGCTCGGCTCCAAAGTCTTGGAGCTCCAACCT	60							
DB	67	CCCCATGGACGCCCTGTGCGGTTCGGGGAGCTCGGCTCCAAAGTCTTGGAGCTCCAACCT	126							
QY	61	GTCGTGCACACAGAAACCCGGACCTCATTCCCTGCTTCCAGAACTCCCTGCTGGGCTG	120							
DB	127	GTCGTGCACACAGAAACCCGGACCTCGCTCCCTGCTTCCAGAACTCCCTGCTGGGCTG	186							
QY	121	GGTGCCCTGCATCTACCTGTGGGTGCCCTGCCCTGCTTACTGTCTTACCTCGGSCACCA	180							
DB	187	GGTGCCCTGCATCTACCTGTGGGTGCCCTGCCCTGCTTACTGTCTTACCTCGGSCACCA	246							
QY	181	TTGTCTGGCTACATCACTCTCCACCTGTCCAAAGCTCAAGATGTCCTGGGTGTCTCT	240							
DB	247	TTGTCTGGCTACATCACTCTCCACCTGTCCAAAGCTCAAGATGTCCTGGGTGTCTCT	306							
QY	241	GCTGTGGTGGCTCTCTGGGGGACCTTTTACTTCTTCCATGGCTGGTCCATGGGCG	300							
DB	307	GCTGTGGTGGCTCTCTGGGGGACCTTTTACTTCTTCCATGGCTGGTCCATGGGCG	366							
QY	301	GGCCCTCGCCCTGTTTCTTGTACCCCTGTGTGGTGGGGTACCACTGCTGCTGGC	360							
DB	367	GGCCCTCGCCCTGTTTCTTGTACCCCTGTGTGGTGGGGTACCACTGCTGCTGGC	426							
QY	361	CACCTGCTGATACAGTATGAGCGCTGCAGGGCGTACAGTCTTCGGGGGCTCTCATAT	420							
DB	427	CACCTGCTGATACAGTATGAGCGCTGCAGGGCGTACAGTCTTCGGGGGCTCTCATAT	486							
QY	421	CTTCTGGTTCCTGTGTGGTCTGGGCCATCGTCCCATTCGCTCCAAAGATCCTTTTACG	480							
DB	487	CTTCTGGTTCCTGTGTGGTCTGGGCCATCGTCCCATTCGCTCCAAAGATCCTTTTACG	546							
QY	481	CAAGCAGAGGGTGAGATCTCAGACCCCTCCGCTTACACACCTTCTACATCCACTTTTC	540							
DB	547	CAAGCAGAGGGTGAGATCTCAGACCCCTCCGCTTACACACCTTCTACATCCACTTTTC	606							
QY	541	CCTGGTACTCTCTGCCCTCATCTTGGCTGCTTCAGGGAGAAACCTCCATTTTCTCCGC	600							
DB	607	CCTGGTACTCTCTGCCCTCATCTTGGCTGCTTCAGGGAGAAACCTCCATTTTCTCCGC	666							
QY	601	AAAGAAATGTCGACCTTAACCCCTACCTTGACACAGCGCTGGCTTCTCCCGCTGTT	660							
DB	667	AAAGAAATGTCGACCTTAACCCCTACCTTGACACAGCGCTGGCTTCTCCCGCTGTT	726							
QY	661	TTTCTGGTGGTTCAAAAGATGGCATCTATGGCTACCGGCATCCCTTGGAGGAGAAGGA	720							
DB	727	TTTCTGGTGGTTCAAAAGATGGCATCTATGGCTACCGGCATCCCTTGGAGGAGAAGGA	786							
QY	721	CCTCTGGTCCCTTAAAGGAAGAGACAGATCCAGATGGTGTGACGAGCTGCTGGAGGC	780							
DB	787	CCTCTGGTCCCTTAAAGGAAGAGACAGATCCAGATGGTGTGACGAGCTGCTGGAGGC	846							
QY	781	ATGGAGGAAGCAGGAAAGACAGACGGCACACAAAGCTTTCAGACGACCTGGGAAAAA	840							
DB	847	ATGGAGGAAGCAGGAAAGACAGACGGCACACAAAGCTTTCAGACGACCTGGGAAAAA	906							
QY	841	TGCTCCGGCAGGACGAGTGTCTGGGTGGCGCCCGCCAGCGCCCGGAAGCCCTCCTT	900							
DB	907	TGCTCCGGCAGGACGAGTGTCTGGGTGGCGCCCGCCAGCGCCCGGAAGCCCTCCTT	966							
QY	901	CCTGAAGGCCCTGTCTGGCCACCTTTCGGCTCCAGCTTCTCATAGTGCCTGCTTCAAGCT	960							
DB	967	CCTGAAGGCCCTGTCTGGCCACCTTTCGGCTCCAGCTTCTCATAGTGCCTGCTTCAAGCT	1026							
Y	961	TATCCAGGACCTGCTCTCTTTCATCAATCCACAGCTGCTCAGCATCTGATCAGGTTTAT	1020							

Db	1027	TATCCAGGACCTGCTCTCTCTTTCATCAATCCACAGCTGCTCAGCATCTGATCAGGTTTAT	1086							
Qy	1021	CTCAACCCCATGGCCCCCTCTGGTGGGCTTCCCTGGTGGGCTGATGTCCTGTG	1080							
Db	1087	CTCAACCCCATGGCCCCCTCTGGTGGGCTTCCCTGGTGGGCTGATGTCCTGTG	1146							
Qy	1081	CTCCATGATGACGTGCTGATCTTACAACACTATTACCACTATCTTCTGACTGGGT	1140							
Db	1147	CTCCATGATGACGTGCTGATCTTACAACACTATTACCACTATCTTCTGACTGGGT	1206							
Qy	1141	GAAGTTTCGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200							
Db	1207	GAAGTTTCGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1266							
Qy	1201	AGTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1260							
Db	1267	AGTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1326							
Qy	1261	CTTTCATGGACCTTTCCT	1320							
Db	1327	CTTTCATGGACCTTTCCT	1386							
Qy	1321	GGGATCTACTTCTCTGCGAGAACCTTAGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCT	1380							
Db	1387	GGGATCTACTTCTCTGCGAGAACCTTAGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCT	1446							
Qy	1381	GCTCTTCTGATTCCTCACTCAACGAGCTGTGGCCGTGAAGATCGGCGCTTCCAGGTAAA	1440							
Db	1447	GCTCTTCTGATTCCTCACTCAACGAGCTGTGGCCGTGAAGATCGGCGCTTCCAGGTAAA	1506							
Qy	1441	GCAATGAAATTTGAAGGACTCGCGCATCAAGCTGATGATGATGATGATGATGATGATGAT	1500							
Db	1507	GCAATGAAATTTGAAGGACTCGCGCATCAAGCTGATGATGATGATGATGATGATGATGAT	1566							
Qy	1501	GCTGCTGAAGCTGTACGCTTGGAGCCAGCTTCTTGAAGCAGGTGAGGCGCATCAGGCA	1560							
Db	1567	GCTGCTGAAGCTGTACGCTTGGAGCCAGCTTCTTGAAGCAGGTGAGGCGCATCAGGCA	1626							
Qy	1561	GGTGAAGCTTCCAGCTGCTGCGCAGCGGCGCTTACCTCCACACCAACACCTTACCTG	1620							
Db	1627	GGTGAAGCTTCCAGCTGCTGCGCAGCGGCGCTTACCTCCACACCAACACCTTACCTG	1686							
Qy	1621	GATGTGACGCTTCTCTGCTGACCTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1680							
Db	1687	GATGTGACGCTTCTCTGCTGACCTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1746							
Qy	1681	AAACAATGTGCTGGAGCGCGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1740							
Db	1747	AAACAATGTGCTGGAGCGCGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1806							
Qy	1741	ACTTCCCTTCAACATGCTGCCCTAGTTAATCAGCACTGACTCAGGCGCTGCTCT	1800							
Db	1807	ACTTCCCTTCAACATGCTGCCCTAGTTAATCAGCACTGACTCAGGCGCTGCTCT	1866							
Qy	1801	GAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1860							
Db	1867	GAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1926							
Qy	1861	GACCATCTCCCGAGGTATGCCATCACCATACACAGTGGCACCTTACCTGGGCCAGGA	1920							
Db	1927	GACCATCTCCCGAGGTATGCCATCACCATACACAGTGGCACCTTACCTGGGCCAGGA	1986							
Qy	1921	CCTGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1980							
Db	1987	CCTGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2046							
Qy	1981	GCTGGGCTGTGGCTGTGGGAGTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2040							
Db	2047	GCTGGGCTGTGGCTGTGGGAGTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2106							
Qy	2041	GAAGCTAGAGGCAAGTGCATGAAGGCTCCGTGGCTATGTGCTGCTGCTGCTGCTGCTGCTG	2100							

Db 2107 GAAGCTAGAGGCAAGTGCATGATGAAGGGCTCCGTGGCCCTATGTGCCCCAGCAGCATG 2166
Qy 2101 GATCCAGAACTGCACTCTTACAGAAAACGTGCTTTTCGGCAAAGCCCTGAAACCCCAAGCG 2160
Db 2167 GATCCAGAACTGCACTCTTACAGAAAACGTGCTTTTCGGCAAAGCCCTGAAACCCCAAGCG 2226
Qy 2161 CTACACGACACTCTGAGGCGCTGCTGCTAGCTGACCTGACCTGAGATGCTGCCTGGTGG 2220
Db 2227 CTACACGACACTCTGAGGCGCTGCTGCTAGCTGACCTGAGATGCTGCCTGGTGG 2286
Qy 2221 GGATCAGACAGAGATTGGAGAAAGGCAATTAACCTGCTGGGGGCCAGCGCGCAGCGGT 2280
Db 2287 GGATCAGACAGAGATTGGAGAAAGGCAATTAACCTGCTGGGGGCCAGCGCGCAGCGGT 2346
Qy 2281 CAGTCTGGCTGAGCTGTTTACAGTAGTGGGATATTTCTGCTGATGACCCACACTGTC 2340
Db 2347 CAGTCTGGCTGAGCTGTTTACAGTAGTGGGATATTTCTGCTGATGACCCACACTGTC 2406
Qy 2341 CGCGGTGCACTCTCATCTGCGCAAGCACATCTTTTGACACGTCATCGGGCCAGAGGCGT 2400
Db 2407 CGCGGTGCACTCTCATCTGCGCAAGCACATCTTTTGACACGTCATCGGGCCAGAGGCGT 2466
Qy 2401 GCTGGCAGGCAAGACGCGAGTGTGTGAGCGACGCGCATTTAGCTTCTGCCCCAGACAGA 2460
Db 2467 GCTGGCAGGCAAGACGCGAGTGTGTGAGCGACGCGCATTTAGCTTCTGCCCCAGACAGA 2526
Qy 2461 CTTGATCATTTGCTAGCTGATGAGACAGGTGCTGAGATGGGCCCGTTACCCAGCCCTGCT 2520
Db 2527 CTTGATCATTTGCTAGCTGATGAGACAGGTGCTGAGATGGGCCCGTTACCCAGCCCTGCT 2586
Qy 2521 GCAGCGCAACGGCTCCTTTGCCAACTTCTCTGCAACTATGCCCGCATGAGGACCAAGG 2580
Db 2587 GCAGCGCAACGGCTCCTTTGCCAACTTCTCTGCAACTATGCCCGCATGAGGACCAAGG 2646
Qy 2581 GCACCTGGAGGACAGCTGGACCGCGTTGGAGGTGACAGAGATGAAGAGGACACTGCTGAT 2640
Db 2647 GCACCTGGAGGACAGCTGGACCGCGTTGGAGGTGACAGAGATGAAGAGGACACTGCTGAT 2706
Qy 2641 TGAAGACACTCAGCAACACACAGGATCTGACAGACAATGATCCATGCTACCTATGTGGT 2700
Db 2707 TGAAGACACTCAGCAACACACAGGATCTGACAGACAATGATCCATGCTACCTATGTGGT 2766
Qy 2701 CCAGAGCAGTTTATGACAGACGTGAGTGCCTCTCTCAGATGGGAGGACAGGCTCG 2760
Db 2767 CCAGAGCAGTTTATGACAGACGTGAGTGCCTCTCTCAGATGGGAGGACAGGCTCG 2826
Qy 2761 GCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGACAGTGCAGAGCGCAAGGC 2820
Db 2827 GCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGACAGTGCAGAGCGCAAGGC 2886
Qy 2821 AGATGGGCACTGACCCAGGAGGAAAGACAGCCATTGGCACTGTGAGCTCAGTGTGTT 2880
Db 2887 AGATGGGCACTGACCCAGGAGGAAAGACAGCCATTGGCACTGTGAGCTCAGTGTGTT 2946
Qy 2881 CTGGGATTATGCAAGCCCTGGGGTCTCTACACGCTGGCCATCTCTCCTGTATGT 2940
Db 2947 CTGGGATTATGCAAGCCCTGGGGTCTCTACACGCTGGCCATCTCTCCTGTATGT 3006
Qy 2941 GGGTCAAAAGTGGCGCTGCCATTGGAGCCAAATGTGTGGCTCAGTGCCTGGCAAAATGATG 3000
Db 3007 GGGTCAAAAGTGGCGCTGCCATTGGAGCCAAATGTGTGGCTCAGTGCCTGGCAAAATGATG 3066
Qy 3001 CATGGCAGACAGTAGACAGAAACAACTTCCCTGAGGCTGGGCGTCTATGCTGCTTTAGG 3060
Db 3067 CATGGCAGACAGTAGACAGAAACAACTTCCCTGAGGCTGGGCGTCTATGCTGCTTTAGG 3126
Qy 3061 AATTCTGCAAGGTTCTTGTGTATGCTGCGAGCCATGTCCTGAGTGGCCATGGCAGCGGTGGCATCCA 3120
Db 3127 AATTCTGCAAGGTTCTTGTGTATGCTGCGAGCCATGTCCTGAGGCTGGGCGTCTATGCTGCTTTAGG 3186
Qy 3121 GGTGCGCGGTGCTTGACACGAGCACTGCTGACAAACAACTACGCTTCGCCACAGTCTT 3180
Db 3187 GGTGCGCGGTGCTTGACACGAGCACTGCTGACAAACAACTACGCTTCGCCACAGTCTT 3246

Qy 3181 CTTTGACACCACACCATCAGGCCGCTCCTGAACCTCTGAACCTCTTCTCAAGGACATCTATGCTGT 3240
Db 3247 CTTTGACACCACACCATCAGGCCGCTCCTGAACCTCTTCTCAAGGACATCTATGCTGT 3306
Qy 3241 TGATGAGGTTCTGGCCCTGTCTATCTCTCATGCTGCTCAANTCTCTTCTCAAGCCCATCTC 3300
Db 3307 TGATGAGGTTCTGGCCCTGTCTATCTCTCATGCTGCTCAANTCTCTTCTCAAGCCCATCTC 3366
Qy 3301 CACTCTTCTGTGCTCATATGGCCAGCACCGCTCTTCACTGTGCTCATCTCTGCCCTGGC 3360
Db 3367 CACTCTTCTGTGCTCATATGGCCAGCACCGCTCTTCACTGTGCTCATCTCTGCCCTGGC 3426
Qy 3361 TGTGCTCTACACCTTAGTGCAGCGCTTCTATGACCCACATCACGGCACTGAAGCGGT 3420
Db 3427 TGTGCTCTACACCTTAGTGCAGCGCTTCTATGACCCACATCACGGCACTGAAGCGGT 3486
Qy 3421 GGAATCAGTCAAGCGCTCACCTATCTACTCCACTTTTCGGAGACAGTGAAGTGCAG 3480
Db 3487 GGAATCAGTCAAGCGCTCACCTATCTACTCCACTTTTCGGAGACAGTGAAGTGCAG 3546
Qy 3481 TGTCTATCCGGCGCTTACAAACCGCAGCGGATTTTGAGATCATCACTGATTAAGTGA 3540
Db 3547 TGTCTATCCGGCGCTTACAAACCGCAGCGGATTTTGAGATCATCACTGATTAAGTGA 3606
Qy 3541 TGCCAAACAGAGAAGTCTGTACCCCTACATCATCTCCAAACCGGTGGCTGAGCATCGGAGT 3600
Db 3607 TGCCAAACAGAGAAGTCTGTACCCCTACATCATCTCCAAACCGGTGGCTGAGCATCGGAGT 3666
Qy 3601 GGAGTCTGTGGGAACTCGCTGGTGTCTTTGCTGCACATTTTGCCTCATCTCGGAGAG 3660
Db 3667 GGAGTCTGTGGGAACTCGCTGGTGTCTTTGCTGCACATTTTGCCTCATCTCGGAGAG 3726
Qy 3661 CAGCTTGAACCCCGGGCTGGTGGGCTTCTGTGTCTCTCTTGCAGGTGACATTTGC 3720
Db 3727 CAGCTTGAACCCCGGGCTGGTGGGCTTCTGTGTCTCTCTTGCAGGTGACATTTGC 3786
Qy 3721 TCTGAACCTGGATGATAGAAATGATGTCAAGATTGGAATCTAACATCTGAGTGTGGAG 3780
Db 3787 TCTGAACCTGGATGATAGAAATGATGTCAAGATTGGAATCTAACATCTGAGTGTGGAG 3846
Qy 3781 GGTCAAGAGTACTTCCAAAGACAGACAGAGCGGCTGGTGGTGGAAAGCAGCGGCC 3840
Db 3847 GGTCAAGAGTACTTCCAAAGACAGACAGAGCGGCTGGTGGTGGAAAGCAGCGGCC 3906
Qy 3841 TCCGAAAGTGGGCCCGCCACCGTGGGAGGTGAGTTCGGGAATTTATCTGTGCGTACCG 3900
Db 3907 TCCGAAAGTGGGCCCGCCACCGTGGGAGGTGAGTTCGGGAATTTATCTGTGCGTACCG 3966
Qy 3901 GCCGGCTAGACCTGTGTGAGAGACCTGAGTGTGATGTGACAGTGGCGGAGAGGT 3960
Db 3967 GCCGGCTAGACCTGTGTGAGAGACCTGAGTGTGATGTGATGGCTCAATGTGCGAGACATCGGCT 4026
Qy 3961 GGGATCTGGCGCGCACTGGGCTGGCAAGTCTTCCATGACCTTTTGCCTGTTCGGCAT 4020
Db 4027 GGGATCTGGCGCGCACTGGGCTGGCAAGTCTTCCATGACCTTTTGCCTGTTCGGCAT 4086
Qy 4021 CCTGGAGCGCGCAAGGTTGAAATCCGATTTGATGGCTCAATGTGCGAGACATCGGCT 4080
Db 4087 CCTGGAGCGCGCAAGGTTGAAATCCGATTTGATGGCTCAATGTGCGAGACATCGGCT 4146
Qy 4081 CCATGACCTGGCTCTCAGCTGACCATCATCCCGAGGACCCCATCTCTCGGGAC 4140
Db 4147 CCATGACCTGGCTCTCAGCTGACCATCATCCCGAGGACCCCATCTCTCGGGAC 4206
Qy 4141 CCTGCGCATGAACCTGACCCCTTCGGCAGTCTACTCAGAGGAGACATTTGGTGGCTTT 4200
Db 4207 CCTGCGCATGAACCTGACCCCTTCGGCAGTCTACTCAGAGGAGACATTTGGTGGCTTT 4266
Qy 4201 GGAGCTCTCCACTGACAGTGTGTGAGTCTCCAGCGGACGCTTGGATTCCTCAGT 4260
Db 4267 GGAGCTCTCCACTGACAGTGTGTGAGTCTCCAGCGGACGCTTGGATTCCTCAGT 4326

QY 241 GCTGTGTCGCTCTCTGGGGGAC--CTTTTTACTCTCTCCATGSCCTGGTCCATGGC 298
Db 307 GCTGTGNNNGTGTCTCTCTGGGACCTTTTTTACTCTCTCCATGSCCTGGTCCATGGC 366
QY 299 CGGGCCCTGCCCTGTTTTTCTTTGTACACCCCTTGGTGTGGGGTCAACATGCTGCTG 358
Db 367 C--GCCCTGCCCTGTTTTTCTTTGTACACCCCTTGGTGTGGGGTCAACATGCTGCTG 424
QY 359 GCCACCTGCTATACAGATATAGCGGCTGCGAGGGGTACAGTCTTCGGGGGTCTCTCAT 418
Db 425 GCCACCTGCTATACAGATATAGCGGCTGCGAGGGGTACAGTCTTCGGGGGTCTCTCAT 484
QY 419 ATCTTCTGTTCTCTGTTGTGGTCTGGGCACTGTCCTCATTCGCTCCAGATCTTTTA 478
Db 485 ATCTTCTGTTCTCTGTTGTGGTCTGGGCACTGTCCTCATTCGCTCCAGATCTTTTA 544
QY 479 GCCAAGCAGAGGGTGAATCTCAGACCCCTTCCGGTTCACACCTTCTACATCCACTTT 538
Db 545 GCCAAGCAGAGGGTGAATCTCAGACCCCTTCCGGTTCACACCTTCTACATCCACTTT 604
QY 539 GGCCTGTTCTCTGCTGCTATCTTTGGCTGCTTCAGGGAGAACTCCATTTTCTCC 598
Db 605 GGCCTGTTCTCTGCTGCTATCTTTGGCTGCTTCAGGGAGAACTCCATTTTCTCC 664
QY 599 GCAAGATGTCACCTTACCCCTTACCCCTGAGACAGCGCTGGCTTCTCTCCGGCTG 658
Db 665 GCAAGATGTCACCTTACCCCTTACCCCTGAGACAGCGCTGGCTTCTCTCCGGCTG 724
QY 659 TTTTCTGTTGTTTCAAGATGGCATCTATGGGTACCGGCATCCCTTGGAGGAGAAG 718
Db 725 TTTTCTGTTGTTTCAAGATGGCATCTATGGGTACCGGCATCCCTTGGAGGAGAAG 784
QY 719 GACCTCTGTTCCCTAAGGAAGAGACAGATCCAGATGTTGTGTCAGCAGCTGCTGAG 778
Db 785 GACCTCTGTTCCCTAAGGAAGAGAGACAGATCCAGATGTTGTGTCAGCAGCTGCTGAG 844
QY 779 GCATGAGGAAGCAGAAAGCAGAGCGGACGACACAAAGCTTCAGCAGACCTGGAAA 838
Db 845 GCATGAGGAAGCAGAAAGCAGAGCGGACGACGACAAAGCTTCAGCAGACCTGGAAA 904
QY 839 AATGCTCCGGGAGGACGAGTGTCTGTTGGTGCCTGGGCCCCAGGCCCCGGAAAGCCCTCC 898
Db 905 AATGCTCCGGGAGGACGAGTGTCTGTTGGTGCCTGGGCCCCAGGCCCCGGAAAGCCCTCC 964
QY 899 TTTCTGAAGCCCTGCTGGCAGCTTCCGGTCCAGCTTCCATATAGTGTCTGCTTCAAG 958
Db 965 TTTCTGAAGCCCTGCTGGCAGCTTCCGGTCCAGCTTCCATATAGTGTCTGCTTCAAG 1024
QY 959 CTATCCAGGACCTGCTCTCTCATCAATCCACAGCTGCTCAGCATCTCTGATCAGGTTT 1018
Db 1025 CTATCCAGGACCTGCTCTCTCATCAATCCACAGCTGCTCAGCATCTCTGATCAGGTTT 1084
QY 1019 ATCTCAACCCATGCCCCCTCTGTTGGGCTTCTGTTGGCTGGGC--TGATGTTCTT 1077
Db 1085 ATCTCAACCCATGCCCCCTCTGTTGGGCTTCTGTTGGCTGGGCTTGATGTTCTT 1144
QY 1078 GT--GCTCATGATGAGTGTGCTGATCTTACAACTATTTACACATATTTGATGTTGACT 1135
Db 1145 GTGTCTTCCATGATGAGTGTGCTGATCTTACAACTATTTACACATATTTGATGTTGACT 1204
QY 1136 GGGGTGAAGTTTGTACTGAGTATGGTGTATCTATACAGGAAGGCTCTGGTTATCAAC 1195
Db 1205 GGGGTGAAGTTTGTACTGAGTATGGTGTATCTATACAGGAAGGCTCTGGTTATCAAC 1264
QY 1196 AACTCAGTCAAGGTCGCTCCATGTTGGGGAAATTTGTCAACCTCATGTGAGTGGATGCC 1255
Db 1265 AACTCAGTCAAGGTCGCTCCATGTTGGGGAAATTTGTCAACCTCATGTGAGTGGATGCC 1324
QY 1256 CAGCGTTTCAAGACCTTGCCGCCCTTCTCAATCTGCTGTGTTGAGCAACCCCTGCAGATC 1315
Db 1325 CAGCGTTTCAAGACCTTGCCGCCCTTCTCAATCTGCTGTGTTGAGCAACCCCTGCAGATC 1384
QY 1316 ATCTGGCGATCTACTTCTCTGGGAGAACCTAGTTCCTCTCTGCTGGTGGAGTCGCT 1375

Db 1385 ATCTGGCGATCTACTTCTCTGGCAGAACCTAGTTCCTCTGCTGGTGGAGTCGCT 1444
QY 1376 TTCATGTCCTTGTCTGATTTCCACTCAACGAGCTGTGGCCGTGAAGATCGCGCCCTTCCAG 1435
Db 1445 TTCATGTCCTTGTCTGATTTCCACTCAACGAGCTGTGGCCGTGAAGATCGCGCCCTTCCAG 1504
QY 1436 GTAAGCAAAATGAATTTAAGGACTCGCGACTCAAGCTGATGAGTGAGATCCTGAACGCC 1495
Db 1505 GTAAGCAAAATGAATTTAAGGACTCGCGACTCAAGCTGATGAGTGAGATCCTGAACGCC 1564
QY 1496 ATCAAGTGTGAAGCTGTACGCTGGAGGCCAGCTTCTTGAAGCAGGTGGAGGGATC 1555
Db 1565 ATCAAGTGTGAAGCTGTACGCTGGAGGCCAGCTTCTTGAAGCAGGTGGAGGGATC 1624
QY 1556 AGCAGAGTGTGAGCTTCCAGCTGTCTGCGACGCGGCTTACCTCCACACCAACCACTTC 1615
Db 1625 AGCAGAGTGTGAGCTTCCAGCTGTCTGCGACGCGGCTTACCTCCACACCAACCACTTC 1684
QY 1616 ACCTGATGTGACGCCCCCTTCTGTTGACCTGTATCACCCTCTGGGTGAGTGTACGCTG 1675
Db 1685 ACCTGATGTGACGCCCCCTTCTGTTGACCTGTATCACCCTCTGGGTGAGTGTACGCTG 1744
QY 1676 GACCAAACTATGTGCTGGAGCGCGAGAGGCCCTTGTGTCTGTGTCTTCTTAAATATC 1735
Db 1745 GACCAAACTATGTGCTGGAGCGCGAGAGGCCCTTGTGTCTGTGTCTTCTTAAATATC 1804
QY 1736 TTAAGACTTCCCTTCAACATGTCTGCCCTAGTTAATCAGCAACCTGACTCAGGCCAGTGTG 1795
Db 1805 TTAAGACTTCCCTTCAACATGTCTGCCCTAGTTAATCAGCAACCTGACTCAGGCCAGTGTG 1864
QY 1796 TCTCTGAACGGATFCCAGCAATTCCTGAGCCAAAGAGAACTTGACCCCTCAGAGTGTGAA 1855
Db 1865 TCTCTGAACGGATFCCAGCAATTCCTGAGCCAAAGAGAACTTGACCCCTCAGAGTGTGAA 1924
QY 1856 AGAAGACCTATCTCCCGAGCTATGCCATCACCATACACAGTGGCACTTCACTTGGGCC 1915
Db 1925 AGAAGACCTATCTCCCGAGCTATGCCATCACCATACACAGTGGCACTTCACTTGGGCC 1984
QY 1916 CAGGACCTGCCCCCTACTCTGCACAGCTTAGACATCCAGGTCCCGAAAGGGGCACTGGTG 1975
Db 1985 CAGGACCTGCCCCCTACTCTGCACAGCTTAGACATCCAGGTCCCGAAAGGGGCACTGGTG 2044
QY 1976 GCGTGTGTGGGCTGTGGCTGTGGGAAATGTCCTGTTGTCTGCTGCTGCTGGAGAG 2035
Db 2045 GCGTGTGTGGGCTGTGGCTGTGGGAAATGTCCTGTTGTCTGCTGCTGGAGAG 2104
QY 2036 ATGAGAAGCTAGAGGCAAAAGTCCATGAAGGGCTCCGTTGGGCTATGTGCCCCAGCAG 2095
Db 2105 ATGAGAAGCTAGAGGCAAAAGTCCATGAAGGGCTCCGTTGGGCTATGTGCCCCAGCAG 2164
QY 2096 GCATGATCCAGAACTGCACTCTTCAGGAAAACGCTGTTTCGCAAGCCCTGAACCCC 2155
Db 2165 GCATGATCCAGAACTGCACTCTTCAGGAAAACGCTGTTTCGCAAGCCCTGAACCCC 2224
QY 2156 AAGCGTTACAGCAGACTCTGGAGGCCCTGTGCCCTGTGTAGCTGACCTGGAGATGCTGCT 2215
Db 2225 AAGCGTTACAGCAGACTCTGGAGGCCCTGTGCCCTGTGTAGCTGACCTGGAGATGCTGCT 2284
QY 2216 GGTGGGATCAGACAGATTTGAGAGAAAGGCAATTAACCTGTCTGGGGCCAGGGCAG 2275
Db 2285 GGTGGGATCAGACAGATTTGAGAGAAAGGCAATTAACCTGTCTGGGGCCAGGGCAG 2344
QY 2276 CGGCTCAGTCTGCTGAGCTGTTTACAGTGTATCCGATATTTTCTGTGATGAGCCA 2335
Db 2345 CGGCTCAGTCTGCTGAGCTGTTTACAGTGTATCCGATATTTTCTGTGATGAGCCA 2404
QY 2336 CTGTCCGGTGTGACTCTCATGTGGCCAAAGCACAATCTTTGACCACTGATCGGGCCAGAA 2395
Db 2405 CTGTCCGGTGTGACTCTCATGTGGCCAAAGCACAATCTTTGACCACTGATCGGGCCAGAA 2464
QY 2396 GCGGTGCTGCGCAGGACAGCGAGTGTGTGAGCAGCGCACTTAGCTTCTCTGCCCGC 2455

Db 2465 GGGTCTGGCAGGCAAGACGGAGTGTGTGTGACCCACGGCATATTAGCTTCTGTGCCCCAG 2524
QY 2456 ACAGACTTCATATTGTGTAGTGTATGGACAGGTGTCTGAGATGGGCCCGTACCCAGCC 2515
Db 2525 ACAGACTTCATATTGTGTAGTGTATGGACAGGTGTCTGAGATGGGCCCGTACCCAGCC 2584
QY 2516 CTGCTGCAGCGCAAGCGCTCTTTTGGCAACTTCTCTGCAACTATGTCCCCCGGATGAGGAC 2575
Db 2585 CTGCTGCAGCGCAAGCGCTCTTTTGGCAACTTCTCTGCAACTATGTCCCCCGGATGAGGAC 2644
QY 2576 CAAGGECACCTGAGGACAGCTGGACCGGTTGGAGGTGACAGAGATGAAGGAGCACATG 2635
Db 2645 CAAGGECACCTGAGGACAGCTGGACCGGTTGGAGGTGACAGAGATGAAGGAGCACATG 2704
QY 2636 CTGATTGAAGACACACTCAGCAACACACAGCGATCTGACAGACAAATGATCCAGTCACTAT 2695
Db 2705 CTGATTGAAGACACACTCAGCAACACACAGCGATCTGACAGACAAATGATCCAGTCACTAT 2764
QY 2696 GTGGTCCAGAACAGTTTATGAGACAGTGTAGTGCCTGTCTCAGATGGGAGGAGACAG 2755
Db 2765 GTGGTCCAGAACAGTTTATGAGACAGTGTAGTGCCTGTCTCAGATGGGAGGAGACAG 2824
QY 2756 GTCTGGCCTGTACCCCGGAGGACCTGGTCCATCAGAGAGGTGCAGGTGACAGAGCG 2815
Db 2825 GTCTGGCCTGTACCCCGGAGGACCTGGTCCATCAGAGAGGTGCAGGTGACAGAGCG 2884
QY 2816 AAGGACAGATGGGCACTGACCCAGGAGGAGAAAGCAGCATTTGGCAGCTGTGGAGCTCAGT 2875
Db 2885 AAGGACAGATGGGCACTGACCCAGGAGGAGAAAGCAGCATTTGGCAGCTGTGGAGCTCAGT 2944
QY 2876 GTGTTCTGGGATTTATGCCAAGCCGTGGGCTCTTACACAGCTGGCCATCTGTCTCCTG 2935
Db 2945 GTGTTCTGGGATTTATGCCAAGCCGTGGGCTCTTACACAGCTGGCCATCTGTCTCCTG 3004
QY 2936 TATGTGGTCAAGTGGCGCTGCCATTTGAGCCATGTGCTCAGTGCCTGGACAAAT 2995
Db 3005 TATGTGGTCAAGTGGCGCTGCCATTTGAGCCATGTGCTCAGTGCCTGGACAAAT 3064
QY 2996 GATGCCATGGCAGACAGTAGACAGAAACACTTCCCTGAGGCTGGGCTCTATGCTGCT 3055
Db 3065 GATGCCATGGCAGACAGTAGACAGAAACACTTCCCTGAGGCTGGGCTCTATGCTGCT 3124
QY 3056 TTAGGAATCTGCAAGGTTCTTGGTGTATGGCAGCCATGGCCATGGCAGCGGTGGC 3115
Db 3125 TTAGGAATCTGCAAGGTTCTTGGTGTATGGCAGCCATGGCCATGGCAGCGGTGGC 3184
QY 3116 ATCCAGGCTGCCGTGTGTTGCACAGGACCTGTGTGCAACAAGATACGCTCGCCACAG 3175
Db 3185 ATCCAGGCTGCCGTGTGTTGCACAGGACCTGTGTGCAACAAGATACGCTCGCCACAG 3244
QY 3176 TCCCTTTTGTACACACACCATATCAGGCGGCATCTGTAACCTCTTCCAAAGACATCTAT 3235
Db 3245 TCCCTTTTGTACACACACCATATCAGGCGGCATCTGTAACCTCTTCCAAAGACATCTAT 3304
QY 3236 GTCCGTGATGAGTGTGCCCCCTGTATCTCATCTGCTGCTCAATTCCTTTTCAAGCC 3295
Db 3305 GTCCGTGATGAGTGTGCCCCCTGTATCTCATCTGCTCAATTCCTTTTCAAGCC 3364
QY 3296 ATCTCCACTCTGTGTGTCATCATGCGCACAGCGCGCTCTTCACTGTGTGTCATCTCGCC 3355
Db 3365 ATCTCCACTCTGTGTGTCATCATGCGCACAGCGCGCTCTTCACTGTGTGTCATCTCGCC 3424
QY 3356 CTGCTGTGCTTACACCTTATGTCAGCGCTTCTATGACGCCACATCAGGCAACTGAAG 3415
Db 3425 CTGCTGTGCTTACACCTTATGTCAGCGCTTCTATGACGCCACATCAGGCAACTGAAG 3484
QY 3416 CGGCTGGAATCAGTCAAGCGCTCACTATCTACTCCCACTTTTCGGAGACAGTGAAGTGT 3475
Db 3485 CGGCTGGAATCAGTCAAGCGCTCACTATCTACTCCCACTTTTCGGAGACAGTGAAGTGT 3544
QY 3476 GCCAGTGTATCCGGGCTTACAACCGCAGCGGGATTTTGAGATCATCAGTGAATCAAG 3535
Db 3545 GCCAGTGTATCCGGGCTTACAACCGCAGCGGGATTTTGAGATCATCAGTGAATCAAG 3604

QY 3536 GTGATGCCAACACAGAGAAGCTGTACCCCTACATCATCTCCAACCGTGGCTGAGCATC 3595
Db 3605 GTGATGCCAACACAGAGAAGCTGTACCCCTACATCATCTCCAACCGTGGCTGAGCATC 3664
QY 3596 GGAGTGGAGTTCGTGGGAACTCGTGGTGTCTTTTGTGCTGCACTATTGTGCGGTCATCGG 3655
Db 3665 GGAGTGGAGTTCGTGGGAACTCGTGGTGTCTTTTGTGCTGCACTATTGTGCGGTCATCGG 3724
QY 3656 AGAGCAGCCTGAACCCGGGGCTGTGGGCTTTCTGTGTCTTACTCTTGTGAGGTGACA 3715
Db 3725 AGAGCAGCCTGAACCCGGGGCTGTGGGCTTTTCTGTGTCTTACTCTTGTGAGGTGACA 3784
QY 3716 TTTGTCTGAACCTGAGTATACGAATGATGTCAAGATTTTGAATCTAACATCGTGGGTGTG 3775
Db 3785 TTTGTCTGAACCTGAGTATACGAATGATGTCAAGATTTTGAATCTAACATCGTGGGTGTG 3844
QY 3776 GAGAGGTTCAAGAGTACTTCCAAAGACAGACAGAGCGCCCTGGGTGTGGAAAGCAGC 3835
Db 3845 GAGAGGTTCAAGAGTACTTCCAAAGACAGACAGAGCGCCCTGGGTGTGGAAAGCAGC 3904
QY 3836 CGCCCTCCGAAAGTTGGCCCCCAGCTGGGGAGTGGAGTTCGGGAATTAATCTGTGCGC 3895
Db 3905 CGCCCTCCGAAAGTTGGCCCCCAGCTGGGGAGTGGAGTTCGGGAATTAATCTGTGCGC 3964
QY 3896 TACCGCGCGGCTAGACCTGTGTGAGAGACCTGAGTGTGATGTGACGCTGACGCTGGCGAG 3955
Db 3965 TACCGCGCGGCTAGACCTGTGTGAGAGACCTGAGTGTGATGTGACGCTGACGCTGGCGAG 4024
QY 3956 AAGGTGGGATCGTGGCGGCTGAGAGTGTGGCAAGTCTTCCATGACCCCTTTGCCCTGTT 4015
Db 4025 AAGGTGGGATCGTGGCGGCTGAGAGTGTGGCAAGTCTTCCATGACCCCTTTGCCCTGTT 4084
QY 4016 CGCATCTCGAGCGCGCAAGGTTGAATCCGAGTGTGAGGCTCAATGTGGCAGACATC 4075
Db 4085 CGCATCTCGAGCGCGCAAGGTTGAATCCGAGTGTGAGGCTCAATGTGGCAGACATC 4144
QY 4076 GGCCTCATGACCTGGCTCTCAGCTGACATCATCCCGCAGGACCCCATCTCTGTTCTCG 4135
Db 4145 GGCCTCATGACCTGGCTCTCAGCTGACATCATCCCGCAGGACCCCATCTCTGTTCTCG 4204
QY 4136 GGGACCTCGCATGAACCTGACCCCTTTCGGCAGCTACTCAGAGGAGGACATTTGGTGG 4195
Db 4205 GGGACCTCGCATGAACCTGACCCCTTTCGGCAGCTACTCAGAGGAGGACATTTGGTGG 4264
QY 4196 GCTTTGGAGCTGTCCACCTGCACAGTGTGTGAGTCTCCAGCGGCGGCTGGACTTC 4255
Db 4265 GCTTTGGAGCTGTCCACCTGCACAGTGTGTGAGTCTCCAGCGGCGGCTGGACTTC 4324
QY 4256 CAGTGTCTCAGAGGGGGGAGAAATCTCAGCGTGGGCGCAGAGGAGCTCGTGTGCTGGCC 4315
Db 4325 CAGTGTCTCAGAGGGGGGAGAAATCTCAGCGTGGGCGCAGAGGAGCTCGTGTGCTGGCC 4384
QY 4316 CGAGCCCTGCTCCGAAAGCGCGCATCTCTGGTGTGTAGAGGCGCCACAGCTGCCATCGAC 4375
Db 4385 CGAGCCCTGCTCCGAAAGCGCGCATCTCTGGTGTGTAGAGGCGCCACAGCTGCCATCGAC 4444
QY 4376 CTGGAGACTGACAACCTCATCCAGGCTACCATCCGACCCAGTTTGAATACCTGCACTGTC 4435
Db 4445 CTGGAGACTGACAACCTCATCCAGGCTACCATCCGACCCAGTTTGAATACCTGCACTGTC 4504
QY 4436 CTGACCTCGCACACCGGCTTAACACTATCATGGACTACACAGGCTCTGCTCTGGAC 4495
Db 4505 CTGACCTCGCACACCGGCTTAACACTATCATGGACTACACAGGCTCTGCTCTGGAC 4564
QY 4496 AAAGAGTAGTAGTGAATTTGATTTCTCAGGCCAACCTCAATTTGACAGTGAAGCATCTTC 4555
Db 4565 AAAGAGTAGTAGTGAATTTGATTTCTCAGGCCAACCTCAATTTGACAGTGAAGCATCTTC 4624
QY 4556 TACGGATGGCCAGAGATGCTGGACTTGCCTAAATATATTTCTGAGATTTCTCTCTGGC 4615
Db 4625 TACGGATGGCCAGAGATGCTGGACTTGCCTAAATATATTTCTGAGATTTCTCTCTGGC 4684

QY	4616	CTTCTCCTGGTTTTTCATCAGGAAGGAATGACACCAAAATATGTCCGCGAATGGACTTG	4677
Db	4685	CTTCTCCTGGTTTTTCATCAGGAAGGAATGACACCAAAATATGTCCGCGAATGGACTTG	4742
RESULT 4			
ABN96910	ID	ABN96910 standard; DNA; 1977 BP.	
XX	AC	ABN96910;	
XX	AC	ABN96910;	
XX	DF	13-AUG-2002 (first entry)	
XX	XX	Gene #3408 used to diagnose liver cancer.	
XX	XX	Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;	
XX	KW	metastatic liver tumour; cytostatic; expression profile; disease sta	
XX	KW	disease progression; drug toxicity; drug efficacy; drug metabolism.	
XX	OS	Homo sapiens.	
XX	FN	WO200229103-A2.	
XX	XX	11-APR-2002.	
XX	XX	02-OCT-2001; 2001WO-US30589.	
XX	PF	02-OCT-2000; 2000US-237054P.	
XX	PR	(GENE-) GENE LOGIC INC.	
XX	PA	Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;	
XX	PI	WPI; 2002-426119/45.	
XX	DR	Diagnosing and detecting the progression of liver cancer,	
XX	PT	hepatocellular carcinoma or metastatic liver tumor in a patient,	
XX	PT	involves detecting the level of expression of two or more genes in a	
XX	PT	liver tissue sample	
XX	XX	Claim 1; SEQ ID NO 3408; 298pp; English.	
XX	CC	The invention relates to a novel method for diagnosing and detecting	
XX	CC	progression of liver cancer, hepatocellular carcinoma or metastatic	
XX	CC	tumour in a patient, and differentiating metastatic liver cancer from	
XX	CC	hepatocellular carcinoma in a patient, involving detecting the level	
XX	CC	expression of two or more genes represented in ABN93503-ABN97455 in a	
XX	CC	tissue sample. The method of the invention has hepatotropic, and	
XX	CC	cytostatic activity. The method is useful for diagnosing and detecting	
XX	CC	the progression of liver cancer, hepatocellular carcinoma and metast	
XX	CC	liver carcinoma in a patient. The method is useful for identifying	
XX	CC	expression profiles which serve as useful diagnostic markers as well	
XX	CC	markers that can be used to monitor disease states, disease progress	
XX	CC	drug toxicity, drug efficacy and drug metabolism.	
XX	CC	Note: The sequence data for this patent did not form part of the prin	
XX	CC	specification, but was obtained in electronic format directly from WFO	
XX	CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX	XX	Sequence 1977 BP; 450 A; 537 C; 513 G; 469 T; 8 other;	
QY	3134	TTGCACACGAGCAGTCGTCACACAAAGATACGCTCGCCACAGTCCTTCTTTGACACACCA	310
Db	1	TTGCACACGAGCAGTCGTCACACAAAGATACGCTCGCCACAGTCCTTCTTTGACACACCA	60
QY	3194	CCATCAGCGCGCATCCTCGAACTGCTTCTCCAAGGACATCATGTGCG--TTTCATCAGGTC	32
Db	61	CCATCAGCGCGCATCCTCGAACTGCTTCTCCAAGGACATCATGTGCGCTTGTAGGAGTTC	120
QY	3252	TGGCCCCGTGTCATCCTCAT-GCTGCTCAATTCCTTCTTCAACGCCATCTCCACATCTTGTG	331
QY	3252	TGGCCCCGTGTCATCCTCAT-GCTGCTCAATTCCTTCTTCAACGCCATCTCCACATCTTGTG	331

Db 1196 CCGAAGAGCCGCTTCCTGGTTTTAGACGAGGCCACAGCTGCCATCGACCTGGAGACTGA 1255
 Qy 4387 CAACCTATCCAGGCTACCATCCGACCCAGTTTGATACCTGCATCTGCTGACCATCGC 4446
 Db 1256 CAACCTATCCAGGCTACCATCCGACCCAGTTTGATACCTGCATCTGCTGACCATCGC 1315
 Qy 4447 ACACGGCTTAACACTATCATGGACTACACAGGCTCTGCTGCTGGACAAAGAGTAGT 4506
 Db 1316 ACACGGCTTAACACTATCATGGACTACACAGGCTCTGCTGCTGGACAAAGAGTAGT 1375
 Qy 4507 AGCTGAATTTGATCTCCAGCAACCTCATTCAGCTAGAGCATCTCTACGGGATGCG 4566
 Db 1376 AGCTGAATTTGATCTCCAGCAACCTCATTCAGCTAGAGCATCTCTACGGGATGCG 1435
 Qy 4567 CAGAGTCTGGACTTGCCTAAATATATCTCTGAGATTTCTCTGCTGCTCTCTCTGCTT 4626
 Db 1436 CAGAGTCTGGACTTGCCTAAATATAT -CTGAGATTTCTCTGCTGCTCTCTCTGCTT 1493
 Qy 4627 TTATCAGGAAGGAATGACACCAATATGTCGGAGATGGACTTGTATGACAAACACTG 4686
 Db 1494 TTATCAGGAAGGAATGACACCAATATGTCGGAGATGGACTTGTATGACAAACACTG 1553
 Qy 4687 GGGCACCTTAAGA-TTTTGCACCTGTAAGTGCCTTACAGGGTAACGTGCTGAATGCT 4745
 Db 1554 GGGCACCTTAAGATTTTGCCTGTAAGTGCCTTACAGGGTAACGTGCTGAATGCT 1613
 Qy 4746 TTATGAGGAAATGATCCCAAGTGTGTAATGACACGCTTAAGTGCACACTAGTTTGA 4805
 Db 1614 TTATGAGGAAATGATCCCAAGTGTGTAATGACACGCTTAAGTGCACACTAGTTTGA 1673
 Qy 4806 GCCAGTTAGACTAGTCCCGGTCTCCGATTCCTCAAGTGTATTTGACACTGAC 4865
 Db 1674 GCCAGTTAGACTAGTCCCGGTCTCCGATTCCTCAAGTGTATTTGACACTGAC 1733
 Qy 4866 TGTTCCTCAATGAGTATTTGAAATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4925
 Db 1734 TGTTCCTCAATGAGTATTTGAAATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1793
 Qy 4926 CTAAAGTTTCGTTCTTTTATTTTAAATGAGTATTTTCTCTGCTGCTGCTGCTGCTGCT 4985
 Db 1794 CTAAAGTTTCGTTCTTTTATTTTAAATGAGTATTTTCTCTGCTGCTGCTGCTGCTGCT 1853
 Qy 4986 GCTGGGTGAGCCACCCCTAGGAATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5045
 Db 1854 GCTGGGTGAGCCACCCCTAGGAATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1913
 Qy 5046 TAAATGAGGAGTACTGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 5078
 Db 1914 TAAATGAGGAGTACTGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1946

RESULT 5
 ID ABL65494
 XX ABL65494 standard; DNA; 1977 BP.
 AC ABL65494;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:3831.
 XX
 DE Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2001194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 22-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 (AVAL-) AVALON PHARM.
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.
 Screening for anti-neoplastic agent involves exposing cells to a
 chemical agent to be tested for anti-neoplastic activity, and
 determining a change in expression of a gene of a signature gene set
 Claim 1; SEQ ID 3831; 44pp; English.
 The present invention describes a method (M1) for screening for an
 anti-neoplastic agent. The method involves exposing cells to a chemical
 agent to be tested for anti-neoplastic activity, determining a change in
 expression of at least one gene (I) of a signature gene set, where (I)
 comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 to ABL701110), or is at least 95% identical to (S), where a change in
 expression is indicative of anti-neoplastic activity. (I) has cytostatic
 activity and can be used in gene therapy. M1 can be used for screening
 an anti-neoplastic agent, and can be used for producing a product which
 is the data collected with respect to the anti-neoplastic agent as a
 result of M1, and the data is sufficient to convey the chemical
 structure and/or properties of the agent. M1 can be used in the
 treatment of cancer such as colon, breast, stomach, lung, thyroid,
 oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

CC carcinoma, papillary carcinoma and Wilm's tumour.

XX Sequence 1977 BP; 450 A; 537 C; 513 G; 469 T; 8 other;

SQ Query Match 34.4%; Score 1749.4; DB 24; Length 1977;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;

QY 3134 TTGCACAGGCACTGTGTCACACAAAGATACGCTGCGCACAGTCTTCTTTTGACACCACA 3193
DB 1 TTGCACAGGCACTGTGTCACACAAAGATACGCTGCGCACAGTCTTCTTTTGACACCACA 60
QY 3194 CCATCAGGCGGCACTGTAAGTCTTCTTCAAGGACATCTATGTCG--TTGATGAGGTTTC 3251
DB 61 CCATCAGGCGGCACTGTAAGTCTTCTTCAAGGACATCTATGTCGCTTTGATGAGGTTTC 120
QY 3252 TGGCCCTGTGTCATCTCAT--GCTGCTCAATTCCTTCAAGGCACTCTCCACTCTTGTG 3310
DB 121 TGGCCCTGTGTCATCTCAT--GCTGCTCAATTCCTTCAAGGCACTCTCCACTCTTGTG 180
QY 3311 GTCATCATGCGGCAAGCAGCGCG--CTCTTCACTGTGCTATGTCATGTCGCGCTGCTG 3367
DB 181 GTCATCATGCGGCAAGCAGCGCGCTTCTTCAAGGCACTCTTCAAGGCACTCTCCACTCT 240
QY 3368 -TACACCTTGTGTCAGGCTTCTATGACGCCACATCACGGCACTGAGCGGCTGGAATC 3426
DB 241 TTAACCTTGTGTCAGGCTTCTATGACGCCACATCACGGCACTGAGCGGCTGGAATC 300
QY 3427 AGTCAGCGGCTCACCTTATCTACCTCCACTTTTCGGAGACAGTGGTGGCCAGTGTTCAT 3486
DB 301 AGTCAGCGG-TCACCTTATCTACCTCCACTTTTCGGAGACAGTGGTGGCCAGTGTTCAT 359
QY 3487 CCGGGCTTCAACCGCAGCGCGGATTTTGGATCATCATGATCATGATCACTAAGTGGATGCAA 3546
DB 360 CCGGGCTTCAACCGCAGCGCGGATTTTGGATCATCATGATCATGATCACTAAGTGGATGCAA 419
QY 3547 CCAGAGAAGTGTCTCCCTACATCATCTCCACCGGTGGCTGAGCATCGAGTGGAGTT 3606
DB 420 CCAGAGAAGTGTCTCCCTACATCATCTCCACCGGTGGCTGAGCATCGAGTGGAGTT 479
QY 3607 CTTGGGGAATCGTGGTGTCTTTCTGCTGCACTATTTGCGTCTATGCGGAGGAGCAGCCT 3666
DB 480 CTTGGGGAATCGTGGTGTCTTTCTGCTGCACTATTTGCGTCTATGCGGAGGAGCAGCCT 539
QY 3667 GAACCGGGGCTGGTGGGCTTTCTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3726
DB 540 GAACCGGGGCTGGTGGG-CTTCTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
QY 3727 CTGGATGATACGAATCATGTCAGATTTTGAATCTAACATCGTGGCTGTGGAGAGGTCAA 3786
DB 599 CTGGATGATACGAATCATGTCAGATTTTGAATCTAACATCGTGGCTGTGGAGAGGTCAA 658
QY 3787 GGAGTACTCCAAGACAGACAGAGCGCCCTGGTGGTGGAGGAGCGCGCCCTCCCGA 3846
DB 659 GGAGTACTCCAAGACAGACAGAGCGCCCTGGTGGTGGAG--CAGCGCCCTCCCGA 716
QY 3847 AGTTGGCCCCCAGCTGGGGAGTGGAGTTCGGGAATTAATCTGCTGCTGCTGCTGCTGCTG 3906
DB 717 AGTTGG-CCCCAGCTGGGGAGTGGAGTTCGGGAATTAATCTGCTGCTGCTGCTGCTGCTG 775
QY 3907 CTTAGACCTGGTGTGAGAGACTGAGTGTGATGTCATGTCAGGCTGGCGAGAAGTGGGAT 3966
DB 776 CTTAGACCTGGTGTGAGAGACTGAGTGTGATGTCATGTCAGGCTGGCGAGAAGTGGGAT 835
QY 3967 CTTGGGCCGCTGGGGCTGGCAAGTCTTCCATGACCCCTTTGCTGCTGCTGCTGCTGCTG 4026
DB 836 CTTGGGCCGCTGGGGCTGGCAAGTCTTCCATGACCCCTTTGCTGCTGCTGCTGCTGCTG 895
QY 4027 GCGGCAAAAGGTGAATCCGCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4086
DB 896 GCGGCAAAAGGTGAATCCGCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
QY 4087 CTTGGCCTCTCAGCTGACCATCATCCCGAGGACCCCATCTCTGCTGCTGCTGCTGCTGCTG 4146

RESULT 6
ABL67998
ID ABL67998 standard; DNA; 1977 BP.
XX
AC ABL67998;

DB 956 CCTCGCTCTCAGCTGACCATCATCCGCGAGACCCCATCTGTCTCTCGGGACCTGCG 1015
QY 4147 CATCAACTGGACCCCTTCGGCAGCTACTCAGAGGAGACATTTGGTGGCTTTGGAGCT 4206
DB 1016 CATCAACTGGACCCCTTCGGCAGCTACTCAGAGGAGACATTTGGTGGCTTTGGAGCT 1075
QY 4207 GTCCCACTGCACACGTTTGTGAGTCTCCAGCCGCGAGCGCTGGAGCTTCCAGTGTCTG 4266
DB 1076 GTCCCACTGCACACGTTTGTGAGTCTCCAGCCGCGAGCGCTGGAGCTTCCAGTGTCTG 1135
QY 4267 GGGCGGGAGAAATCTCAGCTGGGCCAGAGGAGCTGCTGTGCTGCTGGCCCGAGCCCTGCT 4326
DB 1136 GGGCGGGAGAAATCTCAGCTGGGCCAGAGGAGCTGCTGTGCTGCTGGCCCGAGCCCTGCT 1195
QY 4327 CCGCAAGCGCGCATCTCTGTTTGTAGACGAGGCGCACAGCTGCCATCGACCTGGAGCTGA 4386
DB 1196 CCGCAAGCGCGCATCTCTGTTTGTAGACGAGGCGCACAGCTGCCATCGACCTGGAGCTGA 1255
QY 4387 CAACCTCATCCAGGCTACCATCCGACCCAGTTTGTATACCTGACCTGTCTGTGACCATGCG 4446
DB 1256 CAACCTCATCCAGGCTACCATCCGACCCAGTTTGTATACCTGACCTGTCTGTGACCATGCG 1315
QY 4447 ACACCGGCTTAAACACTATATGAGTACACAGGCTTCTGTCTGTGACAAAGGAGTAGT 4506
DB 1316 ACACCGGCTTAAACACTATGAGTACACAGGCTTCTGTCTGTGACAAAGGAGTAGT 1375
QY 4507 AGCTGAATTTGATTCTCCAGCCACCTCATTTGACGCTAGAGGATCTTCTACGGGATGCG 4566
DB 1376 AGCTGAATTTGATTCTCCAGCCACCTCATTTGACGCTAGAGGATCTTCTACGGGATGCG 1435
QY 4567 CAGAGATGCTGGACTTGGCTTAAATATATTTCTGAGATTTCTCTCTGCGCTTCTCTGCTG 4626
DB 1436 CAGAGATGCTGGACTTGGCTTAAATATAT--CTGAGATTTCTCTCTGCGCTTCTCTGCTG 1493
QY 4627 TTCAATCAGGAGGAATGACACCAATATATGTCGCGCAAGTGGACTGTATGACAAACACTG 4686
DB 1494 TTCAATCAGGAGGAATGACACCAATATATGTCGCGCAAGTGGACTGTATGACAAACACTG 1553
QY 4687 GGGGCACTTTAAGA--TTTTCACCTGTAAAGTGTCTTACAGGTAACCTGTCTGCAATGCT 4745
DB 1554 GGGGCACTTTAAGATTTTTCACCTGTAAAGTGTCTTACAGGTAACCTGTCTGCAATGCT 1613
QY 4746 TTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCTTAAGGTACAGCTAGTTTGA 4805
DB 1614 TTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCTTAAGGTACAGCTAGTTTGA 1673
QY 4806 GCCAGTTAGACTAGTCCCGGCTCCCGATTCGCGATTCGCAACTGAGTGTATTTGACACTGCAC 4855
DB 1674 GCCAGTTAGACTAGTCCCGGCTCCCGATTCGCGATTCGCAACTGAGTGTATTTGACACTGCAC 1733
QY 4866 TGTTCCTCAATAACGATTTTATGAAATGACCTCTGCTCTCTCTCTGATTTTTCATATTTT 4925
DB 1734 TGTTCCTCAATAACGATTTTATGAAATGACCTCTGCTCTCTCTCTGATTTTTCATATTTT 1793
QY 4926 CTAAAGTTTCTGTTCTGTTTCTTAAATAAGCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 4985
DB 1794 CTAAAGTTTCTGTTCTGTTTCTTAAATAAGCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 1853
QY 4986 GCTGGCTCAGGCGCACCCCTAGGAACCTCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 5045
DB 1854 GCTGGCTCAGGCGCACCCCTAGGAACCTCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1913
QY 5046 TAAATATGGAGTACTGATGAAATAAATACATCA 5078
DB 1914 TAAATATGGAGTACTGATGAAATAAATACATCA 1946

XX DT 15-MAY-2002 (first entry)
 XX DE Ovary cancer related gene sequence SEQ ID NO: 6335.
 XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 XX KW gene; ds.
 XX OS Homo sapiens.
 XX PN WO200194629-A2.
 XX PD 13-DEC-2001.
 XX PF 30-MAY-2001; 2001WO-US10838.
 XX PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX PA (AVAL-) AVALON PHARM.
 XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI: 2002-188264/24.
 XX PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX Claim 1; SEQ ID 6335; 44pp; English.
 PS

XX The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX
 SQ Sequence 1977 BP; 450 A; 537 C; 513 G; 469 T; 8 other;
 Query Match 34.4%; Score 1749.4; DB 24; Length 1977;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;
 QY 3134 TTGCACGAGGCACTGCTGCACAAAGATACGCTCGCCACAGTCTCTTTGACACCACA 3193
 Db 1 TTGCACGAGGCACTGCTGCACAAAGATACGCTCGCCACAGTCTCTTTGACACCACA 60
 QY 3194 CCATCAGGCGGCATCCTGAACTCTTCCAAAGGACATCTATGTCG--TTGATGAGGTTG 3251
 Db 61 CCATCAGGCGGCATCCTGAACTCTTCCAAAGGACATCTATGTCGCTTTGATGAGGTTG 120
 QY 3252 TGCCCGCTGTCATCTCTCAT--GCTGCTCAATCTCTTCAACGCCATCTCCACTCTTGTG 3310
 Db 121 TGCCCGCTGTCATCTCTCATCTCAACGCCATCTCTTCAACGCCATCTCCACTCTTGTG 180
 QY 3311 GTCATCATGGCCAGCAGCGCG--CTCTTCACTGTGTCTCTCTGCTGCTGCTGCTGCTC 3367
 Db 181 GTCATCATGGCCAGCAGCGGATCTTNACTTGTGGTNNANTGCCCCCTGGGTGCTGCTC 240
 QY 3368 -TACACCTTAGTCAGCGCTTCTATGAGCCACATCACGGCAACTGAAGCGGCTGGAATC 3426
 Db 241 TTACACCTTAGTCAGCGCTTCTATGAGCCACATCACGGCAACTGAAGCGGCTGGAATC 300
 QY 3427 AGTCAGCGCTCACTCTATCTACTCCACTTTTCGGAGACAGTCACTGGTCCAGTGTCTAT 3486
 Db 301 AGTCAGCGG-TCACTCTATCTACTCCACTTTTCGGAGACAGTCACTGGTCCAGTGTCTAT 359
 QY 3487 CCGGGCTTACAAACCGCAGCGGGATTTTGAGATCATCATGATCACTAAGTGGATGCCAA 3546
 Db 360 CCGGGCTTACAAACCGCAGCGGGATTTTGAGATCATCATGATCACTAAGTGGATGCCAA 419
 QY 3547 CCAGAGAAGTGTCTACCCCTATCATCTCTCAACCGGTGGCTGAGCATCGGAGTGGAGTT 3606
 Db 420 CCAGAGAAGTGTCTACCCCTATCATCTCTCAACCGGTGGCTGAGCATCGGAGTGGAGTT 479
 QY 3607 CGTGGGAACTGGGTGCTCTTCTGCTGCACTATTTGCGGCTCATCGGAGGAGGAGCCT 3666
 Db 480 CGTGGGAACTGGGTGCTCTTCTGCTGCACTATTTGCGGCTCATCGGAGGAGGAGCCT 539
 QY 3667 GAACCCGGGCTGGTGGGCTTTCTGTGCTCTACTCTTCTGAGTGCACATTTGCTCTGAA 3726
 Db 540 GAACCCGGGCTGGTGGG-CTTCTGTGCTCTACTCTTCTGAGTGCACATTTGCTCTGAA 598
 QY 3727 CTGGATGATACGAATGATGTCAGATTTTGAATCTAATCATCTGTGGCTGTGAGAGGTCAA 3786
 Db 599 CTGGATGATACGAATGATGTCAGATTTTGAATCTAATCATCTGTGGCTGTGAGAGGTCAA 658
 QY 3787 GGAGTACTCCAGACAGACAGAGAGCGCCCTCTGGGTGGTGGAGGAGGAGGAGGAGCCTCCGA 3846
 Db 659 GGAGTACTCCAGACAGACAGAGAGCGCCCTCTGGGTGGTGGAGGAGGAGGAGGAGCCTCCGA 716

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QY 3847 AGGTGGCCCCACGCTGGGGAGGTGGAGTTCGGGAATATTCTGTGCGCTACCGGCCCGG 3906
Db 717 AGGTGG-CCCAAGTGGAGGTGGAGTTCGGGAATATTCTGTGCGCTACCGGCCCGG 775
QY 3907 CCTAGACCTGTGTGAGAGACCTGAGTCTGCATGTGCACGGTGGCGAGAGGTGGGAT 3966
Db 776 CCTAGACCTGTGTGAGAGACCTGAGTCTGCATGTGCACGGTGGCGAGAGGTGGGAT 835
QY 3967 CGTGGCGGCACTGGGCTGCCAGTCTTCATGACCCCTTTGGCTGTTCGCGATCCTCGA 4026
Db 836 CGTGGCGGCACTGGGCTGGCAAGTCTTCATGACCCCTTTGCCCTGTTCGCGATCCTCGA 895
QY 4027 GCGGCAAGGCTGAATCCGATTGATGGCTCAATGTGGCAGACATCGGCTCCATGA 4086
Db 896 GCGGCAAGGCTGAATCCGATTGATGGCTCAATGTGGCAGACATCGGCTCCATGA 955
QY 4087 CTTGCGCTCTAGCTGACCATCATCCCGCAGAGCCCATCTCTGTTCGGGACCCCTGCG 4146
Db 956 CTTGCGCTCTAGCTGACCATCATCCCGCAGAGCCCATCTCTGTTCGGGACCCCTGCG 1015
QY 4147 CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGAGGACATTTGGTGGCTTTGGAGCT 4206
Db 1016 CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGAGGACATTTGGTGGCTTTGGAGCT 1075
QY 4207 GTCCCACTGCACACGTTTGTGAGCTCCAGCCGCGAGGCTGACATTCAGTGTCTAGA 4266
Db 1076 GTCCCACTGCACACGTTTGTGAGCTCCAGCCGCGAGGCTGACATTCAGTGTCTAGA 1135
QY 4267 GGGCGGGAGAAATCTCAGCGTGGCGCCAGAGGCGAGCTCGTGTGCTGGCCGAGCCCTGCT 4326
Db 1136 GGGCGGGAGAAATCTCAGCGTGGCGCCAGAGGCGAGCTCGTGTGCTGGCCGAGCCCTGCT 1195
QY 4327 CCGCAAGAGCGGATCTCGTGTTCAGAGAGGCGCAGAGCTGCCATCGACCTGGAGACTGA 4386
Db 1196 CCGCAAGAGCGGATCTCGTGTTCAGAGAGGCGCAGAGCTGCCATCGACCTGGAGACTGA 1255
QY 4387 CAACCTCATCCAGGCTACCATCCGACCCAGTTTGTATACCTGCACTGTCCTGACCATCGC 4446
Db 1256 CAACCTCATCCAGGCTACCATCCGACCCAGTTTGTATACCTGCACTGTCCTGACCATCGC 1315
QY 4447 ACACCGCTTTAAACATATCATGTGACTACACAGGCTCCTGTCTCGGCAAAAGGAGTAGT 4506
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QY 4507 AGCTGAATTTGATTCCTCCAGCAACCTCATTCAGAGCTAGAGGCACTTCTACGGGATGGC 4566
Db 1376 AGCTGAATTTGATTCCTCCAGCAACCTCATTCAGAGCTAGAGGCACTTCTACGGGATGGC 1435
QY 4567 CAGAGATGCTGGACTTCCTTAAATATATATCTCAGATTTCTCCTCGCCCTTCTCGTGT 4626
Db 1436 CAGAGATGCTGGACTTCCTTAAATATATAT-CTGAGATTTCTCCTCGCCCTTCTCGTGT 1493
QY 4627 TTCATCAGGAAGGAATGACACCAAAATATGTCCGAGAATGGACTTGATAGCAACACTG 4686
Db 1494 TTCATCAGGAAGGAATGACACCAAAATATGTCCGAGAATGGACTTGATAGCAACACTG 1553
QY 4687 GGGGCACTTAAAG-TTTTGACCTGTAAAGTGCCTTACAGGGTAACTGTGCTGAATGCT 4745
Db 1554 GGGGCACTTAAAGTTTTTAAAGTTTTTAAAGTGCCTTACAGGGTAACTGTGCTGAATGCT 1613
QY 4746 TTAGATCAGGAATGATCCCAAGTGTGAATGACAGCCCTAAGGTACAGCTAGTTGA 4805
Db 1614 TTAGATCAGGAATGATCCCAAGTGTGAATGACAGCCCTAAGGTACAGCTAGTTGA 1673
QY 4806 GCCAGTTAGACTAGTCCCGGCTTCCCGATTCCCAACTGAGTGTATTGACACACTGCAC 4865
Db 1674 GCCAGTTAGACTAGTCCCGGCTTCCCGATTCCCAACTGAGTGTATTGACACACTGCAC 1733
QY 4866 TGTTCCTCAATAACGATTTTATGAAATGACCTCTGTCTCCCTGATTTTTCATATTTT 4925
Db 1734 TGTTCCTCAATAACGATTTTATGAAATGACCTCTGTCTCCCTGATTTTTCATATTTT 1793
QY 4926 CTAAGATTTTCGTTCTGTTTTTAAATAAAGCTTTTTTCTCTCTCGGACAGACAGCT 4995
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Db 1794 CTAAAGTTTCGTTTCTGTTTTTAAATAAAGCTTTTTTCCCTCGAAGACAGCT 1853
QY 4986 GCTGGCTCAGGCCACCCCTAGGAACCTCAGTCTGTACTCTGGGTGCTGCCTGAATCCAT 5045
Db 1854 GCTGGCTCAGGCCACCCCTAGGAACCTCAGTCTGTACTCTGGGTGCTGCCTGAATCCAT 1913
QY 5046 TAAAAATGGAGTACTGATGAATAAAACTACA 5078
Db 1914 TAAAAATGGAGTACTGATGAATAAAACTACA 1946
RESULT 7
AAQ65377
ID AAQ65377 standard; cDNA; 5011 BP.
XX AAQ65377;
XX AC
XX DT 14-OCT-1994 (first entry)
XX Multidrug resistance protein.
XX DE
XX KW Multidrug resistance protein; MRP; H69AR; cancer cell line;
XX stem cell; cardiac muscle; transgenic animal; ss.
XX OS Homo sapiens.
XX FH
XX FT CDS
XX Location/Qualifiers
XX 196..4791
XX /*tag= a
XX WO9410303-A.
XX PN
XX PD 11-MAY-1994.
XX PF 27-OCT-1993; 93WO-CA00439.
XX PR 27-OCT-1992; 92US-0966923.
XX PR 08-MAR-1993; 93US-0029340.
XX PA (TOOH ) UNIV QUEBENS KINGSTON.
XX PI Cole SPC, Deeley RG;
XX WPI; 1994-167460/20.
XX P-PSDB; AAR54928.
XX PT Multi-drug resistance gene - encodes protein capable of
XX conferring multi-drug resistance on cells, useful in diagnostic
XX and treatment methods
XX PS Disclosure; Page 62-68; 101pp; English.
XX CC The multidrug resistant cancer cell line H69AR (ATCC CRL 11350) was
XX used to identify cDNA encoding a novel protein associated with
XX multidrug resistance, MRP. MRP may be expressed in e.g.
XX hematopoietic stem cells or cardiac muscle, or in
XX transgenic animals, or can be used to raise antibodies.
XX SQ Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;
Query Match 34.2%; Score 1737.8; DB 15; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;
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QY 25 CGGGGAGCTCGGCTCCAGTTCGGGACTCCAACTGTGTGCACAGAAAACCCCGA 84
Db 219 CGCGGATGGCTCCGACCGGCTCTGGGACTGGAATGTCACGTGGAATACCAACCCCGA 278
QY 85 CTTCACTCCCTGCTTCCAGAACTCCCTGCTGCCTGGGTGCCCTCATCTACCTCTGGT 144
Db 279 CTTCACTCCCTGCTTCCAGAACTCCCTGCTGCCTGGGTGCCCTCTTTTACCTCTGGC 338
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Qy	145	GC	CGCTGCGCCTGCTACCTGCTACCTGCGGCACCAATGCTCGTGGTACATCATCATCTCTC	204
Db	339	CT	GTGTTCCCTTCTACCTTCTCTATCTCTCCOGACATGACCGAGGCTACATTCAGATGAC	398
Qy	205	CC	ACCTGTCCAAAGCTCAAGATGGTCTGGTGTCTGCTGTGGTGGTCTCTCTGGCGGA	264
Db	399	AC	CTCTCAACAAACCAAACTCCCTTGGGATTTTTGCTGTGGATCGTCTGCTGGCGAGA	458
Qy	265	CC	TTTTTACTCTCTCCATGGCCTGTCATGCGCGGGCCCTGCCCTGTTTCTTTCTTGT	324
Db	459	CT	CTTCTACTCTTTCTGGGAAGAAGTCGGGCATATTTCTGGCCCCCAGTGTTCCTGGT	518
Qy	325	CAC	CCCCCTTGGTGGGGGTACCATGCTGTGGCCACCTCTGTCATACATATGACGC	384
Db	519	CAG	CCCAACTCTCTTTGGGCATCACACGCTGCTTGTCTACCTTTTAAATTCAGCTGGAG	578
Qy	385	GCT	CAGGGCGTACAGTCTTCGGGGTCTCTCATATCTTCTGTGGTTCCTGTGTGGTCTG	444
Db	579	GAG	AAGGGAGTTCAGTCTTCAGGGATCATGCTCACTTCTGTGGTGTGGTGTGGTGTG	638
Qy	445	CG	CATCGTCCCATTCCTGCTCCAAAGATCCTTTTACCAAGGCAGAGGCTGAGATCTCAGA	504
Db	639	TG	CCCTAGCCATCTCGATGATCCAAAATATAGACGCTTAAAGAGGATGCCAGGTGGA	698
Qy	505	CCC	TTCGGCTTACCACACCTTCTACATCCACTTTTGCCTTGGTACTCTCTGCCCTCATCTT	564
Db	699	CT	GTGTCGTGACATCACTTCTACGTCTACTTTTCCCTCTTACTCTTACGCTCGCTT	758
Qy	565	GG	CTGCTCAGGAGAACTCCATTTTCTCCGCAAGAATGTFCAGCCTTAACCCCTA	624
Db	759	GT	CTGTCTTCAGATCGCTCACCCCTGTCTCGGAAACCATCCACGACCCCTAATCCCTG	818
Qy	625	CC	TGAGACACGCGTGGCTTCTCTCCCGCTGTTTCTCTGTGGTGTTCACAAAGATGGC	684
Db	819	CC	CAGATCCAGCGCTCTCTCTGTGAGGATCACCTTCTGTGGATCAGAGGTTGAT	878
Qy	685	CAT	CTATGCTACCGCATCCCTCGAGGAGAGACCTCTGGTCCCTTAAAGGAAGAGA	744
Db	879	TG	TCCGGGGCTACCGCCAGCCCTCGAGGCGAGTCACTCTGGTCTTAAACAGGAGGA	938
Qy	745	CAG	TCCCAGATGGTGTGCGAGCGTCTGTGAGCATGGAGA-----	788
Db	939	CAG	TGGGAACAAGTCTGCTCTTGTGGTAAAGAACTTGAAGAGGAATGCGCAAGAC	998
Qy	789	-----	AGCAGGAAACGACAGCGCACGACACAAGGCTTTCAGCAGCACCTCGGGAAGAA	840
Db	999	TAG	AGCAGCGGTGAAGTGTGTACTCTCCAAAGATCTGCCACGCGCAAGAGAG	1058
Qy	841	TG	CTCGGGGAGGAGGTGCTGTGGTG-----CCCGCCCGCAGGCC	885
Db	1059	TT	CAAGTGGATGCGAATGAGAGGTGAGGCTTGTATGCTCAAGTCCCCACAGAGGA	1118
Qy	886	CC	GGAAGCCTCTCTCTCAAGGCCCTGCTGGCACCTTCGGTCCAGCTTCTCATCAG	945
Db	1119	GT	GGAACCCCTCTCTTTAAGGTGTTATACAAGACCTTTGGGCCCTTACTTCTCATGAG	1178
Qy	946	TG	CTGCTTCAAGCTTATCCAGGACCTGTCTCTTTCATCAATCCACAGCTGTCTCAGCAT	1005
Db	1179	CT	TCTTTCAGGGCATCCAGACCTGATGATGTTTCCGGGCGCGAGATCTTAAGTT	1238
Qy	1006	CT	GATCAGGTTTATCTCAACCCCATGGCCCCCTCTGTGTGGGGTTCCTGTGGTCTG	1065
Db	1239	GCT	ATCAAGTTTCGTGAATGACACGAAGGCCACAGCTGGCAGGGCTACTTCTACACCGT	1298
Qy	1066	GCT	GATGTTCTCTCATCATGACAGTCTGCTGATCTTACAACACTTATACACCTACAT	1125
Db	1299	GCT	GCTGTTTGCTACTGCTGCTGCACACCTCTGCTGTCGACCACTTCCACACATCTG	1358
Qy	1126	CT	TGTGTACTGGGTGAAGTTTCTGCTTCTGGAATCATGGTCTCATCTACAGGAAGCTCT	1185
Db	1359	CT	TGCTAGTGCATGAGGATCAAGACCGTGTCTATGGGGCTCTCTATCGGAAGGCCCT	1418
Qy	1186	GG	TATACCAACTCAGTCAAAACGTGGCTGCCACTGTGGGGAAATTTGTCACCTCATGTC	1245

Db	1419	GGTGATACCAAAATTCAGCCAGAAAATCTCCACGGTGGGGAGATTGTCAACCTCATGTC	1478
Qy	1246	AGTGGATGCCAGCGGTTCATGTGACCTTGGCCCTTCTCCTCAATCTGCTGTGGTCAGCACC	1305
Db	1479	TGTGGAGCTCAGAGTTTCATGACATTCGGCCACGTACATTTACATGATCTGGTCAGCCCC	1538
Qy	1306	CTGCGAGATCATCTGGCGATCTACTTCTCTGGCAGAACCTAGTCCCTCTGTCTCTGGC	1365
Db	1539	CTGTGAAGTCATCTTGTCTCTACCTCTGCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGC	1598
Qy	1366	TGGAGTCGCTTTTCATGGTCTTGCTGTGATTCACATCAACGGAGCTGTGGCCGTGAAGATGCG	1425
Db	1599	TGGAGTGGGGGTGATGGTCTCTCATGGTGGCCGTCAATGCTGTGATGGCATGAAGACAA	1658
Qy	1426	CGCTTTCAGGTAAACAAATGAATGAAGGACTCGCGCATCAAGCTGATGATGAGAT	1485
Db	1659	GAGCTATCAGTGGGCCCATGAAGAGCAAGAACAATTCGATCAAGCTGATGAACGAAT	1718
Qy	1486	CCTGAACGCGATCAAGGTGCTGAAGCTGTACGCTCTGGAGCCCAAGCTTCTCTGAAGCAGGT	1545
Db	1719	TCTCAATGGATCAAAAGTCTAAAGCTTTATGCTCTGGAGCTGGCATTCGAAGCACAAGT	1778
Qy	1546	GGAGGCGATCAGCAGGGTGAGCTCCAGCTGTCTGCGCAGCGGCGCTTACCTCCACACCAC	1605
Db	1779	GCTGGCCATCAGCAGGAGGAGCTGAAGGTGCTGAAGAGTCTGCTACCTGTCAAGCCGT	1838
Qy	1606	AACCCACTTCACCTGATGTGAGCCCGCTTCTCTGGTGACCTGATCACCTCTGGGGTGA	1665
Db	1839	GGGCACTTCACCTGGGTCTGCACGCGCTTCTCTGGTGGCTTGTGTCATGTCGTCCTT	1725
Qy	1666	CGTGTACGTGGACCCAAACAATGCTGTGAGCGCGAGAAGGCCCTTGTGTCATGTCGTCCTT	1785
Db	1899	CGTGACCATTCAGAGAAACAACATCTGGATGCCAGACAGCCTTCGTGCTTTGGCCTT	1958
Qy	1726	GTTTAAATATCTTAAGACTTCCCTCAACATGTGTGCCCCAGTTAATCAGCAACCTGACTCA	1785
Db	1959	GTTTCAACATCTCCGTTTCCCTTGAACATTTCTCCCATGTTCTCCCATGATCGTGCA	2018
Qy	1786	GGCCAGTGTCTCTCAAGCGATCCAGCAATTCCTTGAGCCAGAGAGACTTGACCCCCA	1845
Db	2019	GGCGAGTGTCTCCCTCAACAGCCTGAGGATCTTCTCTCCCATGAGAGCTGGAACCTGA	2078
Qy	1846	GAGTGTGAAGAAGACCATCTCCCAAGC-----TATGCCATCACCATACACAG	1896
Db	2079	CAGCATCGAGCAGCGCTGTCAAGACGGCGGGGCCAGACAGCATCACCGTAGGAA	2138
Qy	1897	TGGACCTTCACCTGGGCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATCAAGGT	1956
Db	2139	TGCCACATTCACCTGGCCAGGAGGAGACCTCCCACTGAATGGCATCACCTTCTCCAT	2198
Qy	1957	CCGAAAGGGGACATGTTGGCCGTGTTGGGGCTGTGGGCTGTGGAGCTCTCCCTGGT	2016
Db	2199	CCCCAGAGTGTGTTGGTGGCCGTGTGGGCCAGTGGGCTGCGGAAGTTGTGTCCTGCT	2258
Qy	2017	GTCTCCCTGTCTGGGAGATGGGAAGCTAGAAGGCAAGTGCACATGAAGGGCTCCGT	2076
Db	2259	CTCAGCCCTTGTGGCTGAGATGAGCAAAAGTGGAGGGCACGTGGCTATCAAGGGCTCGT	2318
Qy	2077	GGCTATGTGCCCAAGCAGGCAATGATCCAGAACTGCATCTTTCAGGAAAAAGTGGTTTT	2136
Db	2319	GGCCTATGTGCCACAGCAGGCCCTGGATTCAGAAATGATTCTCTCCGAGAAAAATCTTTTT	2378
Qy	2137	CGGCAAGCCCTGAACCCCAACCGCTACCAGCAGACTCTGGAGGCTGTGGCTTGGTACG	2196
Db	2379	TGGATGTCAAGTGGAGGAACCATATTTACAGGTCCGTGATACAGGCTGTGGCTCTCC	2438
Qy	2197	TGACCTGGAGATGCTGCCTGTGGGATCAGACAGAGATTGAGAGAGGGCATTAACCT	2256
Db	2439	AGACCTGGAATCTTGCCCACTGGGATCGGACAGAGATTGGGAGAGGGCGTGAACCT	2498
Qy	2257	GTCCTGGGGGCCAGCGGCGGCTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT	2316

Db 2499 GTCTGGGGCAGAGACGCGCTGACGCTGGCCGCGCGCTGTACTCCAACGCTGACAT 2558
QY 2317 TTTCTTGCTGATGACCCACTGTCCGGGTGGACTCTCATGTGGCCCAAGACACATTTTGA 2376
Db 2559 TTACTCTTTCATGATCCCTCTCAGCAGTGGATGCCATGTGGGAAAACACATCTTTGA 2618
QY 2377 CCAGCTCATCGGGCCAGAGCGCTGGCCAGGCAAGACGCGAGTGTGGTGAGCCAGG 2436
Db 2619 AAATGTGATTGGCCCCCAAGGGATGCTGAAGAAACAAGACGGGATCTTGGTCAACGACAG 2678
QY 2437 CATTAGCTTCTCTGCCCCAGACAGACTTCATCATTTGTGTAGCTGATGGACAGGTTCTGA 2496
Db 2679 CATGAGCTACTTGGCAGGTGGACGTCATCATGCTCATGTGATGGCGGCAAGATCTCTGA 2738
QY 2497 GATGGGCCGTACCCACGCTGTGTGACGCCAACGGCTTCTTCCCAACTTTTCTCTGCAA 2556
Db 2739 GATGGGCTCTTACCAGGAGCTGTGGCTCGAGACGGCGCTTCTGCTGAGTTCTCTCGGTAC 2798
QY 2557 CTATGCCCCGATGAGCAACCAAGGCACTGGAGGACAGCTGGACCGGTTGGAAGTGC 2616
Db 2799 CTATGCCCAGCACAGAGGAGGAGGATGAGAGGAAGCGGTCACGGCGTCACGG 2858
QY 2617 AGAGGATAAGGAGGCACTGTGTGAAGACACACTCAGCAACACACAGGATCTGAACAGA 2676
Db 2859 TCCAGGAGGAAGCAAGCAATGAGATGGCAT----- 2894
QY 2677 CAATGATPCCAGTCACTTATGTGTCTCCAGAACAGTATTATGAGACAGCTGAGTGCCTGTCT 2736
Db 2895 -----GCTGGTGACGGACAGTGCAGGGAAGCAACTCAGAGACAGCTCAGCAGCTCCTC 2948
QY 2737 CTCAGATGGGGAGGACAGGCTGGCTGTACCCCGAGGACCTGGTTCATCAGAGAA 2796
Db 2949 CTCCTATAGTGGGGACA-----TCAGCAGGCAACCAACAGCAGCGCACTGACAGAAA- 3003
QY 2797 GGTGCAAGTACAGAGGCGAAGGACAGATGGGCACTGACCCAGGAGGAGAAAGCAGCCAT 2856
Db 3004 ----GCTGAGGCCAAGAGGAGGAGACCTGGAAGCTGATGGAGGCTCAGAGGCGCAGAC 3059
QY 2857 TGGCACTGTGGAGCTAGTGTGTCTGGGATATGCAAGGCCGTGGGGTCTGTATCCAC 2916
Db 3060 AGGCGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTTCTCATCTC 3119
QY 2917 GCTGGCCATCTGTCTCTGTATCTGGTCAAGTGGCGCTGCCATTTGGAGCCATGTGTG 2976
Db 3120 CTTCTCAGCATCTTCTTTTCAATGTGAACCATGTGTCCGCGCTGGCTTCCAACTATTG 3179
QY 2977 GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTACAGAAACAACTTCCCTGAG 3036
Db 3180 GCTCAGCCTCTGGACTGATGACCCCATCTGTCAGGGGACTCAGGAGCACAGGAAGTCCG 3239
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Db 3240 GCTGAGCGTCTATGGAGCCCTGGGCATTTTCAAGGGATCGCCGTGTTTGGCTACTCCAT 3299
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Db 3480 GGCGTCCCTGTTTCAAGCTGATGGTGCTGCTGATCTATCTCTGTCGCCACGCGCCATCGC 3539
QY 3337 CACTGTGGTCACTCTGCCCTGTGCTGTCTACACCTTAGTCAGCGCTTCTATGACG 3396
Db 3540 CGCCATCATATCCGCCCTTGGCTCTACTTCTTCTGTCAGAGGTTCTACGTGGC 3599

QY 3337 CACATCACGGCAACTGAAGCGCTGGAATCAGTCAGCGCTCACCTATCTACTCCACTT 3456
Db 3600 TTCCTCCCGCAGCTGAAGCGCTCGAGTCGTCAGCGCTCCCGGCTATTTCCACTTT 3659
QY 3457 TTCGGAGACAGTACTGTCAGAGTGTCTATCGGGCTTACAACCGCAGCCGGATTTGA 3516
Db 3660 CAACGAGACCTTGTGGGGGTGAGGTCATTCGAGCCTTCGAGGAGCAGGCGCTTCAT 3719
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Db 3900 TTACTCATTTGAGGTCAACACGTACTTGAAGTGGCTGGTTCGGATGTCTCTGAAATGGA 3959
QY 3757 ATCTAACATCTGCTGTGGAGAGGCTCAAGAGTACTCCAAGACAGACAGAGCGCC 3816
Db 3960 AACCAACATCTGCGCTGTGGAGAGGCTCAAGAGTATTTCAGAGACTGAGAGGAGCGCC 4019
QY 3817 CTGGGTGTGGAAGGACGCCCTTCCGAAGGTTGGCCCCACGCTGGGGAGGTGGAAGTT 3876
Db 4020 CTGCAAAATCCAGGAGACACGTCCGCCAGCAGCTGGCCCCAGGTGGCGGAGTGAAT 4079
QY 3877 CCGGAATTTATTTCTGGCTACCGCGCGCTAGACTGTGTGCTGAGAGACTCAGTCT 3936
Db 4080 CCGAAGTACTGCTGCTGCTACCGAGAGGACTGAGCTTCTTCTCAGGACATCAATGT 4139
QY 3937 GCATGTGCAAGGTGGCGAAGGTGGGATCTGGCGCGCACTGGGGCTGGCAAGTCTTC 3996
Db 4140 CACGATCAATGGGGAGAAAAGTTCGGCTGCTGGGGCGGAGGAGCTGGGAAGTCTC 4199
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QY 4057 CCTCAATGTGGCAGACATCGGCTCCATGCTGCTCAGCTGACCATCATCCCGCA 4116
Db 4260 CATCAACATCGCAAGATCGGCTTGCAGCTCCGCTTCAAGATCACCATATCCCCCA 4319
QY 4117 GGACCCCATCTGTCTCGGGGACCTCGCATGAACCTGGACCCCTTCGGCAGCTACTC 4176
Db 4320 GGACCTGTTTGTGTTTTCGGGTTCCCTCCGAATGACCTGACCCATTCAGCCAGTACTC 4379
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Db 4560 GGCCACGCGAGCTGGACCTTGAAGAGGAGGAGCTCATCCAGTCCACCATCCGAGACA 4619
QY 4417 GTTGTATACCTGACCTCTCTGACCATCGGACACGGCTTAACACTATCATGGACTACAC 4476
Db 4620 GTTCGAGGACTGCACCGTCTCTACCATCGGCGCCCGGCTCAACACCATCATGGACTACAC 4679

QY 4477 CAGGTCCTGGTCCGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACTCAT 4536
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RESULT 8
 ID AAT17173 standard; cDNA; 5011 BP.
 AC AAT17173;
 XX AAT17173;
 DT 19-JUL-1996 (first entry)
 XX cDNA encoding multi-drug resistance protein.
 DE MRP; multi-drug resistance protein; small cell lung cancer;
 KW protect; cytotoxicity; therapy; P-glycoprotein; ss.
 KW Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1..195
 FT 5'UTR /*tag= a
 FT CDS 196..4791
 FT /*tag= b
 FT /product= multi-drug_resistance_protein
 FT 3'UTR 4792..5011
 FT /*tag= c
 XX
 XX US5489519-A.
 XX 06-FEB-1996.
 XX 27-OCT-1992; 92US-0966923.
 XX 26-OCT-1993; 93US-0141893.
 XX 27-OCT-1992; 92US-0966923.
 XX 08-MAR-1993; 93US-0029340.
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX
 XX Cole SPC, Deeley RG;
 XX WPI; 1996-115615/12.
 XX P-PSDB; AAR93153.
 XX Multi-drug resistance protein, MRP and DNA encoding it - for
 XX diagnosis and treatment of e.g. small lung cell cancers
 XX
 XX Claim 4; Column 41-52; 50pp; English.

CC The present sequence encodes a multi-drug resistance protein (MRP),
 CC isolated from H69AR, a small cell lung cancer cell line, which is about
 CC 50-fold resistant to doxorubicin as compared to the parental H69 cell
 CC line. The human MRP gene has been mapped to 16p13.1, and is not linked
 CC to either CFTR or MDR genes. The MRP protein is overexpressed in multi-
 CC drug resistant cells independently of overexpression of P-glycoprotein
 CC (a member of a superfamily of membrane proteins that serve to transport
 CC a variety of mols., ranging from ions to proteins, across cell
 CC membranes, and associated with a variety of tumours). Antisense nucleic
 CC acids and splice variants (see AAT14910-14) of this sequence are claimed.
 CC The nucleic acids can be used to protect a drug sensitive cell from
 CC cytotoxicity due to exposure to a drug, or to develop improved forms of
 CC therapy, particularly for small cell lung cancers which exhibit a high
 CC initial response to chemotherapy which is almost always followed by a

CC multi-drug resistance form of the disease.
 XX
 SQ Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;
 Query Match 34.2%; Score 1737.8; DB 17; Length 5011;
 Best Local Similarity 62.2%; Pred. No. 0;
 Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;
 QY 25 CGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAACTCTCTGTGCACACAAACCCGGA 84
 DB 219 CGCCGATGGCTCCGACCCGCTCTGGGACTGGAATGCACGTGAATACCAAGCAACCCGGA 278
 QY 85 CCTCACTCCCTGCTTCCAGAACTCCCTGCTGGGCTGGGTGCCCTGATCTACCTGTGGGT 144
 DB 279 CTTCAACCAAGTGTCTTCAGAACACGGTCTCTGCTGGGTGCCCTGTCTTACCTCTGGGC 338
 QY 145 CGCCCTGCCCTGCTACTTGTCTACCTGGCGGACCAATGTCGTGGGTACATATCTCTC 204
 DB 339 CTGTTTCCCTCTCTACTTCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGAC 398
 QY 205 CCACCTGTCCAAGCTCAAGATGCTGGGTGTCCTGCTGTGGGTCTCTCTGGGCGGA 264
 DB 399 ACCTCTCAACAAACCAAACTCCCTGGGATTTTGTCTGTGATCGTCTGCTGGGCGGA 458
 QY 265 CCTTTTACTCCTTCCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
 DB 459 CCTCTTCTACTCTTCTGGGAAAGATCGGGGCATATCTCTGGCCCACTGTCTCTGCT 518
 QY 325 CACCCCTTGGGTGGGTGCTACCATGCTGTGGGCAACCTCTGCTGATACATGATGAGCG 384
 DB 519 CAGCCCAACTCTCTGGGATCATCACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
 QY 385 GCTGCAGGGGCTACACTCTCGGGGCTCTCATTTATCTCTGCTGCTGCTGCTGCTGCTG 444
 DB 579 GAGGAAGGGAGTTCAGTCTTCAGGGATCATGCTCACTTCTTGGCTGGTAGCCCTTAGTGTG 638
 QY 445 CGCCATCGTCCCATTCGGCTCCAAGATCCCTTTAGCAGGAGAGGGTGAGATCTCAGA 504
 DB 639 TGCCCTAGCCATCTCGATCCAAATATGACAGCTTAAAGAGAGATGCCCAAGTGA 698
 QY 505 CCCCCTCCGCTCACACACCTTCTACATCCACTTTGGCTGGTACTCTCTGCTGCTCTATCT 564
 DB 699 CCTGTTTCGTGACATCACTTCTACGCTACTTCTCCCTTACTCTACTCATTCAGCTGCT 758
 QY 565 GCCTGCTTTCAGGAGAAACCTCCATTTCTCCGCAAGAAATGTCGACCTTAACCCCTA 624
 DB 759 GTCTGTTTCTCAGATCGCTCACCTGTTCTCGAAACCATCCACGACCTTATCCCTG 818
 QY 625 CCCTGAGACCGCTGGCTGCTTCTCTCCGCTGTTTCTTGGTGGTTCACAAAGATGCG 684
 DB 819 CCCAGAGTCCAGCGTTCCTCTCTGTCGAGGATCACCTTCTGCTGGATCACAGGTTGAT 878
 QY 685 CATCTATGCTACCGGCTACCCCTGGAGAGAGAGGACCTCTGCTGCTCCCTAAGAGAGGA 744
 DB 879 TGTCCGGGCTACCGCCAGCCCTGGAGGCGAGTGACCTCTGCTTCTTAAACAAAGAGGA 938
 QY 745 CAGATCCAGATGGTGGTGCAGCAGCTGCTGGAGGATGAGGA----- 788
 DB 939 CAGTCCGGAACAGTCTGCTGCTGTTTGGTAAAGAACTGGAAGAGGAATGCCCAAGAC 998
 QY 789 -----AGCAGGAAACAGCAGCGCAGCAGAGAGGCTTCAGCAGACCTTGGGAAAAA 840
 DB 999 TAGGAAGCAGCGGTGAAGTGTCTGTACTCTCCCAAGGATCTGCTCCAGCCGCAAGAGAG 1058
 QY 841 TCCTTCGCGGAGGAGGAGTGTCTGCTGGTG-----CCCGGCCCAAGGCC 885
 DB 1059 TTCCAAGTGGATGGAATGAGGAGGTGAGGCTTTTGTGCTCAAGTCCCTCCCAAGAGGA 1118
 QY 886 CCGGAGGCTCTCTCTCTCAAGGCCCTGCTGGCCCACTTTCGGCTCCAGCTTCTCTATCAG 945
 DB 1119 GTGGAAACCCCTCTCTGTTTAAAGGTGTATACAAGACCTTTGGGCCCTTCTCTCATGAG 1178
 QY 946 TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTCTCTCATCATCAATCCACAGCTGCTCAGCAT 1005

QY	3157	CAAGATACGGTCGCCACAGTCCTCTTTGACACACACACCATCAGGCCCATCCTGAACTG	3216
DB	3360	CATCTCGGGTCACCAATGAGCTTCCTTTGAGCGGACCCCCAGTGGGAACCTGGSTGAACCG	3419
QY	3217	CTTCTCCAAGGACATCTATGCTGTTGATGAGGTTCTGGCCCTGTCACTCTCCATCTGCTGCT	3276
DB	3420	CTTCTCCAAGSAGCTGGACACAGTGGACCTCCATGATCCGGAGGTCAACAAGATGTTCAAT	3479
QY	3277	CAATTCTCTTCCAAGCCATCTCCACTCTTGTGTGTCATATGCGCAGCAGCGCGCTCTT	3336
DB	3480	GGGCTCCCTCTTCAAGGTCAATTTGGTGCCTGTCATCTGCTATCTGCTGGCCAGCCCATCGC	3539
QY	3337	CACHTGGTCACTCCCTCGCTGTGCTCTACACCTTACTGTGAGCGCTCTCATGCAGC	3396
DB	3540	CGCATCATCATCCCGCCCTTGGCCTCATCTACTTCTTCGTCCAGAGGTTCTACGTGGC	3599
QY	3397	CACATCACGGCAACTGAAGCGGTGGAAATCACTACGCCGCTCACTATCTACTCCCACTT	3456
DB	3600	TTCTCTCCCGCAGCTGAAGCGCTCGAGTCTGGTCAGCGCTCCCGCGTCTATTCCCATTT	3659
QY	3457	TTCGGAGACAGTACTGTTGCCAGTGTCTATCCGGGCTTACAACCGCAGCGGGAATTTGA	3516
DB	3660	CAACGAGACCTTGTCTGGGGTCAAGGCTCATTCGAGCCTTTCAGGAGCAGGAGCGCTTCAT	3719
QY	3517	GATCATCAGTGATACTAAGGTGGATGCCAACAGAGAAGCTGTACCCCTACATCATCTC	3576
DB	3720	CCACGAGTGCCTGAAGGTGGACGAAACCAAGAAGCCCTATTACCCCAAGCATCTGCGC	3779
QY	3577	CAACCGGTGGCTGAGCATCCGAGTGGAGTTCTGTGGGAACCTGCCTGTGCTCTTTGCTGC	3636
DB	3780	CAACAGTGGCTGGCGCTCGGCTGGAGTGTGTGGCAACTGCATCGTTCTGTTGCTGC	3839
QY	3637	ACTATTTCGGCTATCGGAGAGAGAGCGCTGAACCCGGGGCTGTGGGCTTCTCTGTGTC	3696
DB	3840	CTGTGTTGGCGGTGATCTCCAGCAGACGCTCAGTGTCTGGCTTGTGTGGGCTCTCAGTGT	3899
QY	3697	CTACTCTCTTGCAGTGCACATTTGCTCTGAATCGATGATACGAATGATGTCAGATTTGGA	3756
DB	3900	TTACTCATTTGCAGGTACCCAGCTACTTGAATGGCTGGTTCGGATGTCTCTGAATGGA	3959
QY	3757	ATCTAATACGTGGGTGTGGAGAGGTCAAGAGTACTTCCAAGACAGAGACAGAGCGCC	3816
DB	3960	AACCAACATCGTGGCGCTGGAGAGGCTCAAGAGTATTTCAGAGACTGAGAAGGAGCGCC	4019
QY	3817	CTGGGTGGTGAAGCAGCGCCCTCCGAGAGTTGGCCCCCAGCTGGGAGGTGAGTT	3876
DB	4020	CTGGCAATTCACAGGAGACAGTCCGCCCCAGCAGCTGGCCCCAGTGGGGCGAGTGAAT	4079
QY	3877	CCGGAATATTCTGTGCGCTACCGGCCGGCTAGACCTGTGCTGAGAGACCTGAGTCT	3936
DB	4080	CCGGAACTACTGCCCTACCGAGAGACCTGGACTTCGTTCTCAGGCACATCAATGT	4139
QY	3937	GCATGTACAGTGGCGAGAAAGTGGGATCGTGGCGGCACCTGGGCTGGCAAGTCTTC	3996
DB	4140	CACGATCAATGGGGAGAAAAGGTTCGGCATCTGTGGGCGGACGGAGCTGGGAAGTCGT	4199
QY	3997	CATGACCCCTTTCCTGTTCCGCATCTTGGAGCGCGCAAGGGTGAATCCGCAATTGATGG	4056
DB	4200	CCTGACCTTGGGCTTATTTCGGATCAACGATCTGTCCGAAGGAGATCATCATCATGG	4259
QY	4057	CCTCAATGTGGCAGACATCGGCTCCCATGACTCGCTCTCAGTGAACATCATCCGCA	4116
DB	4260	CATCAACATCGCCAGATCGGGCTGCAGACCTCCGCTTCAAGATCACCATCATATCCCCA	4319
QY	4117	GGACCCCATCTCTTTCGCGGAACCTGCGCATGAACCTGGACCCCTTCGGCAGCTACT	4176
DB	4320	GGACCCCTGTTTGTGTTTCGGGTTTCCCTCCGAATGAACCTGGACCCCATCAGCAGTACT	4379
QY	4177	AGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCACCTCCACACGCTTTGTGAGTCCCA	4236
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RESULT 9

AAV31497

ID AAV31497 standard; cDNA: 5011 BP.

XX
AC AAV31497;

XX
DT 14-AUG-19

Human mul

XX
KW

KW
XX
multidrugOS Homo sapi
XX

Key
5' UTR

FT	.	
FT	CDS	

11
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FT
FT

XX
PN US5766880

XX
PD 16-JUN-19XX
PF 05-JUN-19XX
PR 05-JUN-19

PR	27-OCT-19
PR	08-MAR-19

PR	26-OCT-19
PR	20-MAR-19

XX
PA (TOOH) UI

XX Cole SP,
PI

XX	WPI; 1998
DR	

XX
DR P-PSDB; A/

PT DNA encoded:

QY 1897 TGGCAGCTTACCTTGGCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGT 1956
DB 2139 TGGCAGCTTACCTTGGCCAGGACGACCCCTCCACACTGAATGGCATCACCTTCCCAT 2198
QY 1957 CCCGAAAGGGGACTGGTGGCCGTGTGGGGCTGTGGGCTGTGGGAAGTCCCTCCGGT 2016
DB 2199 CCCGAAAGGTGCTTGGTGGCCGTGTGGCCAGGTGGGCTGGGAAAGTGTGCCCTGCT 2258
QY 2017 GTCGCCCCCTGCTGGGAGAGATGGAGAAGCTAGAAGCAAGTGCACATGAAGGGCTCCGT 2076
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QY 2077 GGCCTATGTGCCCCAGCAGGATGGATCCAGAACTGCATCTTTCAGAAACAGTGCTTTT 2136
DB 2319 GGCCTATGTGCCACAGAGCCCTGGATTGAGATGATCTCTCCGAGAAAATCATCTTTT 2378
QY 2137 CGGCAAGCCCTGCAACCCCAAGCGCTACCAGCAGACTCTGGAGGCGCTGCGCTTGTAGC 2196
DB 2379 TGGATGTACGCTGGAGAACCATTTACAGTCCGTGTACAGGCGCTGTGCCCTCCTCC 2438
QY 2197 TGAOCTGGAGATGCTGCCCTGGTGGGATCAGACAGATTTGGAGAGAAGGGCAATTAACCT 2256
DB 2439 AGACCTTGAATACTTGCACAGTGGGATCGACAGAGATTGGGAGAAGGGCTGAACT 2498
QY 2257 GTCTGGGGCCAGGCGCAGCGGTGAGTCTGGCTGAGCTGTTTACAGTGTGCCGATAT 2316
DB 2499 GTCTGGGGACAGAGACGCGGTGAGCCTGGCCGCGGCGGTGTAATCCAAAGCTGACAT 2558
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DB 2559 TTACCTTCTGATGATCCCTCTACAGTGGATGCCATGTGGGAAACACATCTTTGA 2618
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QY 2437 CATTAAGTTCCTGCCCCAGACAGACTTCATCATGTGTGTAGCTGTATGGACAGGTGTGGA 2496
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DB 2739 GATGGCTCTTACAGGAGCTGCTGGCTGAGACCGCGCTTCCGTGAGTTCCTGCGTAC 2798
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DB 2859 TCCAGGGAAGGAAGCAAAATGGAGATGGCAT----- 2894
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DB 3420 CTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGTCTCAAGATGTTCT 3479
QY 3277 CAATTCCTCTTCAACGCCATCTCCACTCTTGTGGTCACTATAGTCAGCGCTTCTATG 3336
DB 3480 GGCTCCTCTTCAACGTCTATGCTGGTCTGCTGCTGCTTATCTGCTGGCCACGCCATCG 3539
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DB 3540 CGCATCATCATCCGCCCTTGGCTCTACTTCTTCTGCTCCAGAGTCTTACGTGGC 3599
QY 3397 CACATCAGGCAACTGAAGGGTGGAACTCAGTCAGCGCTCACTATCTACTTCTCCACT 3456
DB 3600 TTCTCCCGGAGCTGAAGCGCTCGAGTGGTTCAGCGCTCCCGCTCTATTCCCATTT 3659
QY 3457 TTCGAGAGACAGTGTGCTGCCAGTGTCTCCGGGCTTACAAACCGCAGCGGATTTGA 3516
DB 3660 CAACGAGACCTGCTGGGGTCAAGCTTCTGAGGCTTCGAGGACAGAGCGCTTCTAT 3719
QY 3517 GATCATCAGTGTACTAAGTGGATGCCAACACAGAAAGTCTACCCCTACATCATCTC 3576
DB 3720 CCACAGAGTGAACCTGAAGTGGACGAGAACAGAGGCTATTACCCAGCATCTGGC 3779
QY 3577 CAACGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGAACTGCTGGTGTCTTGTCTGC 3636
DB 3780 CAACAGTGGCTGGCGCTGCGGTGGAGTGTGTGGCAACTGCACTGCTTGTCTGC 3839
QY 3637 ACTATTTGGCGTCATCGGAGGAGCAGCTGAAACCGGGCTGAGGCTTCTCTGTC 3696
DB 3840 CTTGTTGGGTGATCTCCAGGACAGCTCAGTGTGGCTTGGTGGGCTCTCAAGTGC 3899
QY 3697 CTACTCTTGCAGGTGACATTTGCTGAACTGGATGATACGAATGATGTCAAGTTTGA 3756
DB 3900 TTACTCATTTGAGGTCAACCATCTTGAATGGCTGGTTCGATGTCTCAATGGA 3959
QY 3757 ATCTAACATCTGGCTGTGGAGGCTCAAGAGTACTCAAGACAGACAGAGAGCGCC 3816
DB 3960 AACCAACATCTGGCGTGGAGGCTCAAGGATTTTTCAGAGACTTGAAGAGCGCC 4019
QY 3817 CTGGTGTGGAGGAGCGCGCTCCCGAAGTGTGGCCCCCAGGCTGGGCGGAGTGGAGT 3876
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QY 3877 CGGAAATTTCTGTGCGCTACCGCGCCCTAGACCTTGGTCTGCTGAGAGACTGAGTCT 3936
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DB 4140 CACGATCAATGGGGAGAAAAGTTCGGCATCTGTGGGGCGGAGCGGAGTGGAACTGC 4199
QY 3997 CATGACCTTTCCTTCCGCTCTGTGAGGCGCAAGGCTGAAATCCGATTCATG 4056
DB 4200 CTTGACCTTGGCTTATTTCCGATCAACGAGTGTCCGAGGAGAGATCATCATGATGG 4259
QY 4057 CCTAATGTGCAGACATCGGCTCCATGACCTGGCTCTCAGCTGACCATCATCCGCA 4116

Db 3004 ----GCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATGAGGCTGACAAGGGCGACAG 3059
QY 2857 TGGCACTGTGGAGCTCAGTGTGTCTGGGATATGCAAGGCCGTGGGGCTCTGTATCCAC 2916
Db 3060 AGGCAAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119
QY 2917 GCTGGCCATCTGCTCTCTGTATCTGGGTCAAGCTGGGCTGCCATTGGAGCCCAATGTGTG 2976
Db 3120 CTTCCTCAGCATCTCTCTTTCAATGTATACCAATGTGTCCCGCTGGCTTCCCAACTATTG 3179
QY 2977 GCTCAGTGCCCTGGCAAAATGATCCCATGGCAGACAGTAGACAGAAACAACACTTCCCTCTGAG 3036
Db 3180 GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACAAAGTCCG 3239
QY 3037 GCTGGGGCTTACTGCTGTCTTTAGGAATTCGAAGGGTCTTGGGTGATGCTGGCAGCCAT 3096
Db 3240 GCTGAGCGCTATGAGAGCCCTGGGCAATTCACAAGGATCGCGGTGTCTTGGCTACTCCAT 3299
QY 3097 GGCATGGCAGCGGTGGCATCCAGGCTGCCGTGTGTTCACACAGGCACTGCTGCACAA 3156
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QY 3157 CAAGATACGCTCCCAAGCTCTCTTTGACACACACCATCAGCGCGCATCTGTAAGCTG 3216
Db 3360 CATCTCGGCTACCCATGAGCTTCTTTGAGCGGACCCCAAGTGGAACTGCTGTAACCG 3419
QY 3217 CTTCCTCAAGGACATCTATGTCTGATGAGGTCTTGGGCCCTGTCTATCTCATGCTGCT 3276
Db 3420 CTTCCTCAAGGAGCTGGACAGTGGACTCCATGATCCCGGAGGTCTATCAAGATGTTCTAT 3479
QY 3277 CAATCTCTCTTCAAGCCATCTCCACTCTTGTGGTCTATCATGCGCCAGCACCGGCTCTT 3336
Db 3480 GGCTCCCTGTTCAAGCTCATTTGGTGCCTGCATCGTATTCCTGCTGCCACGCCCACTCGC 3539
QY 3337 CACTGTGGTCTATCTCCCTGCTGTCTTACACCTTTAGTCAGCGCTTCTATGACGC 3396
Db 3540 CGCCATCATCATCCCGCCCTTGGCCCTATCTACTTCTTCGTCACAGGTTCTACGTGGC 3599
QY 3397 CACATCAGGCAACTCAAGCGGTGGAATCAGTCAGCGGTCACTATCTACTCCCACTT 3456
Db 3600 TTCTCTCCGGCAGCTGAAGCGCTCGAGTGGTCAAGCGCTCCCGGTCTATTTCCTCATTT 3659
QY 3457 TTCGGAGACAGTGACGTGGCTGATCTGCTGCGGCTTACAACCGCAGCGGATTTTGA 3516
Db 3660 CAACGAGACTTGTCTGGGCTCAGCGTCAATTCAGCTTCGAGGACAGAGCGCTTCAT 3719
QY 3517 GATCATCTAGTACTAAGTGGATGCCAACAGAGAAAGCTGTACCCCTACATCATCTC 3576
Db 3720 CCACCAAGTGAACCTGAAGTGGACGAGAACCAGAGGCTATTACCCAGCATCGTGC 3779
QY 3577 CAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGAACTCGGTGGTCTCTTTGCTGC 3636
Db 3780 CAACAGGTGGCTGGCGTGGCTGAGTGTGTGGGCAACTGCATCGTCTGTCTGTCTGC 3839
QY 3637 ACTATTTCGCTCATCGGAGGAGCGCTGAAACCGGCGCTGGTGGCTTTCTCTGTCTC 3696
Db 3840 CTGTTTGGCGTGAATCTCCAGCAGAGCTCAGTCTGCTGGTGGGCTCTCAAGTCTC 3899
QY 3697 CTACTCTTGCAGGTGACATTTTCTCTGAATCGGATGATACGAATGATCTCAGATTTGA 3756
Db 3900 TTACTCATTTGAGGTCAACACGCTACTTGAATCTGGCTGGTTCGATCTCATCTGAATGA 3959
QY 3757 ATCTAACATCTGGTGTGGAGGCTCAAGGAGTACTCCAGACAGACAGACAGCGCC 3816
Db 3960 AACCAACATCTGGCGTGGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAGCGCC 4019
QY 3817 CTGGTGGTGGAGGAGCAGCGCTTCCGAAAGTGTGGCCCTCCACGTTGGGAGGTGAGTT 3876
Db 4020 CTGGCAATTCAGGAGACACGCTCCCGCCAGCAGCTGGCCCCAGTGGCGGAGTGAAT 4079
QY 3877 CCGGAATATTCTGTGCGCTACCGCGCGGCTTAGACCTGGTCTGCTCAGAGACTGAGTCT 3936
Db 4080 CCGGAATCTACTGCTGCGCTACCGGAGAGACCTGGACTTCGTTCTCAGGCACATCATGT 4139

QY 3937 GCATGTGCACCGTGGCGAGAAAGTGGGGATCGTGGCCGCACTGGGGTGGCAAGTCTTC 3996
Db 4140 CACGATCAATGGGGAGAAAAGTTCGGCATCGTGGGGCGGAGCTGGGAAGTCTGTC 4199
QY 3997 CATGACCTTTTGGCTGTTCGCATCTCGGAGCGGCAAGGTTGAAATCCGCAATGATGG 4056
Db 4200 CCTGACCTTGGCTTATTTTCGATCAACGAGTCTGCGGAAGGAGAGATCATCATGATGG 4259
QY 4057 CCTCAATGTGACACATCGGCTTCCATGACCTCGCTCTCAGCTGACCATCATCCCCA 4116
Db 4260 CATCAACATCGCAAGATCGGCTGACGACTCGCTTCAAGATCACCATCATCCCCA 4319
QY 4117 GGACCCCATCTGTCTTCGGGACCTGCGCATGAACCTGACCCCTTCGCAAGTACTC 4176
Db 4320 GGACCTTGTCTTTCGGGTTCCTCCGAATGAACCTGACCCATTCAGCCAGTACTC 4379
QY 4177 AGAGGAGCATTTGGTGGCTTTGGAGCTCTCCACCTGCACAGCTTGTGAGTCTCCA 4236
Db 4380 GGATGAAGAAGTCTGGAGCTCCCTGGAGCTGGCCACTGAAGGACTTCTGTCTCAGCCCT 4439
QY 4237 GCGGCAAGGCTTGACTTCCAGTCTCAGAGGCGGGGAGAAATCTCAGCTGGGCGCAG 4296
Db 4440 TCCTGACAAGCTAGACCATGATGTGCAAGAGCGGGGAGAACTCAGTCTCGGCGACG 4499
QY 4297 GCAGCTGTGTGCTGCGGAGCCCTGCTCCGCAAGAGCGCATCTCTGTTTATAGCA 4356
Db 4500 CCAGCTTGTGTGCTAGCCGCGGCTCTGAGGAAGACGAAGATCTTGTGTTGATGA 4559
QY 4357 GGCACAGCTGCCATCCAGCTGGAGACTGACAACCTCATCCAGCTACCATCCGACCCA 4416
Db 4560 GGCACGCGAGCGTGGACCTGGAACGAGGACCTCATCCAGTCCACCATCCGAGACA 4619
QY 4417 GTTGTATPACTGCACTGTCTGACCATCGCACCGGCTTAACACTATCATGGACTACAC 4476
Db 4620 GTTCGAGGACTGCACCTCTCATCCATCGCCACCGCTCAACACCATCATGGACTACAC 4679
QY 4477 CAGGTCCTGTGCTTGACAAAGAGTAGTAGTGAATTTGATTTCTCCAGCCAACTCAT 4536
Db 4680 AAGGCTGATCTGCTTGGACAAAGAGAAATCCAGGAGTACGGCGCCCATCGGACCTCT 4739
QY 4537 TGCAGCTAGAGGAGCATCTTCTACGGGTGGCCAGAGATGCTGGACTTGCCTAAATATAT 4596
Db 4740 GCAGCAGAGAGGTCTTTCTACAGACTGGCCAAAGACGCGGCTTGGTGTGAGCCCCAGA 4799
QY 4597 CTTGAGATTTTC 4607
Db 4800 GCTGGCATATC 4810

RESULT 11
AAX21976
ID AAX21976 standard; cDNA; 5011 BP.

XX AAX21976;
AC
XX
DT 18-MAY-1999 (first entry)
XX Human multidrug resistance-associated protein coding sequence.
DE
XX
KW Multidrug resistance-associated protein; MDR; human; diagnosis;
KW MDR tumour cell identification; cancer therapy; ds.
OS Homo sapiens.
XX
XX US5882875-A.
XX
PD 16-MAR-1999.
XX
PF 05-JUN-1995; 95US-0462109.
XX
PR 05-JUN-1995; 95US-0462109.
PR 27-OCT-1992; 92US-0966923.

Db 1719 TCTCAATGGGATCAAGTGTAAAGCTTTATGCTGGAGCTGGCAATTCAGAGGACAAGGT 1778
QY 1546 GGAGGGATCAGGCGAGGTGAGCTCCAGCTGCTCGGCACGCGCGCTACCTCCACACAC 1605
Db 1779 GCTGGCCATCAGGCGAGGAGCTGAAGGTGCTGAAGAAGTCTGCCCTACCTGTCAGCGGT 1838
QY 1606 AACCACCTTCACCTGGATGTCGACGCCCTTCTGCTGACCTGATCACCCTCTCGGGTGA 1665
Db 1839 GGGCACCTTCACCTGGTCTGCGACGCCCTTCTGCTGACCTTGTGACATTTGCGGTCTA 1898
QY 1666 CGTGTAGCTGGACCCAAACAAATGCTGGAGCGCGGAGGCGCTTTGTGCTGTGTCCTT 1725
Db 1899 CGTGACCAATTTGAGGAGAACAACTCTCTGGATGGCCACAGACGCTTCGTGCTTTGGGCTT 1958
QY 1726 GTTTAATATCTTAAGACTTCCCTCAACATCTGCCCTCCAGTAACTAATCAGCAACCTGACTCA 1795
Db 1959 GTTCAACATCTCCGGTTTCCCTTGAACTTCTCCCATGGTCTATCAGCAGCTCGTGCA 2018
QY 1786 GGCAGTGTGCTCTGAAACGGATCCAGCAATTCCTGAGCCAGAGGAACCTTGACCCCCA 1845
Db 2019 GCGAGTGTCTCCTCAAGCGCTGAGGATCTTCTCTCCATGAGGAGCTGGAACTGA 2078
QY 1846 GAGTGTGGAAGAAAGAACCATCTCCOCAGC-----TATGCCATCACCATACACAG 1896
Db 2079 CAGCATCGAGCGAGCGCTCTCAAGACGCGGCGGCGCACGAACAGCATACCGGTGAGGAA 2138
QY 1897 TGGCACCCTTACCTTGGCCCGACAGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGT 1956
Db 2139 TGGCACAATTCACCTGGGCGAGGAGGACGACCTCCCACTCAATGGCATCACCTTCTCCAT 2198
QY 1957 CCGGAAAGGGGCACTGTGTGCGCTGTGTGGGCGCTGTGGGCTGTGGGAAGTCTCCCTCGGT 2016
Db 2199 CCGGAGGTGCTTTGTGTGCGCTGTGTGGCGAGGTGGGCTGCGGAAGTGTGCCCTGCT 2258
QY 2017 GTCTGCCCTCTGGGAGAGATGAGAGAGCTTAGAAGGCAAGTGCACATGAAGGCGTCCGT 2076
Db 2259 CTCAGGCCCTTGTGGCTGAGATGGACAAAGTGGAGGGGACGCTGGCTATCAAGGGCTCCGT 2318
QY 2077 GGCCTATGTGCCCGACAGCATGGATCCAGAACTGCACCTTTCAGAGAAACGTCCTTTT 2136
Db 2319 GGCCTATGTGCCAGCAGCGGCTGGATTCAGATGATCTCTCCGAGAAACATCCCTTTT 2378
QY 2137 CGGCAAGGCCCTGAACCCCAAGCGCTACACAGCAGACTCTGGAGGCTGTGCTGTGCTAGC 2196
Db 2379 TGGATGTCAGCTGGAGGAACCATATTACAGTCCGCTGATACAGGCTGTGCCCTCTCC 2438
QY 2197 TGACCTGGAGATCTGCTGGTGGGATCAGACAGAGATTGGAGAGAGGCGCATTAACCT 2256
Db 2439 AGACCTGGAAATCTGCCAGTGGGATCGGACAGAGATTGGGAGAGAGGCGGTGAACCT 2498
QY 2257 GTCTGGGGCCAGCGCAGCGGTGCTGCTGCTCGAGCTGTTTACAGTGTATGCCGATAT 2316
Db 2499 GTCTGGGGACAGCAGCGGCTGAGCTGTGGCCGGGCGGTGACTTCCAAACGCTGACAT 2558
QY 2317 TTTCTTGTGGATGACCCCACTGTCCCGGTGGACTCTCATGTGGCCCAAGCACATCTTTGA 2376
Db 2559 TTACCTTTCGATGATCCCTCTCAGCAGTGGATGCCATGTGGGAAAACACATCTTTGA 2618
QY 2377 CCAGCTATCGGGCCAGAGGCGTGTGGCAGGACAGACGCGAGTGTGTGACGACGG 2436
Db 2619 AAATGTGATTTGGCCCCCAAGGGATGTGAAGAAACAAAGACGCGGATCTTGTGCAGCACAG 2678
QY 2437 CATTAAGCTTCTGCCCGACAGACACTTCATATTGTGCTAGCTGATGGACAGGTGCTGA 2496
Db 2679 CATGAGCTACTTCCCGAGCTGGAGCTCATATCTGATGAGTGGCGGCGGAGATCTCTGA 2738
QY 2497 GATGGGCGGCTACCCAGCCCTGCTGCGAGCGCAACGCGCTCTTTTGCCAACTTCTCTGCAA 2556
Db 2739 GATGGGCTCTACCAAGAGCTGCTGCTGAGACGCGGCTTCCGCTGAGTTCTCTGCGTAC 2798
QY 2557 CTATGCCCGGATGAGGACCAAGGCGACCTTGGAGGACAGCTGGACCGCGGTGGAAGGTGC 2616

Db 2799 CTATGCCAGCAGACAGCAGGAGCAGGATGCAGAGGAGAAACGGGTCACGGGCTCAGCGG 2858
QY 2617 AGAGCATTAAGAGGAGCAGCTGCTGATTTGAAGACACACTCAGAAACACACAGGATCTGACAGA 2676
Db 2859 TCCAGGGAAGGAACAAAGCAAAATGGAGATGGCAT----- 2894
QY 2677 CAATGATCACTCACTATGTGGTCCAGACAGTTTATGAGACAGCTCAGTGCCCTGTC 2736
Db 2895 -----GCTGGTGGAGCAGTGCAGGGAAGCACTGCAGAGCAGCTCAGCAGCTCTCTC 2948
QY 2737 CTCAGATGGGAGGAGACAGGCTGCGCCTGTATCCCGGAGGACCTTGGGTCCATCAGAGAA 2796
Db 2949 CTCCTATAGTGGGACA---TCAGCAGSCACCAACAACAGCACCCAGACTGCGAGAA- 3003
QY 2797 GGTGCAAGTGCACAGGCGAAGGAGATGGGCACTGACCCAGAGGAGAGAAAGCAGCCAT 2856
Db 3004 ----GCTGAGGCCAAGAGGAGGAGACCTGGAAGCTGATGGAGGCTGACAAGGCGCAGAC 3059
QY 2857 TGGCACCTGTGAGGCTCAGTGTGCTTGGGATATGCCAAGGCGGTGGGCTCTGTATCCAC 2916
Db 3060 AGGCAAGTCAAGCTTTCCTGTTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119
QY 2917 GCTGGCCATCTGTCTCTGATGTGGGTCAAAGTGGGCTGCGCATTTGGAGCCAATGTGTG 2976
Db 3120 CTTCCTCAGCATCTTCCCTTTCATGTGTAACTGTGTCCCGGCTGGCTTCCAATATTG 3179
QY 2977 GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAAACAACTTCCCTGAG 3036
Db 3180 GCTCAGGCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGGACACAGAAAGTCG 3239
QY 3037 GCTGGGCTCTATCTGCTTTAGGAATCTCAAGGGTCTTGTGGTGTGCTGGGAGCCAT 3096
Db 3240 GCTCAGGCTCTATGAGGCCCTGGGCAATTTCAACGGGATGCGCGTGTGGCTACTCCAT 3299
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Db 3300 GGCCTGTGCCATCGGGGATCTTGGCTTCCGCTGTCTGCAGCTGGACCTGCTGCACAG 3359
QY 3157 CAAGTATGCTGCGCACAGTCTTCTTTGACACCAACCATCAGCCGCGCATCTCTGAACTG 3216
Db 3360 CATCTCGGCTCACCCATGAGCTTCTTTGAGCGGACCCCACTGGGAAACCTGGTGAACCG 3419
QY 3217 CTCTCTCAAGGACATCTATGCTGTTGATGAGTGTGCGCCCTGTCACTCTCATCTCTGCT 3276
Db 3420 CTCTCTCAAGGAGCTGGACACAGTGGACTCCATGATCCGAGGATCATCAGATGTTTCA 3479
QY 3277 CAATCTCTTCAACGCCATCTCCACTCTTTGTGTCATCATGCGCCAGCAGCCGCTCTT 3336
Db 3480 GGGCTCCTCTTCAACGCTCATTTGCTGCTGCTGCTGCTGCTGCGCCACGCCCATCGC 3539
QY 3337 CACTGTGCTCATCTGCGCCCTGGCTGTGCTTACACCTTGTGAGAGCGCTTCTATGACAGC 3396
Db 3540 CGCATCATCATCCCGCCCTTGGCCCTCATCTACTTCTTCTGCTCCAGAGGTTCTAGCTGGC 3599
QY 3397 CACATCACGGCACTGAAGGCGCTGGAATCAGTCAGCGGCTCACTTACTCTCTTCTTCT 3456
Db 3600 TTCTCTCCGCGAGCTGAAGGCGCTCGAGTCTGAGCGCTCCCGGCTCATATCCCATTT 3659
QY 3457 TTGCGAGACAGTACTGCTGCCAGTGTATCCGGGCTTACACCGCAGCAGCCGGAATTTGA 3516
Db 3660 CAACGAGACCTTGTGGGGTCAAGCTCATTTGAGGCTTTCAGGAGGAGGAGCGCTTCAT 3719
QY 3517 GATCATCAGTGTACTAAGGTGGATGCCAACCCAGAGAGCTGTACCCCTATCATCATCTC 3576
Db 3720 CCACGAGTGTGACCTGAAGGTGGAGAGAACAGAAAGGCTTATTACCCAGCATCGTGGC 3779
QY 3577 CAACGCTGCTGAGCATCGAGTGGAGTTCGTGGGAACTGCGGTGGTCTTTGTGCTG 3636
Db 3780 CAACAGTGTGCTGCGGCTGCGGCTGTGAGTGTGTGGGAACTGCACTGCTTCTGTTGCTG 3839
QY 3637 ACTATTGCGGCTCATCGGAGGAGCAGCTGAACCCGGGCTGGTGGGCTTCTGCTGTC 3696
Db 3840 CCGTGTGGGCTGATCTCCAGGCACAGCCCTCAGTGTGCTGGCTTGGTGGGCTCTCAGTGT 3899

Db 339 CTGTTTCCCTTCTACTCTCTATCTCTCCGACATGACCGGCTACATTCATGAC 398
Qy 205 CCACCTGTCCAAGTCAAGATGGTCTCTGGGTGTCTGCTGGTGCCTCTCTGGGCGGA 264
Db 399 ACCTCTCAACAAACAAACAACTGCTGGGATTTTGTGCTGGATCGTCTGCTGGCGAGA 458
Qy 265 CTTTCTTACTCCTTCCATGCGCTGGTCCATGGCGGGCCCTGCGCCCTGTTTCTTTGT 324
Db 459 CCTCTTACTCTTTCTTGGGAAAGTCGGGGCATATTCCTGGCCCGAGTGTCTCTGGT 518
Qy 325 CACCCCTTGGTGTGGGGTCAACATGCTGCTGCCACCTCTGTGATACAGATGAGCG 384
Db 519 CAGCCCACTCTTGGGCATCACCAGCTGCTTACCTTTTAATTCAGCTGGAGAG 578
Qy 385 GCTCGAGGGGTACAGCTTGTGGGGTCTCTCAATATCTTCTGTTCTGTGTGGTGTG 444
Db 579 GAGGAAGGAGTTCAGTCTTCAGGGATCATGCTCACTTTCTGGCTGGTAGTGTG 638
Qy 445 CGCCATGTCCTCCATTCGCTCCAGATCTTTTACGCAACCTCTGTGATACAGAGGTGAGATCTAGA 504
Db 639 TGCCCTAGCCATCTGAGATCCAAATATGACAGCCTTAAAGAGGATGCCCGAGTGA 698
Qy 505 CCCCTTCGGCTTACCACCTCTTACATCCACTTTGCCCCTGGTACTCTCTGCCCTCATCTT 564
Db 699 CTTGTTCTGACATCACTTTTACGTCTACTTTTCCCTTACTCTTACTTACGTGCTT 758
Qy 565 GGCCTGCTCAGGAGAAACCTCCTATTTTCTCGCAAGAAATGTCAGCCCTAACCCCTA 624
Db 759 GTCCCTGTTTCTCAGATGGCTCACCCCTGTTCTCGAAACCATCCAGCACCCCTAATCCCTG 818
Qy 625 CCCTGACAGCAGCTGGCTTCTCTCCCGCTTTTCTGTTCTGTTCTCACAAGATGGC 684
Db 819 CCCAGATCAGCGCTTCTTCTGTCGAGATCACTTCTGTTGATCATCAGGGTTGAT 878
Qy 685 CATCTATGGCTACCGGATCCCTGGAGGAGAGGACTCTGTGCTCCTAAAGGAAGAGA 744
Db 879 TGTCCGGGCTACCGCAGCCCTGGAGGCGAGTGAACCTCTGTGCTTAAACAGAGGA 938
Qy 745 CAGATCCAGATGGTGTGACGAGCTGTGAGGAGCATGAGGA- 788
Db 939 CAGCTCGGAACAAGTCTGTCTGTTTGGTAAAGAACTGGAAGAAGAAATGCGCCAGAG 998
Qy 789 -----ACGAGAAAGACAGCGGCACACACAGGCTTCAGCACCTGGGAAAA 840
Db 999 TAGAAGACGCGGTGAAGTTGTGTACTCTCCTCAAGGATCTGCCAGCGGAAAGAGAG 1058
Qy 841 TGCTCCGGGAGGACGAGGTGTGTGCTGGTG-----CCCGGCCAGGCC 885
Db 1059 TTCCAAGTGGATGCGAATGAGGAGGTGAGGCTTTGATCGTCAAGTCCACAGAGGA 1118
Qy 886 CCGAAGCCCTCTCTGAAGCCCTGTGGCCACCTTCGGCTCCAGCTTCCTCATCAG 945
Db 1119 GTGGAACCCCTCTCTGTTAAGTGTATACAGACCTTTGGGCCCTTCTCTCATGAG 1178
Qy 946 TGCTGCTTCAAGCTATCAGGACCTGTCTCTTCTCATCAATCCACAGCTGCTCAGCAT 1005
Db 1179 CTTCCTTCAAGCCATCCACAGCTGATGATGTTTCCGGCCGCGAGATCTTAAAGTT 1238
Qy 1006 CTGATCAGGTTTATCTCCAACCCCTGCGCCCTCTCTGTTGGGCTTCTGTGGCTGG 1065
Db 1239 GCTCATCAAGTTCGTGAATGACACGAAGGCCCGCAGCTGSCAGGGCTACTTTCACACCGT 1298
Qy 1066 GCTGATGCTTCTGTCTCATGATGATGCTGCTGATCTTACACACTATTACCACTACAT 1125
Db 1299 GCTGCTGTTTGTCACTGCTGCTGCTGAGACCTCTGCTGCTCAGCAGTACTTCCACATCTG 1358
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Db 1359 CTTGCTAGTGGCATGAGGATCAAGACCGCTGTCTATTTGGGCTGTCTATCGAAGGCCCT 1418
Qy 1186 GGTATACCAACTCAGTCAAGAGTGGCTGCTGCTGCTGAGGAAATGCTCAACCTCATGTC 1245
Db 1419 GGTGATCACCAATTCAGCCAGAAATCCTCCAGGCTGGGAGATGTCACCACTCATGTC 1478

Qy 1246 AGTGATGCCCGACGCTTTCATGGACCTTGCCCTTCCCTCAATCTGCTGTGTGACACCC 1305
Db 1479 TGTGACGCTCAGAGGTTTCATGGACTTGGCCACGTACATTAACATGATCTGTGACGCC 1538
Qy 1306 CTTGAGATCACTCTGGGATCTACTTCTCTGGCAGAACCTAGTCTCTGTCTGTCTGCG 1365
Db 1539 CTTGAACTCATCTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1598
Qy 1366 TGGAGTCTCTTTCATGCTTCTGCTGATCCACTCAAGGAGCTGTGGCGTGAAGATGG 1425
Db 1599 TGGAGTGGGCTGATGGTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1658
Qy 1426 CGCCTTCCAGCTTAAAGCAATGAAGACTCGGCATCAAGCTGATCAGTGAAGAT 1485
Db 1659 GACGTATCAGGTGGCCCATGAGAGCAAGCAATCGGATCAAGCTGATGAAGCAAT 1718
Qy 1486 CTTGAACGGCATCAAGTGTGAAGCTGTAGCCTGGGAGCCAGCTTCTCTGAAGCAGGT 1545
Db 1719 TCTCAATGGGATCAAGTGTAAAGCTTATGCTGGGAGCTGGCATCAAGCAAGGT 1778
Qy 1546 GGAGGCTATCAGGAGGCTGAGCTCCAGCTGCTGCGCAGCGGCGCTACCTCCACACCAT 1605
Db 1779 GCTGGCCATCAGGAGGAGGCTGAAGTGTGAAGAGTGTGCTGCTGCTGCTGCTGCTGCT 1838
Qy 1606 AACCACTTCACTGGATGTGAGCCCTTCTGCTGACCCCTGATCACCCTCTGGGTGA 1665
Db 1839 GGGCACTTCACTGGGTCTGACGCCCTTCTGCTGGCTTGTGCAATTTGCGCTCTA 1898
Qy 1666 CTTGATCTGGACCCAAACAATGTGCTGGAGCCGAGAGGCTTGTGTCTGTGTCTT 1725
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Qy 1726 GTTAAATCTTAAAGCTTCCCTCAACATGCTGCCCACTTAATCAGCAACTGACTCA 1785
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Qy 1786 GGCAGTGTGTCTCTGAACGGATCCAGCAATTCCTGAGCCAAAGAGGAACTTGACCCCA 1845
Db 2019 GGCAGTGTCTCCCTCAACGCCCTGAGGATCTTCTCTCCATGAGGAGCTGGAACCTGA 2078
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Db 2079 CAGCATCGAGCGAGCGCTGTCAAGAGCGGGGGGACGAAACAGCATCACCGTGAGAA 2138
Qy 1897 TGGCACCTTCACTTGGCCAGGACCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1956
Db 2139 TGCCACATTCACCTGGCCAGGAGGACCTTCCACACTGAATGGCATCACCTTCTCCAT 2198
Qy 1957 CCCGAAAGGGGACTGTGGCCCTGTGGGCTGTGGGCTGTGGGAAAGTCTCCCTGCT 2016
Db 2199 CCCGAAAGGTCTTGTGTGGCGTGTGGGCGAGGTGGGCTGCGGAAAGTGTCCCTGCT 2258
Qy 2017 GTCGCGCTGCTGGAGAGATGGAGAGCTAGAAGGAAAGTGCACATGAAGGGCTCGT 2076
Db 2259 CTCAGCCCTTCTGTGCTGAGATGGACAAAGTGGAGGGGACCTGGCTATCAAGGGCTCGT 2318
Qy 2077 GGCCTATGTGCCCGCAGGCGATGATCCAGAACTGCACTCTTCAGGAAAAAGTCTTTT 2136
Db 2319 GGCCTATGTGCCACAGCAGGCTGATTCAGAAATGATCTCTCCGAGAAACATCTTTT 2378
Qy 2137 CGGAAAGCCCTGAACCCCAAGCCTTACAGCAGACTTGTGAGGCTGTGCTGTGCTAGC 2196
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Qy 2197 TGACCTGGAGATGCTGCTGTGGGATCAGACAGATTTGGAGAGAGGCGATTAACCT 2256
Db 2439 AGACCTTGAATCTTGGCCAGTGGGATCGGACAGATTTGGCAGAGAGGCGGTGAACCT 2498
Qy 2257 GTCTGGGGGCGAGCGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2316
Db 2499 GTCTGGGGGACAGAGCAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2558

QY	2317	TTTCTTGCTGGATGACCCCACTGTGCCGGTGGACTCTCATGTGGCCAAGACAATCTTTGA	2378
DB	2559	TTACCTCTTCGATGATPCCCTCTCACAGTGGATGCCATTGTGGAAAAACATCTTTGA	2618
QY	2377	CCACGTCTATCGSGCCNAGRAGCGTGTCTGGCAGGCAGAAGCCGAGTCTGCTGGTAGCCACGG	2436
DB	2619	AAATGTGATTTGGCCCCAAGGGGATCTGAAGAACAAAGACGGGATCTTGGTCACGCACAG	2678
QY	2437	CATTAGCTTCCTGCCCCAGACAGACTTCATCTATTGTCTAGCTGATGGACAGGTGCTGA	2496
DB	2679	CATGAGCTACTTTGCCGAGTGGAGCTCATCTCATGTCATGATGGCGGCAAGATCTCTGA	2738
QY	2497	GATGGCCGGTPACCAGCCCTGCTGCAGCGCAACGGCTCCTTTGGCAAATTTCTCTGCAA	2556
DB	2739	GATGGCTCTCTACCAGGAGCTCTGGCTCGAGACGGCGCTTCGCTGAGTTCTCGGTATC	2798
QY	2557	CTATGCCCCCAGTAGAGGCAAGGCACTCTGGAGGACACTGGACCGGTTGGAAAGGTGC	2616
DB	2799	CTATGCCAGCAGAGCAGGACGAGTGCAGGAGGAACGGGTCACGGGGTCTAGCGG	2858
QY	2617	AGAGGATAAGGAGGCACTGCTGATTGAAGACACACTTCAGCAACCAACGATCTGACAGA	2676
DB	2859	TCCAGGGAAGCAAGCAATGGAGTAATGGCAT-----	2894
QY	2677	CAATGATCCAGTCACTATGTGGTCCAGAAAGCAAGTTTATGACAGACTGAGTGCCCTGTC	2736
DB	2895	-----GCTGGTGACGGACAGTGCAGGGAAGCACTGCAGACAGCAGTCTCAGCAGTCTCTC	2948
QY	2737	CTCAGATGGGAGGACAGGGTCGGCTGTACCCGGAGGCACTTGGGTTCATTCAGAGAA	2796
DB	2949	CTCCTATATAGTGGGGACA---TCAGCAGGCACCAACAGCACCGCAGAACTTCGAGAAA-	3003
QY	2797	GGTGAGCTGACAGAGCGCAAGGCAGATGGGCACTTGACCCAGGAGGAGAAAGCAGCCAT	2856
DB	3004	---GCTGAGGCCAAGAGGAGGACCTGGAAGCTGATGGAGGTGCACAGCGGCAGAC	3059
QY	2857	TGGCACTGTGAGCTCAGTGTGTCTTGGATTTATGCCAAGCGCTGGGCTCTGTACCAC	2916
DB	3060	AGGGCAGTCAAGCTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC	3119
QY	2917	GCTGGCACTGTCTCCGTATGTGGGTCAAGTGGGCTGCCATTGGAGGCCAATGTGTG	2976
DB	3120	CTTCTCAGCATFTCTCTTTTCATGTGTAACCATGTGTCGGCGCTGGCTTCCAACATTTG	3179
QY	2977	GCTAGTGCCTTGGCAAAATGATGCCATGGCAGACAGTAGACAGAAACAACATCTCCCTGAG	3036
DB	3180	GCTCAGCCTCTGGACTGATGACCCCATGTCNAOCCGACTCAGGAGCACACGAAAGTCCG	3239
QY	3037	GCTGGGCTCTATGCTGCTTTAGGAATTTCTGCAAGGGTTCTTTGGTGATGCTGGCAGCCAT	3096
DB	3240	GCTGAGCTCTATGGAGCCCTGGGCATTTCAAGGGATCGCCGTGTTGGCTACTCCAT	3299
QY	3097	GGCCATGGCAGGGTGGCATCCAGGCTGCCGTGTGTGACACAGGCACTGCTGCACAA	3156
DB	3300	GGCCGTGTCATCGGGGGATCTTGGCTTCOCGTGTCTGCACGTGGACCTGCTGCACAG	3359
QY	3157	CAAGATACGCTCGCCACAGTCTCTTTTGACACCACCATCAGCGCCGATCCTGAACTG	3216
DB	3360	CATCCTGGGTCAACCATGAGCTCTTTGGGGGACCCCCAGTGGGAACCTGGTGAACCG	3419
QY	3217	CTTCTCAAGGACATCTATGTGTTGATGAGGTCTTGGCCCTGTGATCTCATCTGCTGTGT	3276
DB	3420	CTTCTCAAGGAGCTGGACACAGTGGACTTCCATGATCCCGAGGTCAATCAAGATGTTCA	3479
QY	3277	CAATTCCTTCTCAAGCCATCTCCACTCTTGTGTGTCATCATGCGCCAGCAGCCGCTCTT	3336
DB	3480	GGGCTCCCTGTTCAACGTCATTTGGTGGCTGTCATCGTTATCTGCTGGCCACGCGCATGCG	3539
QY	3337	CACGTGTGCTCTCTGCCCCCTGGGTGCTCTACACCTTAGTGCAGCGCTTCTATGCGAGC	3396
DB	3540	CGCCATCATCATCGGCCCTTGGCCCTCATCTACTCTTCTGTCAGAGGTTCTACGTGGC	3599
QY	3397	CACATFCAGGCAACTGAAGCGGCTGGAATCAGTCAGCGGCTCACCTATCTACTCCCACTT	3456

[illegible]

Db 2319 GGCCTATGTCACAGAGCCCTGGATTCAAGATTGATCTCTCGAGAAACATCCCTTTT 2378
 QY 2137 CGGCAAGCCCTGAACCCCAAGGCTACACAGCAGACTCTGAGGCCCTGTGCTTGTAGC 2196
 Db 2379 TGGATGTCAGCTGGAGGAACCATATTACAGTCCGTGATACAGGCTGTGCCCTCCTCCC 2438
 QY 2197 TGACCTGGAGATGCTGCTGTGGGATCAGACAGAGATTGGAGGAAGGGCATTAACCT 2256
 Db 2439 AGACCTTGAATCTGCCAGTGGGATCGGATCGACAGAGATTGGGAGAAGGCGGTGAACCT 2498
 QY 2257 GTCTGGGGGACGGCAGCGGCTCAGTCTGGCTCGAGCTGTTTACAGTGATGCGGATAT 2316
 Db 2499 GTCTGGGGGACAGACAGCGGCTGAGCTTGGCCCGGCGCTGACTCCACGCTGACAT 2558
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 QY 2557 CTATGCCCCGATGAGACCAAGGACCTTGGAGACAGCTGTGACGCCGCTTGGAAAGTGC 2616
 Db 2799 CTATGCGACACAGACGAGCAGGATGTCAGAGAGAACGGGTCACGGGCGTCAGCGG 2858
 QY 2617 AGAGTAAGAGGAGCTGCTGATTGAAGACACACTCAGCAACACAGCATCTGACAGA 2676
 Db 2859 TCAGGGAAGGAAGCAAGCAATGGAGATGGCAT----- 2894
 QY 2677 CAATGATCCAGTCAACCTATGTGTGTCAGAGACAGTATTATGAGACAGCTGAGTGCCTGTC 2736
 Db 2895 -----GCTGGTGACGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGTCTC 2948
 QY 2737 CTCAGATGGGAGGACAGGCTGGCTGTACCCCGGAGGACCTGGGTCCATCAGAGAA 2796
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 Db 3240 GCTGAGCGTCTATGAGCCCTTGGGCAATTCACAAGGATGCGCGTGTGGCTACTCCAT 3299
 QY 3097 GGCATGAGCAGGGGTGGCATTCAGCGCTGCCGCTGTGTGTGACAGCACTGTGTGCACAA 3156
 Db 3300 GGCGGTGTCCATCGGGGGATCTGTGGCTTCCGCTGTCTGCACGTGGACCTGTGTGCACAG 3359
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Db 3360 CATCTCGGGTCAACCATGAGCTTCTTTGAGGGGACCCCTAGTGGGAACCTGGTGAACCG 3419
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 Db 3420 CTTCTCAAGGAGCTGGACACAGTGCATCCATGATCCGGAGGTTCATCAAGATGTTAT 3479
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 Db 4200 CTTGACCTGGGCTTATTCGGATCAACGATCTGCCAAGGAGAGATCATCATGATGG 4259
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DB 3480 GGGTCCCTTCTCAAGCTCATGGTGCCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 3539
QY 3337 CACTGTGTGTCATCTCCCTGCTGCTCTACACCTTAGTGACGCTTCTATGACG 3396
DB 3540 CGCATCATCATCCCGCCCTTGGCTCATCTACTTCTTCTGTCAGAGGTTCTACGTGGC 3599
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DB 3600 TTCTCTCCCGCAGCTGAAGCGCTGAGTGGTCAAGCGCTTCCCGCTCTATTTCCCATTT 3659
QY 3457 TTCGGAGACGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3516
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QY 3517 GATCATCATGATATTAAGTGGATGCCAACACGAGAGAGCTGCTACCCCTACATCATCTC 3576
DB 3720 CCACAGAGTGAACCTGAGGTGGACGAGAACGAGAGGCTATTACCCAGCATCTGTCG 3779
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QY 3637 ACTATTTCGCTCATCGGAGGAGCAGCTGAACCGGGGCTGAGCGGCTTCTGCTGTC 3696
DB 3840 CCGTGTGGGTGATCTCCAGGACAGCGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3899
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DB 3960 AACCAACATCGTGGCGTGGAGAGCTCAAGGAGTATTCAGAGACTGAGAAGGAGCGCC 4019
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QY 3937 GCATGTGCAGGTGGCGAGAGTGGGATCGTGGCGGCTGAGCTGGCGGCTGAGCTGCTGCT 3996
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Job time : 715.101 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:10 ; Search time 8364.83 Seconds
(without alignments)
17670.781 Million cell updates/sec

Title: US-09-647-140A-5

Perfect score: 5079

Sequence: 1 cccatggagccctgtgcg.....ctgatgaataaaactacag 5079

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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7: gb.ph.*
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15: em.ba.*
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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5079	100.0	5079	9	AF104943	AF104943 Homo sapi
2	5073.2	99.9	5117	9	AF083552	AF083552 Homo sapi
3	5071.6	99.9	5117	9	AB010887	AB010887 Homo sapi
4	5071.6	99.9	5193	6	AX443141	AX443141 Sequence
5	5056	99.5	5142	9	AF085690	AF085690 Homo sapi
6	4895.4	96.4	5291	9	AF085691	AF085691 Homo sapi
7	4892.4	96.3	4948	9	HSY17151	Y17151 Homo sapien
8	4828.8	95.1	5346	9	AF085692	AF085692 Homo sapi
9	4636.4	91.3	4762	9	AF009670	AF009670 Homo sapi
10	4586.8	90.3	4762	6	A64692	A64692 Sequence 58
11	3186.4	62.7	5174	10	AB010467	AB010467 Rattus no
12	3152.4	62.1	5107	10	AF072816	AF072816 Rattus no
13	1749.4	34.4	1977	6	AX333322	AX333322 Sequence
14	1749.4	34.4	1977	6	AX333826	AX333826 Sequence
15	1745.8	34.4	1977	6	AX410761	AX410761 Sequence
16	1737.8	34.2	5011	6	SATHMRP	X78338 Synthetic a
17	1737.8	34.2	5011	6	AR070198	AR070198 Sequence
18	1737.8	34.2	5011	6	AR093439	AR093439 Sequence
19	1737.8	34.2	5011	6	I17455	I17455 Sequence 1
20	1737.8	34.2	5011	9	HUMRPX	L05628 Human multi
21	1736.2	34.2	5011	6	AR070199	AR070199 Sequence
22	1736.2	34.2	5011	6	AR093440	AR093440 Sequence
23	1612.6	31.8	4587	10	AF022908	AF022908 Mus muscu
24	1612.6	31.8	5889	6	AR070200	AR070200 Sequence
25	1612.6	31.8	5889	6	AR093441	AR093441 Sequence
26	1516.2	29.9	1565	9	HSU83659	U83659 Human multi
27	1372	27.0	2242	9	AF154001	AF154001 Homo sapi
28	1209.2	23.8	5817	5	AF486830	AF486830 Raja erin
29	1207.8	23.8	5473	3	AY069827	AY069827 Drosophil
30	1173.8	23.1	182222	2	AC123374	AC123374 Rattus no
31	1109	21.8	5407	4	OC249144	Z49144 O. cuniculus
32	1096.4	21.6	4864	9	HSCMRP	X63395 H.sapiens m
33	1096.4	21.6	4868	9	HSU63970	U63970 Human canal
34	1096.4	21.6	5586	6	A64635	A64635 Sequence 1
35	1094.8	21.6	4659	9	AF410948	AF410948 Macaca mu
36	1094.8	21.6	4868	6	E15807	E15807 Human mRNA
37	1094.8	21.6	5300	6	AX410727	AX410727 Sequence
38	1094.8	21.6	5300	9	HSU49248	U49248 Human canal
39	1075.6	21.2	4934	4	CFA315401	AJ315401 Canis fam
40	1057.6	20.8	4509	9	AF168791	AF168791 Homo sapi
41	1057.4	20.8	4512	6	AX282510	AX282510 Sequence
42	1057.4	20.8	4535	9	AF076622	AF076622 Homo sapi
43	1048.4	20.6	5016	4	CFA18220	Y18220 Canis famli
44	1042	20.5	4632	10	AF282773	AF282773 Mus muscu
45	1035.6	20.4	4632	10	AF282772	AF282772 Mus muscu

ALIGNMENTS

RESULT 1	AF104943	AF104943	5079 bp	mRNA	linear	PRI 12-JAN-1999
LOCUS	Homo sapiens ABC transporter MOAT-D (MOAT-D) mRNA, complete cds.					
DEFINITION	Homo sapiens ABC transporter MOAT-D (MOAT-D) mRNA, complete cds.					
ACCESSION	AF104943					
VERSION	AF104943.1	GI:4140699				
KEYWORDS						
SOURCE	Homo sapiens.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	1 (bases 1 to 5079)					
	Belinsky, M.G., Bain, L.J., Balsara, B., Testa, J.R. and Kruh, G.D.					
	Characterization of MOAT-C and MOAT-D, new members of the MRP/CMOAT					
	subfamily of transporter proteins					

[illegible]

[illegible]

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Db	2581	GCACCTGGAGGACAGCTGGACCGCGTTGGAAGTGCAGAGGATAAAGAGGCACTGCTGAT	2640
QY	2641	TGAAGACACACTCAGCAACACACGGATCTGACAGACAATGATCCAGTCACCTATGTGGT	2700
Db	2641	TT	2700
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Db	3301	CACCTCTGTGGTCATCATGGCCAGACGCGCTCTTTCACGAGACAGTCACTGGTGGCCAG	3360
QY	3361	TGTGCTCTACACCTTAGTGACGCGTCTATGACAGCCACATCAGGCCACTCAAGCGGCT	3420
Db	3361	TGTGCTCTACACCTTAGTGACGCGTCTATGACAGCCACATCAGGCCACTCAAGCGGCT	3420
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Db	3421	GGAATCAGTCAGCCGCTCACCTTATCTACTCCCACTTTTCGGAGACAGTCACTGGTGCCAG	3480
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ORIGIN

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Matches 5075; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 3
AB010887
LOCUS

DEFINITION Homo sapiens mRNA for multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2), complete cds.
AB010887
VERSION AB010887.1 GI:3132269
KEYWORDS multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2).

SOURCE Homo sapiens cell_line:Caco-2 cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
AUTHORS Kiuchi,Y., Suzuki,H., Hirohashi,T., Tyson,C.A. and Sugiyama,Y.
TITLE cDNA cloning and inducible expression of human multidrug resistance associated protein 3 (MRP3)
JOURNAL FEBS Lett. 433 (1-2), 149-152 (1998)
MEDLINE 98409330
REFERENCE 2 (bases 1 to 5117)
AUTHORS Kiuchi,Y., Suzuki,H., Hirohashi,T. and Sugiyama,Y.
JOURNAL Direct Submission
TITLE Submitted (02-FEB-1998) Yuichi Sugiyama, Graduate School of Pharmaceutical Sci., The University of Tokyo, Department of Pharmacueticals, Hongo 7-3-1, Bunkyo-ku, Tokyo 113, Japan
(E-mail:BXG05433@niftyserve.or.jp, Tel:+81-3-3812-2111, Fax:+81-3-5800-6949)

FEATURES
source

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REFERENCE
AUTHORS 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Burgess, C.E., Conley, P.B., Grosse, W.M., Hart, M., Kekuda, R.,
Shimkets, R.A., Spytek, K.A., Szekeres, E.S., Tomlinson, J.E.,
Topper, J.N. and Yang, R.B.
TITLE Proteins and nucleic acids encoding same
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FEATURES Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
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REFERENCE 1 (bases 1 to 5291)
AUTHORS Fromm,M.F., Leake,B., Roden,D.M., Wilkinson,G.R. and Kim,R.B.
TITLE Human MRP3 transporter: identification of the 5'-flanking region,
genomic organization and alternative splice variants
JOURNAL Biochim. Biophys. Acta 1415 (2), 369-374 (1999)
MEDLINE 99107643
PUBMED 9889399
REFERENCE 2 (bases 1 to 5291)
AUTHORS Fromm,M.F., Leake,B., Roden,D.M., Wilkinson,G.R. and Kim,R.B.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Pharmacology, Vanderbilt University, 572
MRB1, Nashville, TN 37232, USA
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RESULT 7
HSY17151
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DEFINITION Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3).
ACCESSION Y17151
VERSION Y17151.2 GI:4826562
KEYWORDS ABC3 protein; MRP3 gene; multidrug resistance protein 3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Koenig, J., Rost, D., Cui, Y. and Keppler, D.
TITLE Characterization of the human multidrug resistance protein isoform MRP3 localized to the basolateral hepatocyte membrane
JOURNAL Hepatology 29 (4), 1156-1163 (1999)
MEDLINE 99197095
PUBMED 10094960
REFERENCE
AUTHORS Koenig, J.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1998) J. Koenig, DKFZ Heidelberg, Abteilung
Tumorbiochemie, Im Neuenheimer Feld, 280 D-69120 Heidelberg, FRG
COMMENT On May 13, 1999 this sequence version replaced gi:3087793.
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BASE COUNT 1011 a 1453 c 1364 g 1120 t

ORIGIN

Query Match 96.3%; Score 4892.4; DB 9; Length 4948;
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AUTHORS Kool, M., van der Linden, M., de Haas, M., Scheffer, G.L., de
Vree, J.M.B., Smith, A.J., Jansen, G., Peters, G.J., Ponne, N.,
Scheper, R.J., Elferink, R.P.J.O., Baas, F. and Borst, P.
MRP3, an organic anion transporter able to transport anti-cancer
drugs
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (12), 6914-6919 (1999)
MEDLINE 99289572
PUBMED 10359813
REFERENCE 2 (bases 1 to 4762)
AUTHORS Kool, M., de Haas, M., Ponne, N.J., Baas, F. and Borst, P.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1997) Molecular Biology, The Netherlands Cancer
Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
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RESULT 10

A64692

LOCUS

A64692 4762 bp

DNA

linear

PAT 29-MAR-1999

DEFINITION Sequence 58 from Patent WO97/3111.

ACCESSION A64692

VERSION A64692.1 GI:4530758

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

unclassified.									
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AUTHORS	Oude, E.R., Paulusma, C.C., Bosma, P.J., Borst, P., Evers, R., Kool and Marcel.								
TITLE	A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM								
JOURNAL	Patent: WO 9731111-A 58 AUG-1997;								
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DEFINITION Rattus norvegicus mRNA for multidrug resistance-associated protein
(MRP)-like protein-2 (MLP-2), complete cds.
ACCESSION AB010467
VERSION AB010467.1 GI:3242459
KEYWORDS multidrug resistance-associated protein (MRP)-like protein-2
(MLP-2).
SOURCE Rattus norvegicus (strain:Sprague-Dawley) adult male colon cDNA to
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ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (sites)
AUTHORS Hirohashi,T., Suzuki,H., Ito,K., Ogawa,K., Kume,K., Shimizu,T. and
Sugiyama,Y.
TITLE Hepatic expression of multidrug resistance-associated protein-like
proteins maintained in eisel hyperbilirubinemic rats
JOURNAL Mol. Pharmacol. 53 (6), 1068-1075 (1998)
MEDLINE 98279126
REFERENCE 2 (bases 1 to 5174)
AUTHORS Hirohashi,T.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceutical
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Fax:81-3-5800-6949)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrihan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
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Avalon Pharmaceuticals (US)
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[illegible]

Search completed: December 18, 2002, 17:17:03
Job time : 8422.83 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:25 ; Search time 3824.06 Seconds
(without alignments)
19096.316 Million cell updates/sec

Title: US-09-647-140A-7
Perfect score: 4509
Sequence: 1 atggccgcgcctgagcc.....ccagagtcagcctggctc 4509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_estl.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_eston.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	652.8	14.5	947	14	BQ645685	BQ645685 AGENCOURT
2	623.4	13.8	655	9	AL596779	AL596779 DKFZp451H
3	434.4	9.6	566	12	BG834418	BG834418 352634 MA
4	415.6	9.2	558	12	BG610482	BG610482 326419 MA
5	395.6	8.8	701	13	B1147240	B1147240 602913152
6	393.4	8.7	838	12	BF539254	BF539254 602054722

7	332.8	8.7	603	13	BI338028	BI338028 361675 MA
8	384.6	8.5	1977	11	U66674	U66674 Homo sapien
9	382.8	8.5	474	10	AG670647	AG670647 114778 MA
10	360.6	8.0	471	12	BG834170	BG834170 352284 MA
11	359	8.0	471	12	BG834171	BG834171 352285 MA
12	334	7.4	570	10	AW318859	AW318859 un08ell.y
13	327.8	7.3	518	14	BM826384	BM826384 K-EST0098
14	319.4	7.1	541	10	BE014336	BE014336 125901 MA
15	314	7.0	314	13	BI036283	BI036283 CM3-NT024
16	312	6.9	1080	13	BI221221	BI221221 602939585
17	310.2	6.9	477	14	T69749	T69749 YOI412.s1
18	300.8	6.7	896	14	BQ434553	BQ434553 AGENCOURT
19	298	6.6	888	14	BQ687464	BQ687464 AGENCOURT
20	285	6.3	368	10	AW485631	AW485631 67105 MAR
21	282.4	6.3	898	14	BQ690370	BQ690370 AGENCOURT
22	277.8	6.2	1006	14	BM804774	BM804774 AGENCOURT
23	276.4	6.1	1125	14	BM799798	BM799798 AGENCOURT
24	272.2	6.0	1068	13	BI147070	BI147070 602913321
25	271.6	6.0	541	10	AW108440	AW108440 un30f09.x
26	270.2	6.0	743	13	BI687138	BI687138 603314982
27	266.6	5.9	694	13	BM251797	BM251797 BOP101000
28	266.6	5.9	983	11	AK006128	AK006128 Mus muscu
29	265.4	5.9	1914	11	U66684	U66684 Homo sapien
30	263.6	5.8	618	10	AV661510	AV661510 AV661510
31	262.8	5.8	767	13	BI329076	BI329076 602980201
32	261.2	5.8	298	12	BF815129	BF815129 MR2-C1012
33	260.2	5.8	474	9	AI032554	AI032554 ov69g06.s
34	260.2	5.8	696	12	BG328614	BG328614 602427877
35	259.8	5.8	503	9	AA537850	AA537850 vj34f02.r
36	259	5.7	480	14	H94404	H94404 yv17h10.r1
37	257.4	5.7	958	13	BI330408	BI330408 602983414
38	255.6	5.7	936	14	BQ920393	BQ920393 AGENCOURT
39	253.8	5.6	801	13	BI664268	BI664268 603289021
40	251.6	5.6	698	13	BM626308	BM626308 170006874
41	249.4	5.5	800	12	BC205053	BC205053 RST24472
42	248.8	5.5	2727	11	EC026509	EC026509 Mus muscu
43	247.8	5.5	572	13	BI843062	BI843062 fr02f04.y
44	247	5.5	720	10	AW013471	AW013471 pc071KS.W
45	246.2	5.5	617	13	BJ001995	BJ001995 BJ001995

ALIGNMENTS

RESULT 1
BQ645685
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ645685
AGENCOURT_8414907 NIH_MGC_100 Homo sapiens cdna clone IMAGE:6271971
5', mRNA sequence.
BQ645685
BQ645685.1 GI:21769857
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 947)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2449 row: j column: 04
High quality sequence start: 18
High quality sequence stop: 645.
Location/Qualifiers

FEATURES

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source
1. .947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6271971"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 198 a 290 c 257 g 202 t
ORIGIN

Query Match 14.5%; Score 652.8; DB 14; Length 947;
Best Local Similarity 95.3%; Pred. No. 6.4e-142;
Matches 738; Conservative 0; Mismatches 27; Indels 9; Gaps 6;

Qy 1 ATGGCCGCGCTGTGAGCCCTGCGCGGGGAGGGGCTGGAACACAGACAGAGCTGAA 60
Db 43 ATGGCCGCGCTGTGAGCCCTGCGCGGGGAGGGGCTGGAACACAGACAGAGCTGAA 102
Qy 61 CTGCGCCGACAGCCTGCTGAGCCTGTGCTCTCTGGAACAGACAGAGGCTGTGGTACCC 120
Db 103 CTGCGCGCAGCAGCCTGCTGAGCCTGTGCTCTCTGGAACAGACAGAGGCTGTGGTACCC 162
Qy 121 CCCATGTACCTCGGATG-TCCCCACTCTTCAAAGCCAAAGATGCTGTGGATTGCGCCCTCAT 180
Db 163 CCCATGTACCTCGGATG-TCCCCACTCTTCAAAGCCAAAGATGCTGTGGATTGCGCCCTCAT 222
Qy 181 GGCTACCTCGGATG-TCCCCACTCTTCAAAGCCAAAGATGCTGTGGATTGCGCCCTCAT 239
Db 223 GGCTACCTCGGATG-TCCCCACTCTTCAAAGCCAAAGATGCTGTGGATTGCGCCCTCAT 282
Qy 240 AGTCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTGGAAATCCAAAGGAGGAGCCCTGA 299
Db 283 AGTCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTGGAAATCCAAAGGAGGAGCCCTGA 342
Qy 300 GGCCCCAGAAATCTCATTCATCTACTGTGTGGCTACACAGATGAGCTTCGCGAGTGT 359
Db 343 GGCCCCAGAAATCTCATTCATCTACTGTGTGGCTACACAGATGAGCTTCGCGAGTGT 402
Qy 360 CCTGATTACACCGAGAGGAGGAGGAGTCCAGTCTCTGAGTGTCTGTTTGGTTACTG 419
Db 403 CCTGATTACACCGAGAGGAGGAGGAGTCCAGTCTCTGAGTGTCTGTTTGGTTACTG 462
Qy 420 GCTTCTGTGCTTTGCTGTCCAGCTACCAAGCTGCCAGAGGCTCCGGAGGCGGTT 479
Db 463 GCTTCTGTGCTTTGCTGTCCAGCTACCAAGCTGCCAGAGGCTCCGGAGGCGGTT 522
Qy 480 CCAGAGGAGCCTGTCCGCCACCTGTCCACCTACTATGCTGTCTGTGTGGTGGCACA 539
Db 523 CCAGAGGAGCCTGTCCGCCACCTGTCCACCTACTATGCTGTCTGTGTGGTGGCACA 582
Qy 540 GTTTGTGCTGTCTGCTGGCGGATCAACCCCTCTTCCCTGAAAGACCCCGAGCAGTC 599
Db 583 GTTTGTGCTGTCTGCTGGCGGATCAACCCCTCTTCCCTGAAAGACCCCGAGCAGTC 642
Qy 600 TAACCCCTGTCCAGAGACTGGGGAGGCTTCCCTCCAAAGCCACG-TTCTGTGGGGTTT 658
Db 643 TAACCCCTGTCCAGAGACTGGGGAGGCTTCCCTCCAAAGCCACGTTTCTGTGGGGTTT 702
Qy 659 CTGCGCTGGTCTGAGGGGATACA--GGAGGCCACT--GAGACCAAGACCTCTGTGTCG 714
Db 703 CTGCGCTGGTCTGAGGGGATACAAGGGAGGCGCCTGTGGAGACCAAGACCTCTGTGTCG 762
Qy 715 CTT--GGGAGAGAAACTCTCT--CAGAAGAACTGTGTTTCCCGGCTTGAAAGGAG 765
Db 715 CTT--GGGAGAGAAACTCTCT--CAGAAGAACTGTGTTTCCCGGCTTGAAAGGAG 765
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Db 763 CTTTGGAGAGAAACTCTCTCAAAAGAACTTGTTTCCCGGCTTGAAAAAG 116

RESULT 2
LOCUS AL596779 655 bp mRNA linear EST 14-AUG-2001
DEFINITION DKF2p451H201_r1 451 (synonym: hlccl) spinal cord Homo sapiens cDNA
clone DKF2p451H201 5', mRNA sequence.
ACCESSION AL596779
VERSION AL596779.1 GI:15154475
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 655)
AUTHORS Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
TITLE EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
JOURNAL Unpublished (1999)
COMMENT Contact: Poustka A.J.
Department Leirach
Max-Planck-Institute for Molecular Genetics
Innestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKF2p451H201) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..655
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p451H201"
/clone_lib="451 (synonym: hlccl) spinal cord"
/tissue_type="human spinal cord"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 116 a 220 c 175 g 144 t
ORIGIN

Query Match 13.8%; Score 623.4; DB 9; Length 655;
Best Local Similarity 99.8%; Pred. No. 4.1e-135;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGCGCCCTGTGAGCCTGCGCGGGGAGGGGCTGGAACACAGACAGAGCTGAA 60
Db 31 ATGGCGCGCCCTGTGAGCCTGCGCGGGGAGGGGCTGGAACACAGACAGAGCTGAA 90
Qy 61 CTGCGCGCCACAGCCTGCTGAGCCTGTCTTCTCTGAGAACAGCAGGCTCTGGGTACCC 120
Db 91 CTGCGCGCCACAGCCTGCTGAGCCTGTCTTCTCTGAGAACAGCAGGCTCTGGGTACCC 150
Qy 121 CCCATGTACCTCTGGTCTCTGGTCCCATCTTCTACCTCTCTTCCATCCACCATGSCCGG 180
Db 151 CCCATGTACCTCTGGTCTCTGGTCCCATCTTCTACCTCTCTTCCATCCACCATGSCCGG 210
Qy 181 GGCTACCTCCGATGTCCCATCTCTTCAAGCAAGATGGTGTGGATTCGCCCTCAT 240
Db 211 GGCTACCTCCGATGTCCCATCTCTTCAAGCAAGATGGTGTGGATTCGCCCTCAT 270
Qy 241 GTCCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTGGAAATCCAAAGGAGGAGCCTGAG 300
Db 271 GTCCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTGGAAATCCAAAGGAGGAGCCTGAG 330
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QY 301 GCCCAGATTCCTCATCTACTCTGCTGGCTCACCAGATGAGCTTCGCAAGTTC 360
D 331 GCCCAGAAATTCCTCATCTACTCTGCTGGCTCACCAGATGAGCTTCGCAAGTTC 390
QY 361 CTGATTCACACCGAGAGAGAAAGGAGTCCAGTCACTGGAGTGTCTTTGGTTACTGG 420
D 391 CTGATTCACACCGAGAGAGAAAGGAGTCCAGTCACTGGAGTGTCTTTGGTTACTGG 450
QY 421 CTTCTGCTGTCTCTGCTGGAGTACCAACGCTGCCAGCAGGCTCCGGAGCGGGCTTC 480
D 451 CTTCTGCTGTCTCTGCTGGAGTACCAACGCTGCCAGCAGGCTCCGGAGCGGGCTTC 510
QY 481 CAGAGCAGCCTGTCCGCCAGCTGTCCACCTACCTATGCTGTCTCTGCTGGTGGCAG 540
D 511 CAGAGCAGCCTGTCCGCCAGCTGTCCACCTACCTATGCTGTCTCTGCTGGTGGCAG 570
QY 541 TTTGTGCTGTCTCTGCTGGGAGTCAACCCCTCTCTCCCTGAAGACCCCGCAGTCT 600
D 571 TTTGTGCTGTCTCTGCTGGGAGTCAACCCCTCTCTCCCTGAAGACCCCGCAGTCT 630
QY 601 AACCCCTGTCCAGAGCTGGGGCAG 625
D 631 AACCCCTGTCCAGAGCTGGGGCAG 655

RESULT 3
BG834418 566 bp mRNA linear EST 25-MAY-2001
LOCUS 352634 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
DEFINITION BG834418
ACCESSION BG834418
VERSION BG834418.1 GI:14199678
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 566)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR primers
FORWARD: AGGAACACCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 113 row: H column: 23
Seq primer: ATTAGTGACATATAG.
FEATURES
Location/Qualifiers
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10p"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 83 a 185 c 166 g 132 t
ORIGIN

Query Match 9.6%; Score 434.4; DB 12; Length 566;
Best Local Similarity 85.6%; Pred. No. 7.4e-91;
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Matches 483; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 2772 CATCCAATAGCGAGGGTGAAGCCACATGACCTGGCTTACCTGCTGCGCTGGGCAC 2831
D 2 CATGCATATGCGAGGGTGAAGGCTACCATGTACCTGACCTACCTGGAGCGCTGGGCAC 61
QY 2832 CCCCCTCTCCCTCTAGCGACTCTTCCTCTTCCTCTGCCAGCAAGTGGCTCTCTTCTGCG 2891
D 62 CCCCCTCTCCCTCTATACACTGTTCCTCTCTCCAGCAAGTGGCTCTCTTCTGCG 121
QY 2892 GGGCTACTGGCTGAGCGTGTGGCGGACACCTGCTAGGTGGCAGCAGACGAGGC 2951
D 122 TGGCTATTGGCTGAGCGTGTGGCGGACACCTACCGTGGAGCGGACGACACAGGC 181
QY 2952 AGCCCTGTGGTGGCGGATCTTCGGGCTCTCGGCTGTCTCCAGCCATTGGGCTGTTGC 3011
D 182 AGCCCTGTGGGCTGGGCTCTTCGGGCTCTCGGCTGCCCTCCAGCAATGGGCTCTTTC 241
QY 3012 CTCATAGGCTGGGTGCTCTAGTGGGCGCGGCGCATCCAGTTCCTCTCCAGAGGCT 3071
D 242 CTCATGGCCACGGTGTCTTAGTGGGATCCGGGATCCACCTCTCTTCGGGAGCT 301
QY 3072 CCTGTGGATGTGGTGGGATCTCCCATCAGCTTCTTTGAGCGGACACCATGGTCACT 3131
D 302 CCTGTGGACGTGGCGCGGTCTCTATCGGCTTCTTTGAGCAGACGCCATCGGAACCT 361
QY 3132 GCTAAACCGCTTCTCAAGGAGACAGACAGCGTGTAGCTGGGATTCAGCAAACTCCG 3191
D 362 GCTGAACCGCTTCTCGAAGGAGACAGACATAGTGAATGGGATCCAGACAGATGGC 421
QY 3192 GTCCCTGCTGATGTACGCTTTGGACTCTCTGGAGGTGACGCTGGTGGCAGTGGCTAC 3251
D 422 GTCTTTGCTGATGTATGCTTCGGGCTCTCTGGAAGTGGCCCTGGTGTGACAGTGGCC 481
QY 3252 CCCACTGGCCACTGGGCCATCTGCCACTGTTCTCTCTAGCTGGGTGGTTCAGAGCCT 3311
D 482 CCCACTGGCTGTGTGGCGCTCTGCTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 3312 GTATGTGTAGCTCATGCCAGCT 3335
D 542 GTATGTGGCCAGCTGTGCCAGCT 565

RESULT 4
BG610482 558 bp mRNA linear EST 17-APR-2001
LOCUS 326419 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
DEFINITION BG610482
ACCESSION BG610482
VERSION BG610482.1 GI:13660461
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 558)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 113 row: H column: 23
Seq primer: ATTAGTGACATATAG.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10p"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 83 a 185 c 166 g 132 t
ORIGIN
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[illegible]


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source
1. 471.
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 67 a 145 c 159 g 100 t
ORIGIN
Query Match 8.0%; Score 360.6; DB 12; Length 471;
Best Local Similarity 85.4%; Pred. No. 1.3e-73;
Matches 402; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 3259 GCCACTGTGGCCATCTCCACTGTTTCCTCTACGCTGGGTTTCAGAGCCCTGTATGTG 3318
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GCTGTTGTGGCGCTCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 3319 GTTACCTATGCCAGCTGAGAGCCTTGGAGTCAGCCAGCTACTCGTCTCTCTCTCTCT 3378
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GCCAGCTCTGTGCCAGCTCAGAGCCCTGGAGTCAGCCAGCTACTCTCTCTCTCTCTCT 120
QY 3379 ATGGCTGAGACCTTCCAGGCGACAGTCAGTGTCCGGGATTCGGAACCCAGGCCCTTT 3438
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GTGGCTGAGACATCCAGGCGGGAGTCATCAGGGCTTCCGAGCCCGAGGCCCTTTT 180
QY 3439 GTGGCTCAGAACATGCTCGCTAGTAGTAAAGCCAGAGGATCAGTTTCCCGGACTGGTG 3498
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GTGGCTCAGAACATGCTCGCTAGTAGTAAAGCCAGAGGATCAGTTTCCCGGACTGGTG 240
QY 3499 GCTGACAGTGGCTTCCAGGCGGCAATGTGAGCTTCCTGGGATGGCTGTGTTGCGAGCC 3558
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GCTGACAGTGGCTTCCAGGCGGCAATGTGAGCTTCCTGGGATGGCTGTGTTGCGAGCC 360
QY 3559 GCCAGCTGTGCTGTGAGCAAGCCACCTCAGTGTGGGCTCTGGGCTTCTCTCTCTCT 3618
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GCCCTGTGCTGTGCTGTGAGCAAGCCACCTCAGTGTGGGCTCTGGGCTTCTCTCTCT 360
QY 3619 TCTGCTGCCCTCCAGGTGACCCAGACATGTCAGTGGGTTGTTCCGCACTGGACAGACCTA 3678
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 TCCGCTGCCCTCCAGGTGACCCAGACATGTCAGTGGGCTGTCAGTGGGCTGTCGAGCTGG 420
QY 3679 GAGAACAGCATCTGTGTCAGTGGAGCGGATGTCAGGACTATGCTCTGGAGCCCT 3729
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 GAGAGCAGCATCTGTGTCAGTGGAGCGGCTGAGGAGTACGCCCTGACACCC 471

RESULT 11
BG834171 471 bp mRNA linear EST 25-MAY-2001
LOCUS
DEFINITION BG834171
ACCESSION BG834171
VERSION BG834171.1 GI:14199213
KEYWORDS EST.
SOURCE
pig.
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 471)
AUTHORS
Fahrenkrug,S.C., Frenking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.,
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

```

```

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCAGTCAGCAGCG
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Location/Qualifiers
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and 30 embryos."
BASE COUNT 67 a 144 c 160 g 100 t
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Best Local Similarity 85.1%; Pred. No. 3.1e-73;
Matches 401; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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Db 1 GCTGTTGTGGCGCTCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
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Db 61 GCCAGCTCTGTGCCAGCTCAGAGCCCTGGAGTCAGCCAGCTACTCTCTCTCTCTCTCT 120
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RESISTANCE-ASSOCIATED PROTEIN ; mRNA sequence.
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VERSION AW318859.1 GI:6748403
KEYWORDS EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 570)
AUTHORS
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T.,

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QY 376 AGGAAAAGGGAGTCCAGTCATCTCGAGTGGAGTGTGTTGGTACTGGCTTCTCTGCATTGTC 435

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.

BASE COUNT 52 a 105 c 79 g 78 t

ORIGIN

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Job time : 3852.31 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:49:35 ; Search time 109.187 Seconds
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16388.716 Million cell updates/sec

Title: US-09-647-140A-7

Perfect score: 4509

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Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 479
; LENGTH: 5728
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010466
US-09-917-800A-479

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Db 4033 CTG 4092
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; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; CURRENT APPLICATION NUMBER: US/09/967,768A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1977)
; OTHER INFORMATION: n=a,t,g or c
US-09-967-768A-190

Query Match 8.5%; Score 384.6; DB 10; Length 1977;
Best Local Similarity 55.8%; Pred. No. 4,1e-85;
Matches 811; Conservative 0; Mismatches 631; Indels 12; Gaps 4;
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RESULT 8

US-09-925-299-157
; Sequence 157, Application US/09925299
; Patent No. US2002055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 1448


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; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1007
; LENGTH: 4395
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-1007

Query Match          6.0%; Score 271.4; DB 9; Length 4395;
Best Local Similarity 46.0%; Pred. No. 4.6e-57;
Matches 1185; Conservative 0; Mismatches 1366; Indels 24; Gaps 7;

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QY 3196 CTGCTGATGTACGCCCTTTGGACTCTCGAGGCTCAGCCTGTGTGGCAGTGGCTACCCCA 3255
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Db 3007 TCCATCCAGACATTTGCTACAAGTGGTGTGCTCTCTGTGGCTGTGGCGTGTATCTCT 3066

QY 3256 CTGGCCACTGTGGCCATCTCTGCGCATGTTTCTCTCTACGCTGGGTTTCAGAGCCTGTAT 3315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3067 TGGATGCAATACCTTGGTTCCCTTGGAAATCATTTTCTTCGCGGATATTTT 3126

QY 3316 GTGTTAGCTCATGCCAGCTGAGACGCTTGGAGTGCAGCTTCCAGACAACTCCGGTCC 3375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3127 TTGGAACGTCAAGAGATGTGAAGCGCTTGAATCTACAACCTCGGAGTCCAGTGTTTTCC 3186

QY 3376 CACATGGCTGAGAGCTTCCAGGGCAGCACAGTGTGTCGGGCATTTCCGAACCCAGGCCCC 3435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3187 CACTTGTCACTTCTCTCCAGGGGCTCTGCAACCATCCGGGCATACAAAGCAGAGAGAGG 3246

QY 3436 TTTGTGGCTCAGAAACAATGCTCGGTAGATGAAGCCAGAGGATCACTTTCCCGGAGTG 3495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3247 TGTCAAGAACTGTTTATGTCACACACAGGATTTACATTCAGAGGCTTGGTCTCTTTTGG 3306

QY 3496 GTGGCTGACAGGTGGCTTGGGCGCAATGTGAGCTCTCTGGGGAATGCCCTGGTGTTCGA 3555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3307 ACAACCTCCGCTGGTTCGCGCTCCGCTCTGGATGCCATCTGTGCCATGTTTTCATCATC 3366

QY 3556 GCCGCCACGTGTCTGTGTGAGCAAGCCACCTCAGTGTCTGGCCTGTGGGCTTCTCT 3615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3367 GTTGCCTTTGGTCCCTGATTTCTGGCAAAACTCTGATCCCGGGCAGGTTGTTTGGCA 3426

QY 3616 GTCTCTGCTGCCCTCCAGGTGACCCAGACACTGACGTGGGTTGTTCGCAACTGGACAGAC 3675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3427 CTGCTCATGCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCAGAAAGTGCCTGAA 3486
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QY	3676	CTAGAGAACAGCATGCTGTCACTGGAGGGATGTCAGGACTATGCTGTGACGCCCAAGGAG	3735
Db	3487	GTTGGAATATGATGATCTCAGCTAGAAAGGGTCATTGAATACACAGACCTTTGAAAAAGAA	3546
QY	3736	GCTCCCTGGAGGCTGCCACATGTGCAGCTACGCCCTTCACTAGGGCGGCGCAGATC	3795
Db	3547	GCACCTTGGGAATATCAGAAACGCCACCA---CCAGCTGGCCCCATGAAGAGGAGTGATA	3603
QY	3796	GAGTTCGGGAGCTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTGGCTGTGCAGGGCTG	3855
Db	3604	ATCTTTGCAATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGGTACTGAACATCTG	3663
QY	3856	TCCTTCAAGATCCACGACGAGGAGAAGGTGGGCATCTGTTGCGACGACCGGGCAGGGAAG	3915
Db	3664	ACAGCACTCATTTAAATACAGAAAAAGGTGGCAGTGTGGGAAAGAACGGAGCTGGAAAA	3723
QY	3916	TCCTCCCTGGCAGTGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGTGGGATCTGGATC	3975
Db	3724	AGTTCCTCATCTCAGCCCTTTTATAGTT---GTCAGAACCCGAAGGTAAAAATTTGGATT	3780
QY	3976	GACGGGGTCCCCATTTGCCACGCTGGGGCTGACACACATGCGCTCCAGGATCAGCATCATC	4035
Db	3781	GATAAGATCTTGACAACTGAAATTTGCACTTCACGATTTAAGGAAGAAAACTCAATCATA	3840
QY	4036	CCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGGGGATGAACCTGACCTGCTGTGCAGGAG	4095
Db	3841	CCTCAGGAACCTGTTTTGTTTCTACCTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG	3900
QY	4096	CACCTGGACGAGGCTATCTGGGACGCCCTGGAGACGGTGCAGCTCAAGGCTTGGTGGCC	4155
Db	3901	CACACGGATGAGGAATCTGGAAATGCCCTTACAGAGGTACAACTTAAAGAAACCATTTGAA	3960
QY	4156	AGCTGCCCGGCCAGCTGAGTACAAAGTGTGCTCACGAGCGGAGGACCTGAGCGTGGCC	4215
Db	3961	GATCTTCTCTGTTAAATGGATCTGAATTAGCAGAAATCAGGATCCAATTTTAGTGTGGA	4020
QY	4216	CAGAAACAGCTCCTGTGCTGCGAGTGCCTCTCCGGAGACCCAGGATCCATCTCATCTCTG	4275
Db	4021	CAAAGCAACTGGTGTGCTTGCAGGGCAATTTCTCAGGAAATAATCAGATATTGATTATT	4080
QY	4276	GACGAGGCTACTGCTGCCGTGGACCCCTGGCAGGAGCTGCAGATGCAGGCCATGCTCGGG	4335
Db	4081	GATGAAGCGACGGCAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAAAATCCCG	4140
QY	4336	AGCTGGTTTGACAGATGCACATGTGCTGCCAATTCGCCACCGCTCGCTCCGTGATGGAC	4395
Db	4141	GAGAAATTTGGCCACTGCACCGTGTAACTTACACAGATTTGAACACCATTTATTGAC	4200
QY	4396	TGTGCCGGGTCTTGTCATGGACAAGGGCGAGTGGCAGAGCGCGCACGCCG---GCC	4452
Db	4201	ACGGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAGAAATATGATGAGCCGTATGTT	4260
QY	4453	CAGCTGTGCCCGAAGAGGGCCTGTTTTACAGATGCGCCGAGGAGTCAAGCCCTGG	4507
Db	4261	TTTGTCGAAAAATAAGAGAGAGCTATTTTACAAAGATGTGCAACAACTGGGCAAGG	4315

RESULT 12

US-10-012-896-536
; Sequence 536, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:

[illegible]

QY 2536 GCCTCGTGTCTTCTGATCAGCCACACACCCAGGAGATAGAGAGAGAGAAACA 2595
Db 2035 GATTTTGGGTCCCTTTTAAAGAGGATAATGAGAAAGTGAACAACCTCCAGGTCCAGGA 2094
QY 2596 GAACCTGGACAGACACCAAGACCCAGAGACCTCTGACGAGGAGGCCGAGCTT 2655
Db 2095 ACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG-----GTCTCAACAAT 2149
QY 2656 AGACGGAGAGGTCCATCAAGTACGTCCTGAGAAAGACCGTACCACCTTCAGAAAGCCAG 2715
Db 2150 CTTCTAGACCCCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGTCCAG 2209
QY 2716 ACAGAGGTTCTCTGATCAGCCCTGACAGGCGAGGATGCGCCAGCAAGAGACAGATC 2775
Db 2210 TTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTCAGGGCTATTAAGAATT 2269
QY 2776 CAATACGGCAGGTTGAAGCCACAGTGCACCTGGCCCTACTCGTGGCTGGGACCCCC 2835
Db 2270 ACTTCAGAGCTGGTCACTAGATTGTTCTTCAATTTTCTTATTCCTTAACACTGCAG 2329
QY 2836 CTCTGCTCTACGCACTCTTCTCTCTCTGCCCCAAGTGGCCCTCTCTGCCGGGGC 2895
Db 2330 CTCAGGTTGCCCTATGTGCTTCAAGATTGCTGGCTTTTCATACTGGGCAACAACAAAGTA 2389
QY 2896 TACTGCTCAGCCTGTGGCGGACGACGCCCTGCAGTAGTGGGAGCAGAGCGAGGAGCC 2955
Db 2390 TGTAAATGTCACTGTAAATGAGGAGGAGAAATGTAAACGAGAGCTAGATCTTAACTG-- 2447
QY 2956 CTGGTGGCGGATCTTGGGCTCTCTCGCTGTCTCAAGCCATTTGGCTGTTTGGCTCC 3015
Db 2448 GTACTTAGGAATTTATCAGTTTAACTGTAGTACCGTTCTTTTGGGATAGCAAGATC 2507
QY 3016 ATGGCTGGGGTCTCCTAGGTGGGGCCCGGCATCCAGTTGCTCTTCCAGAGGCTCCTG 3075
Db 2508 TCTATTGGTATTCTACGTCTTGTAACTCTTCAACAACCT--TGCAACAACAATGTTT 2565
QY 3076 TGGGATGTGGTGGATCTCCCATCAGCTCTTTTGGCGGACACCCCATTTGGTCACTGCTA 3135
Db 2566 GAGTCAATTTCTGAAAGCTCCGGTATTATTTTGTATAGAAATCCAATAGAGAAATTTTA 2625
QY 3136 AACCGCTTCTCAAGGAGACACACAGGTGTGAGTGGACATTCAGACAAACCTCCGGTCC 3195
Db 2626 AATCGTTTCTCCAAAGACATTGACACTTTGGATGATTGCTGCCGTGAGCTTTTAGAT 2685
QY 3196 CTGCTGATAGCCTTTGGACTCTCGAGGTACAGCCCTGGTGGTGCAGTGGGTACCCCA 3255
Db 2686 TTCTATCCAGACATTGCTACAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTGATTCTCT 2745
QY 3256 CTGGCCACTGTGGCCATCTGCGCACTGTTTCTCTCTAGCTGGGTTTCAGAGCCTGTAT 3315
Db 2746 TGGATGCGCAATACCTTGGTTCCCTTGGAAATCAATTTTCTTCGGCGATATTTT 2805
QY 3316 GTGGTTAGCTATCCAGCTGAGAGCTTGGAGTCAAGCCAGCTACTCTGCTGTCTGCTCC 3375
Db 2806 TTGGAAACCTCAAGAGATGTGAGCGCTTGGAAATCTAACAACCTCGAGTCCAGTGTTC 2865
QY 3376 CACATGGCTGAGACGTTCCAGGGACACACAGTGGTCCGGGCAATTCGAAACCCAGGCCCC 3435
Db 2866 CACTTGTCTATCTTCTCCAGGGCTCTGGACCATCCGGGCAATACAAAGCAGAGAGAGG 2925
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Db 2926 TGTAGGAACTCTTTGATGATCAGACACAGGATTTTACATTCAGAGGCTTGGTCTGTTTGG 2985
QY 3496 GTGGCTGACAGTGGCTTCCGCGCAATGTGGAGTCTCTCGGGAATGGCCTGTGTTTGA 3555
Db 2986 ACAACGTCCGCTGGTTCGCGCTCGTCTGGATGGCCATCTGTGCCATGTTTGTCAATC 3045
QY 3556 GCGGCCAGCTGTGCTGTGAGCAAGCCCACTCAGTGTGGCTCGTGGGCTTCTCT 3615
Db 3046 GTTGCCCTTTGGGTCCTGATCTGGCAAAACTCTGGATGCGCGGAGGTTGGTTTGGCA 3105

QY 3616 GTCTCTGCTCCCTCCAGGTGACCCAGACACTGTCAGTGGGTTGTTCCGAACTGGACACAC 3675
Db 3106 CTGTCTTATCCCTCTACGCTCATGGGATGTTTCAGTGGTGTGTTCGACAAAGTGTCTGAA 3165
QY 3676 CTAGAAACAGCATCGTGTGAGTGGAGCGATGAGCACTATGCTGTGACGCCCAAGGAG 3735
Db 3166 GTTGAGAAATATGATGATCTCAGTAGAAGGTCTATTGAATACACAGACCTTGAAGAAAGA 3225
QY 3736 GTCTCCCTGGAGGTGCCCATGTGAGCTCAGCCCCCTGGCTCAGGGCGGCGAGATC 3795
Db 3226 GCACCTTGGGAATATCAGAAACGCCCACTA---CCAGCCTGGCCCCATGAAGGAGTGATA 3282
QY 3796 GAGTTCGGGACATTTGGGCTAAGATGCGGACCTGAGCTCCGCTGGCTGTGTCAGGGGCGTG 3855
Db 3283 ATCTTTGACAATGTGAATTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCATCTG 3342
QY 3856 TCCTTCAAGATCCACGAGGAGAGGTGGGATCTGTGGCAGGACCGGGGCGAGGGAAG 3915
Db 3343 ACAGCACTCATTAATCACAAGAAAGGTGGCATTTGGGAAGAACCGGAGCTGGAAAAA 3402
QY 3916 TCCTCCCTGGCCAGTGGGCTGCTGCGCTCCAGAGGACGCTGAGGTTGGATCTGGATC 3975
Db 3403 AGTCCCTCATCTCAGCCCTTTTAGATT---GTCAGAACCCGAAGGTAAATTTGGATT 3459
QY 3976 GACGGGTCCCATTTGCCAGCTGGGCTGCACACACTGCGCTCCAGGATCAGCATCATC 4035
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QY 4036 CCCAGGACCCCATCTCTCTGCGGATGAACCTCGACCTCGACCTCTCGCAGGAG 4095
Db 3520 CTTGAGAACCTGTTTGTCTACTGGAAACAATGAGGAAACCTCGGATCCCTTTAATGAG 3579
QY 4096 CACTCGACAGAGCTATCTGGGAGCCCTGGAGACGCTGACGCTCAAAGCCTTGGTGGCC 4155
Db 3580 CACACGGATGAGAACTGTGGAATGCCCTTACAAGAGGTACAACCTTAAAGAAACCATTTGAA 3639
QY 4156 AGCTGCCCGCCAGCTGACAGTACAGTGTGCTGACCGAGCGGAGGACCTGAGCGTGGC 4215
Db 3640 GATCTTCCCTGGTAAATGGATCTGAATTAGCAAGATTCAGGATCCCAATTTTAGTGTGGGA 3699
QY 4216 CAGAAACAGCTCTGTCTGGCAGCTGCTCTCCGGAAGACCCAGATCTCATCTG 4275
Db 3700 CAAAGACAACCTGCTGCTTCCAGGCAATCTCAGGAAATATCAGATTTGATTATT 3759
QY 4276 GACAGGCTACTGCTGCTGGACCTCGGACGAGCTGCGAGAGCTGAGAGCCCATGCTCGG 4335
Db 3760 GATGAGCGACGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3819
QY 4336 AGCTGTTTGCAGTGCCTGCTGCCATTTGCCACCGCTCGCTCGCTGATGGAC 4395
Db 3820 GAGAAATTTGCCACTGCACCGTGTAACTTGCACACAGATTTGAACACCATTTATTGAC 3879
QY 4396 TGTGCCCGGTTCTGTGCTATGGACAAGGCGAGGTGCGAGAGCGGCGAGCCG---GCC 4452
Db 3880 AGCACAAGATATGTTTTAGATTACAGAAAGCTGAAGAAATATGATGACCGCTGATT 3939
QY 4453 CAGCTGCTGGCCAGAGGCCCTGTTTACAGACTGGCCAGGAGTCAAGGCTGG 4507
Db 3940 TTGCTGCAAAATAAGAGAGGCTTATTTTACAAGATGTTGCAACAACCTGGGCAAGG 3994

RESULT 13

US-09-759-143-536
; Sequence 536, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.

QY	3676	CTAGAGAACAGCATCGTCTCAGTGAGCGGATGCAGGACTATGCTCTGGACGCCCAAGGAG	3733
Db	3166	GTTGAGAATAATGATGATCTCAGTGAAGAGGGTCATTGTAATACACAGACCTTGAAACAGAA	3225
QY	3736	GCTCCTCGGAGGCTGCCACACATGTGCAGCTCAGCCCCCTCGCCCTCAGGCGGGCAGATC	3795
Db	3226	GCACCTTGGGAATATCAGAAACGCCCAACA--CCAGCCTGSCCCCATGAAGAGTGTATA	3282
QY	3796	GAGTTCGGGACTTTGGCTTAGATGCCGACCTGAGCTCCCTCGCTGGCTGTGCAAGGCGTGG	3855
Db	3283	ATCTTTGACAATGTGAACCTTCATGTFACAGTCCAGGTGGGCCCTTCGTACTGAAGCATCTG	3342
QY	3856	TCCTTCAAGATCCACGAGGAGAGAGTGGGCATCTGTGGCAGCACCGGGGCAGGGAAG	3915
Db	3343	ACAGCACTCAATTAATACACAGAAAGCTTGGCAITTTGGGAAGAACCGGACCTGGAANA	3402
QY	3916	TCCTCCCTGGCCAGTGGGCTGCTGGGGCTTCAGAGGACGCTGAGGGTGGGATCTGGATC	3975
Db	3403	AGTTCCCTCATCTCAGCCCTTTTTAGATT--GTCAAGAACCCGAAGGTAAAAATTTGGATT	3459
QY	3976	GACGGGTCCCCATTGGCCACGTGGGGCTGCACACACTCGGCTCCAGGATCAGCATC	4035
Db	3460	GATAGATCTTTGACACATGGAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCAT	3519
QY	4036	CCCAGGACCCCATCTCTTCCCTGGCTCTCTCGGATGAACCTCGACCTGCTGCAGGAG	4095
Db	3520	CCTCAGGAACCTGTTTGTCTTCACTGGAAACATGAGGAAAAACCTCGATCCCTTTAATGAG	3579
QY	4096	CACTCGGACGAGGCTATCTGGGCAGCCCTGGAGAGGCTGCAGCTCAAAGCCTTGGTGGCC	4155
Db	3580	CACACGGATGAGAACTGTGGAATGGCTTTACAAGAGGTACAACTTTAAAGAAACCAATTGAA	3639
QY	4156	AGCCTGCCCGGCCAGCTCAGCTACAAGTGTGCTGACCGAGGCGGAGCACTGAGCGTGGGC	4215
Db	3640	GATCTTCTGTGTAATATGATACTGAATTAGCAGAATCAGGATCCAATTTAGTGTGGA	3699
QY	4216	CAGAAACAGCTCTGTGTCCTGGCAGTGCCTTCTCCGAGAGACCCAGATCCTCATCTG	4275
Db	3700	CAAAAGCAACTGGTGTGCCTTTGCCAGGGCAATCTTCAGGAAAAATCAGATATTGATTATT	3759
QY	4276	GACGAGGCTACTGCTCGCTGGACCCCTGGCACGGAGCTGCAGATCAGGCCCATGCTCGGG	4335
Db	3760	GATGAAGCAGCGCAATATGATATCCAAAGAACTGATGAGTTTAATACAAAAAATCCGG	3819
QY	4336	AGCTGGTTTGCACAGTGCAGCTGTGCTGCCCAATGCCCCACCGCCTCGCTCATCTGATG	4395
Db	3820	GAGAAATTTGCCCACTGCACCGTGTCTACCAATTTGCACACAGATTTGAACACCACTTAT	3879
QY	4396	TGTCGCCGGTTCCTGGTATGCGAAAGGGCAGGTGGCAGAGAGCGGCAGCCCG--GCC	4452
Db	3880	AGCCACAAGATAATGGTTTTAGATTCAGGAAGACTGAAGAATAATGATGACCGGTATGTT	3939
QY	4453	CAGCTGTGCCCCAGAAGGGCTGTTTTACAGACTGGCCCCAGGAGTCAAGGCTGG	4507
Db	3940	TTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTCTGGCGAAGG	3994

RESULT 14

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RES-09-780-669-536
; Sequence 536, Application US/097808669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.

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Db 2035 GATTTTGGCTCCCTTTTAAAGAGGATAATGAGAAAGTGRACAACTCCAGTTCACGA 2094
QY 2596 GNACTTGGAGCAGACCAAGACCCAGAGCCACTCTGACAGGAGGAGGCCGCTT 2655
Db 2095 ACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTCGGTTTG-----GTCTCAACAAT 2149
QY 2656 AGACGCGAGAGTCCACTCAAGTCAGTCCCTGAGAGGAGCCGTACCACITCAGAACGCCAG 2715
Db 2150 CTTCTAGACCTCCTTTGAAAGATGCTGCTGGAGAGCAAGATACAGAGAATGTCCCA 2209
QY 2716 ACAGAGTTCTCTTGATGACCCCTCACAGGCGAGGATGCCAGGAGGAGACAGCATC 2775
Db 2210 TTACATATCAGAGAGAACCGTTCTGAGGAAGTTGGTTTTCAGGCGCTATAGAAT 2269
QY 2776 CAATAGCGCAGGGTGAAGGCCACAGTGCACCTGGCCCTACCTGCGTGGCGTGGCCACCC 2835
Db 2270 ACTTCAGAGCTGGTCTCACTGGATGTCTTCATTTCTTCTTCTCTAAACACTGCAG 2329
QY 2836 CTCTGCCCTTACGCACCTCTCTCTCTCTGCGAGCAAGTGGCTCTCTGCGGGGC 2895
Db 2330 CTCAGTTGCCATGTGCTTCAAGTGTGGTCTTCTATCTGGGCAAAACAAAGTA 2389
QY 2896 TACTGGCTGAGCCTGTGGGCGAGCACCTCTGCAGTGTGGTGGCGAGCAGCGAGCC 2955
Db 2390 TGCATAATGTCACTGTAAATGGAGGAGGAATGTAAACGAGAGCTAGATCTTAATG-- 2447
QY 2956 CTGGTGGCGGATCTTCGGGCTCTCGGCTGTCTCAAGCCATTTGGGCTTTGCCCTCC 3015
Db 2448 GTACTTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTTTTGGCATAGCAAGATC 2507
QY 3016 ATGGCTGGGTGCTCCTAGTGGGCGCGGCATCCAGTTGCTCTCCAGAGGCTCCTG 3075
Db 2508 TCTATTGGTATCTACGCTCTTGTAACTCTTCAAACTT--TGCACAAAAATGTTT 2565
QY 3076 TGGATGTGTGCGATCTCCACTCAGCTCTTTTGGCGGACACCCCATTTGGTCACTGCTA 3135
Db 2566 GAGTCAATCTCGAAGCTCCGGTATTATCTTTGATGAAATCCAAATGAGGAATTTA 2625
QY 3136 AACCGCTTCTCCAGGAGACAGACAGGTTGACGTGGACATTCACAGAAACCTCGGTCC 3195
Db 2626 AATCGTTTCTCAAAGACATTTGGACACTTGGATGATTTGCTGCGCGCTGACGCTTTTAGAT 2685
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QY 3316 GTGTTTACCTATCCAGCTGAGACGCTTGGAGTACGACGCTACTGCTGCTGCTGCT 3375
Db 2806 TTGAAACGCTCAGAGATGTGAAGCGCTCGGAATCTCAACTCGGAGTCCAGTGTCTTCC 2865
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Db 2926 TGTCAAGAACTGTGTGATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTCTTTT 2985
QY 3496 GTGCTGACAGGTGGCTTGGGCAATGTGGAGCTCTTGGGAATGGCTGGCTTTTGA 3555
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QY 3616 GTCTCTGCTCCCTCCAGGTGACCCAGACACTGCAAGTGGTGTGCTCAACTGGACAGAC 3675
Db 3106 CTGCTCTATGCCCTCACGCTCATGGGATGTTTCAAGTGGTGTGCTGACAAAGTGTCTGAA 3165

QY 3676 CTAGAGAACAGCATCTGTGTAGTGAGCGGATGCAGACTATGCTTGGACGCCAAGGAG 3735
Db 3166 GTTGAAGATATGATGATCTCTAGTAGAAAGGTCATTTGAATACACAGACCTTGAAGAAGAA 3225
QY 3736 GCTCCCTGAGGCTGCCACATGTGAGCTCAGCCCCCTTGGCTCAGGGCGGCGAGATC 3795
Db 3226 GCACCTTGGGAATATCAGAAACGCCCA---CCAGCCTTGGCCCTTGAAGAGTGTATA 3282
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QY 3976 GACGGGTCCCATTTGCCACGCTGGGCTGCACACACTGCGCTCCAGGATCAGCATCATC 4035
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Db 3520 CCTCAGGAACCTGTTTGTCTACCTGGAACAATGAGGAAAAACCTGATCCCTTTAATGAG 3579
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Db 3640 GATCTTCTGTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3699
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Db 3760 GATGAAGCGAGCGCAAAATGTGATCCAGAACTGATGATTAATAAATAAATAAATAA 3819
QY 4336 AGCTGTTTGCACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4395
Db 3820 GAGAAATTTGCCCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3879
QY 4396 TGTGCGCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4452
Db 3880 AGCGACAAGATAATGTTTGTAGATTCAGGAAGCTGAAAGAAATATGATGAGCGCTATGTT 3939
QY 4453 CAGCTGCTGGCCCAAGGCGCTGTTTACAGACTGGCCCGAGGATGAGGCGCTGG 4507
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RESULT 15

US-09-822-827-536
; Sequence 536, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140

Db 3403 AGTCCCTCATCTCAGCCCTTTTATGATT---GTCAGAACCCGAGGTAAATTTGGATT 3459
QY 3976 GACGGGTCCCATTTGCCACGCTGGGCTGCACACACTGCGCTCCAGGATCAGCATATC 4035
Db 3460 GATAAGATCTTGACAACCTGAAATTTGGACTTCACGATTTAAGGAAGAAAATGTCATATCATA 3519
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Db 3580 CACACGATGAGGAACCTGGAATGCCCTTACAAGAGGTACAACTTAAGAAACCAATTGAA 3639
QY 4156 AGCTGCCCGGCCAGCTGCAGTACAAGTGTCTGACCGAGCGGAGCCTGAGCGTGGC 4215
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QY 4276 GACGAGCTACTGTGCTGCGTGGACCCCTGGCACGGAGCTGCAGATGCAGGCCATGCTGGG 4335
Db 3760 GATGACGGAGCGCAATGTGGATCCAAAGACTGATGAGTTAATACAAAAAATCCGG 3819
QY 4336 AGCTGTTTGACAGTGCACCTGTGCTGCCCATTTGCCACCGCCTCGCTCGGTGATGGAC 4395
Db 3820 GAGAAATTTGCCACTGCACCGTCTAACCATTCACACAGATTGAACACCATTTATGAC 3879
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Db 3940 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAGG 3994

Search completed: December 18, 2002, 21:44:23
Job time : 202.187 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:05:00 ; Search time 89.9185 Seconds
(without alignments)
15378.431 Million cell updates/sec

Title: US-09-647-140A-7

Perfect score: 4509

Sequence: 1 atggcgcgcctgctgagcc.....ccagagtcagcctggtc 4509

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1227.6	27.2	5011	3	US-08-463-179A-3
5	1227.6	27.2	5011	3	US-08-461-384B-3
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42 271.4 6.0 6140 4 US-09-439-313-536 Sequence 536, App
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45 264 5.9 5232 4 US-08-972-927-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-463-092B-3
; Sequence 3, Application US/08463092B
; Patent No. 5766880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,092B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:

Db 3296 CCATGGCGTGTCCATCGGGGGATCTTGGCTTCCGCTGTCTGCACGTGGACCTGCTGC 3355
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Qy 3557 CGGCCAGTGTGCTGTGTGAGCAAGCCACCTAGTGTGGCTGTGCTGCTGCTGCTGCTG 3616
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Qy 3617 TCTGTGCTCCCTCAGTGACCCAGACACTGCACTGGTGTGTCGCAACTGGACAGACC 3676
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Qy 3677 TAGAAGACAGCTGCTGTGATGAGCGGATGCGAGCTATGCTCCCTGGACGCCCAAGAGG 3736
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Qy 3737 CTCCTGTGAGGCTGCCACATGTGAGCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 3796
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Db 4616 CACAGTTCGAGACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4675
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Db 4676 ACACAAGGCTGATGCTTGGACAAAGGAGAAATCCAGAGTACGGCGGCCCATCGGACC 4735
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Db 4736 TCTGCGCAGCAGAGCTGCTTCTTACAGCATGSCCAAGACGCGGCTTGGT 4787

RESULT 3

US-08-460-907B-3
; Sequence 3, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-460-907B-3

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Best Local Similarity 55.8%; Pred. No. 4e-281;
Matches 2538; Conservative 0; Mismatches 1934; Indels 80; Gaps 7;

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QY 1737 GGCCAGGCTTCTGCTGCTTCTCCATCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
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RESULT 4

US-08-463-179A-3
Sequence 3, Application US/08463179A
Patent No. 6001563
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.179A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: POI-002CP8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:

Db 1077 TGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAAGGAGTGGAAACCCCTCTCTGTT 1136
QY 900 GAAGGCCATCTGGCAGGTGTTTCATTCTACCTTCCTCCCTGGGACCCCTCAGCCCTCATCAT 959
Db 1137 TAAGTGTTTATACAGACCTTTTGGGCCCTTACTTCTTCATCAGCTTCTCTTCAAGGCCAT 1196
QY 960 CAGTGAATGCTTTCAGGTTCACGTGTCCTCCCAAGCTGTCTCAGCCCTTTTCTCGAGTTTATGG 1019
Db 1197 CACAGACCTGATGATGTTTTCCGGGCCCGCAGATCTTAAAGTTGCTCATCAAGTTCTGTAA 1256
QY 1020 TGATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCTCTCCGCGTGTCTGATGTCTCTCAGC 1079
Db 1257 TGACACGAAGGCCCCAGAGACTGCGAGGGCTACTTCTACACCGTGTCTGTTTGTCACTGC 1316
QY 1080 CTGCGCTGCAAAAGCGCTTTTGAACAGCAGAACATGTACAGGCTCAAGGTGCGCGCAGATGAG 1139
Db 1317 CTGCGCTGCAAGCCCTCGTGTCTGCACAGACTTCCACATCTGCTCGTCAAGTGGCATGAG 1376
QY 1140 GTTGGGGTGGCCATCAGTGGCCTGGTGTACAGAAAGGTCTCTGGCTCTGTCCAGGGCTC 1199
Db 1377 GATCAAGCCGTGTCTTATTTGGGGCTGTCTATCGGAAGGCCCTGGTGATCACCAATTCAGC 1436
QY 1200 CAGAAAGGCCAGTGGCGGTGGTGTGTGTCAATCTGTGTCTCGTGGAGCTGCGAGCGCT 1259
Db 1437 CAGAAATCTCCACGGTCCGGGAGATTCTCAACCTCATGTCTGTGGACGCTCAGAGGTT 1496
QY 1260 GACCGAGAGCGTCTTACTACCTCAACGGGCTGTGGCTGTCTCGTGTGATCGTGTGTCTG 1319
Db 1497 CATGGACTTGGCCACGATACATTAACATGATCTGGTCAAGCCCTTCAAGTCTATCCTTGC 1556
QY 1320 CTTCTGTCTATCTTGGCAGCTCTCTGGGGCCCTCCGGCCCTCACTGCCATCGCTGTCTTCT 1379
Db 1557 TCTCTACCTCTGTGGCTGAATCTGGGCCCTTCCGCTCTGGCTGGAGTGGCGGTGATGGT 1616
QY 1380 GAGCCTCTCTCTCAATTTCTTCTATCTCAAGAAAGAAACCAACCATCAGAGGAGCA 1439
Db 1617 COTCATGGTGGCCGCTCAATGTGTGATGCGATGAAGACCAAGACGATATCAGSTGGCCCA 1676
QY 1440 ANTGAGCAGAGGACTCAGCGGACGGCTCACCAGCTCTATCTCAGGAATCTCGAAGAC 1499
Db 1677 CATGAAGAGCAAGACAACTCGGATCAAGCTGATGAACGAAATTTCTCAATGGGATCAAGT 1736
QY 1500 CATCAAGTTTCAATGTGGGAGGAGCCCTTCTGGACAGAGTCTTGGGACCTCGGAGGCCA 1559
Db 1737 GCTAAGCTTTATGCTGGAGCTGGCATTCAAGACAGAGGTGCTGGCCATCAGGCAGGA 1796
QY 1560 GGAGCTGGGCGCTTGGGACCTCGGCGCTCTCTTCTCTGTGTGTGTGTGTGTGTGTGTGT 1619
Db 1797 GGAGCTGAAGGTGCTGAAGAAGTCTGCGCTTACCTGTGTCAGCGGTGGGCACTTCACTGGGT 1856
QY 1620 AGTGTCTACATTTCTGTGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1679
Db 1857 CTGCAAGCCCTTCTGTGGGCTTGTGCACATTTGGCGTCTACGTGACCATTGACGAGAA 1916
QY 1680 TGCTA---TGAATCAGAGAAAGCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAA 1736
Db 1917 CAACATCTGGATGCCAGACGCTCTGTGTCTTGGCGCTTGTTCACACATCTCTCGGTT 1976
QY 1737 GGCCACAGGCTTTCCTGCGCTTCTCATCCACTCCCTCTGTCAGGCGCGGCTGTCTTTGA 1796
Db 1977 TCCCTGAAACATCTCCCATGCTCATCAGCAGCATCTGTCAGGCGAGTGTCTCCCTCAA 2036
QY 1797 CGCTGTGTCTACCTTCTCTGTCTGCTGAAGAAGTGTGACCTGTGTGTGTGTGTGTGTGTGT 1856
Db 2037 AGCCCTGAGGATCTTCTCTCCATGAGAGCTGGAACCTGACAGCATCAGCGAGCGGC 2096
QY 1857 CTCTGGAAGCGCTCGGGAGGATTTGATCATCACATACAGTGTGCACCTTCTGCGCTGGTC 1916
Db 2097 TGTCAAGACGCGGGGACAGACAGCATCACOGTGAAGATGCCAATTCACCTGGGC 2156
QY 1917 CCAGGAAGCCCTCTCTGCTCTCCAGATAAACCCTCAGCGTGCCCGAGGGTGTGTGTGT 1976
Db 2157 CAGGAGCGACCCCTCCACATGAATGGCATCACCTTCTCCATCCCGGAAGGTGCTTTGTGT 2216

QY 1977 GGCTGTTGTCTGCTCCAGTGGGGGAGGAAAGTCTCTCCTGTCTGTCGCGCCCTCTCTTGGGGA 2036
Db 2217 GGCGGTGGTGGGCGAGTGGGCTCGCGAAAGTGTCTCCTGTCTCAGCCCTCTTTGGGTGA 2276
QY 2037 GCTGTCAAAAGGTGAGGGGTTCTGAGCATCGAGGTGCTGTGGCCCTACGTGCGCCACGGA 2096
Db 2277 GATGGACAAGTGGAGGGGACGTGGCTATCAAGGGCTCGGTGGCCCTATGTGTGCCACAGCA 2336
QY 2097 GGCTGGGTGAGAAACACCTCTCTGTGTAGAGAAATGTGTCTCGGCGAGGAGCTGGACCC 2156
Db 2337 GGCTGGATTCAGATGATCTCTCCGAGAAACATCTTTTGGATGTACGTGGGAGGA 2396
QY 2157 ACCTGGCTGGAGAGTACTAGAGCCTGTGCCCTGCAGCCAGATGTGGACACTTTCCTCC 2216
Db 2397 ACCATATTACAGTCTCGGTGATACAGGCTGTGCCCTCTCCAGACCTTGAATTCCTGCC 2456
QY 2217 TGAGGGAATCCACACTTCAATTGGGAGGAGGACATCAATCTCTCCGAGGCGCAGAGCA 2276
Db 2457 CAGTGGGATCGGACAGAGATTGGCGAAGGGCGTGAACCTGTCTGGGGACAGAGCA 2516
QY 2277 GCGGCTGAGCCTGCGCCGGGCTGTATACAGAAAGGCAAGCTGTGTACCTGTGGATGACCC 2336
Db 2517 GCGGCTGAGCCTGCGCCGGGCTGTACTTCAAGCTGTACATTTACCTCTTCGATGATCC 2576
QY 2337 CCTGGCGGCTGGATGCCACCTTGGCCAGCATGTCTTCAACAGGTCTATTGGGCGCTGG 2396
Db 2577 CCTCTCAGCAGTGGATGCCATTTGGGAAACACATCTTTGAAATGTGATTTGGCCCAA 2636
QY 2397 TGGGCTACTCCAGGGAACACGAGTCTCTGTGACGACGCACTCCACATCTTCCGCCCA 2456
Db 2637 GGGGATGCTGAAGAACAAAGACGCGGATCTTGGTCACGACAGCATGAGCTACTTGGCCGA 2696
QY 2457 GGCTGATTTGATCATAGTGTGCGCAATGGGCGCATCGCAGAGATGGTTCCTACCAGGA 2516
Db 2697 GGTGAGCTCATCATCTGTCATGAGTGGCGCAAGATCTCTGAGATGGCTCTTACCAGGA 2756
QY 2517 GCTTCTCAGAGGAAGGGGCGCTCTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2576
Db 2757 GCTGTCTGGCTCGAGAGCGGCGCTTCG-CTGAGTCTCTGCTGCTACCTATGCCAGCAGAGC 2815
QY 2577 TAGAGAGAGGAGAAACAGAACTTGGACCCAGCACCAAGGCCCCAGAGGACCTCTGC 2636
Db 2816 AGGAGCAGATGTCAGAGGAGAACGGGTTCAGGGCGTCAAGGCTCCAGGGAAGAGCA 2875
QY 2637 AGCAGAGGCGCGAGCTTAGACGCGAGAGGTCCATCAAGTCAAGTCTCTCTGAGAG-- 2691
Db 2876 AGCAATGGAGAAATGGCATGCTGTGACGACAGTGCAGGGAAGCAACTGCAGAGACAGC 2935
QY 2692 -----GACCGTACCCTTCAGAGGCCCA-- 2716
Db 2936 TCAGCAGCTCCTCTCTATAGTGGGGACATCAGCAGGCGCACACAGACCGCAGAAC 2995
QY 2717 CAGAGTTTCTCTGATGACCTTGACAGGCGAGGATGGCCAGAGGAAAGACAGCATCC 2776
Db 2996 TGCAGAAAGCTGAGGCCCAAGAGGAGGAGACTTGGAGCTGTATGGAGGCTGACAGGCGC 3055
QY 2777 AATACGGCAGGTGAAGGCCACAGTGTGCTGCGCTTACCTGTGCGGTGGCGTGGGACCCCC 2836
Db 3056 AGACAGGCGAGGTCAAGCTTTCGCTGTACTGGGACTACATGAAGGCCCATCGGACTCTTCA 3115
QY 2837 TCTGCTCTACGCACTTCTCTCTCTCTGCGCAGCAAGTGGCTCTCTTCTGCGGGGCT 2896
Db 3116 TCTCTCTCTCAGCATCTTCTCTTTTCACTGTGTAACTATGTCTCGGCGCTGGCTTCCA 3175
QY 2897 ACTGGCTGAGCCTGTGGGCGAGCAGCTCTCAGTAGTGGGCGAGCAGCAGCAGCAGCC 2956
Db 3176 ATTGGCTCAGCTCTGAGCTGATGACCCCATCTGTCAAGGAGCTCAGGACACAGNAAG 3235
QY 2957 TGGGTGGCGGATCTTGGGCTCTCTGCGTGTCTTCCAAGCCATTTGGCTTTTGGCTCCA 3016
Db 3236 TCCGGCTGAGCGGTATGAGGCGCTTGGGCATTTTCAAGGGATCGCGCTGCTTTGGCTACT 3295

QY	3017	TGGCTGGGTGCTCTCTAGTGTGGGGCCGGGCATCCAGAGTTGCTTTCACAGAGGCTCTCTGT	3076
Db	3296	CCATGGCCGTGTCATCGGGGGGATCTTGCTTCCCGCTGCTGCAGCTGGACGTGCTGC	3355
QY	3077	GGGATGTGGTGCCATCTCCCATCAGCTTCTTTGAGGGGACACCCATTGGTTCACCTGCTAA	3136
Db	3356	ACAGCATCTCTGGCGGTCACCCATCAGCTTCTTTGAGGGGACCCCACTGGGAACCTGCTGA	3415
QY	3137	ACCGCTTCTCCAAAGGAGACAGACACGTTTGACGTGGACATTCACAGACAACCTCCGGTCCC	3196
Db	3416	ACCGCTTCTCCAAAGGAGCTGGACACAGTGCATGCATGATCCGGAGGTTCATCAAGATGT	3475
QY	3197	TGCTGATGTACGCCCTTTGGACTCCTGGAGGTACAGCTGGTGTGGCAGTGGCTTACAGGCTGTATG	3316
Db	3476	TCATGGGCTCCCTGTTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCA	3535
QY	3257	TGGCCACTGTGGCCATCTCTGCCACTGTGTTCTCTACGCTGGTTCAGAGGCTGTATG	3316
Db	3536	TCGCCGCCCATCATCATCTCCCGCCCCCTTGGCTCATCTACTTCTTCGTCAGAGGTTCTAGG	3595
QY	3317	TGGTTTAGCTCATCGCCAGCTGAGACGGCTTGGAGTTCAGCCAGCTACTGCTGTCTGTCTGCC	3376
Db	3596	TGCTTCTCTCCCGCAGCTGAAGCGCTCGAGTCGTCAGCCGCTCCCGGCTCTATATCC	3655
QY	3377	ACATGGCTGAGAGCTTCCAGGCGACACAGTGTGGGCAATTCGGAACCCAGGCCCCCT	3436
Db	3656	ATTTCAACGAGACCTTGTCTGGGGTCAAGGTCATTTCGAGCCTTCAGGAGCAGGAGCGT	3715
QY	3437	TTGTGGCTCAACAATGCTCCGCTAGATGAAGCCACGAGGATCAGTTTCCGCGACTGG	3496
Db	3716	TCATCCACACAGAGTCACTGAAGTGGAGGAGACGAAAGGCCATTATACCCAGCATCG	3775
QY	3497	TGGCTGACAGTGGCTTGGCGCAATGTGGAGCTCTCTGGGAATGGCCTGGTGTGTTCAG	3556
Db	3776	TGGCCACAGGTGGCTGGCCGTGGCGGTGGAGGTGTGGCAACTGCATCTGTCTGTGTG	3835
QY	3557	CCGCCACGTGTCTGTGTGAGCAAGCCCACTCAGTGTGGCCTCGTGGGCTTCTCTGT	3616
Db	3836	CTGCCCTGTTTCGGTGATCTCCAGGCACAGCCTCAGTGTGGCTTGGTGGGCTCTCAG	3895
QY	3617	TCCTGTCTCCCTCCAGGTGACCCAGACACTGCAGTGGGTGTTTCGCAACTGGACAGACC	3676
Db	3896	TGCTCTACTCATGTGAGGTACACAGTACTTGAATGGCTGGTTCGGATGTCATCTGAAA	3955
QY	3677	TAGAAACAGCATCTGTTCAGTGGAGCGGATGCAGGACTATGCCTGGAGGCCCAAGGAGG	3736
Db	3956	TGGAACAACATCTGTGGCCGTGGAGAGGCTCAGGAGTATTTCAGAGACTGAGAAGGAGG	4015
QY	3737	CTCCCTGGAGGCTGCCACATGTGAGCTCAGCCCCCTCGCCCTCAGGGCGGGCAGATCG	3796
Db	4016	CGCCCTGCCAAATCCAGGAGACAGTCCGCCCCACGACGCTGGCCCCAGGTGGGCCGAGTGG	4075
QY	3797	AGTTCGGGACTTTGGGCTAAGATGCCGACCTCAGCTCCCGCTGGCTGTGCAGGCGGTGT	3856
Db	4076	AATTCGGGAATCTGCTGCGCTACCGAGAGGACCTTGCATCTGCTCTCAGGCACATCA	4135
QY	3857	CTTCAAGATCCACGACGAGAGAAGTGGGCATCTGTTGGCAGGACCGGGGCGAGGAGT	3916
Db	4136	ATGTCAGATCAATGGGGGAGAAAGTTCGGCATCTGTGGGCGGACCGGAGCTGGGAAGT	4195
QY	3917	CCTCCTGGCCAGTGGGCTGTCTGGGCTCCAGGAGGAGCTGAGGGTGGGATCTGGATCG	3976
Db	4196	CGTCCCTGACCTGGGCTTATTCGGATCAACGAGTCTGCCGAAGGAGATCATCATCG	4255
QY	3977	ACGGGCTCCCATTTGGCCAGCTGGGGCTGCACACACTTCCGCTTCAGGATCAGCATCC	4036
Db	4256	ATGGCATCAACATCGCCAAAGATCGGCTGCACGACCTCCCGTTCAAGATCACCATCATCC	4315
QY	4037	CCCAGGACCCCATCTCTTCCCTGGCTCTCTGCGGATGAACCTTCGACCTCTGTCAGAGC	4096
Db	4316	CCCAGGACCCCTGTTTGTTCGCGTTCCCTCCGAATGAACCTGGAGCCCATTCAGCCAGT	4375
QY	4097	ACTCGGACGAGGCTATCTGGCGAGCCCTGGAGAGCGGTGCAGCTCAAAAGCCTTGGTGCCA	4156

RESULT 5
 US-08-461-384B-3
 : Sequence 3, Application US/08461384B
 : Patent No. 6025473
 : GENERAL INFORMATION:
 : APPLICANT: Cole, Susan P.C.
 : APPLICANT: Deeley, Roger G.
 : TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
 : STREET: Queen's University at Kingston
 : CITY: Kingston
 : STATE: Ontario
 : COUNTRY: CANADA
 : ZIP: K7L 3N6
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: ASCII text
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/461.384B
 : FILING DATE: 05-JUN-95
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/966,923
 : FILING DATE: 27-OCT-1992
 : APPLICATION NUMBER: 08/029,340
 : FILING DATE: 8-MAR-1993
 : APPLICATION NUMBER: 08/141,893
 : FILING DATE: 26-OCT-1993
 : APPLICATION NUMBER: 08/407,207
 : FILING DATE: 20-MAR-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Steeg, Carol Miernicki
 : REGISTRATION NUMBER: 39,539
 : REFERENCE/DOCKET NUMBER: Q1547
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (613) 545-2342
 : TELEFAX: (613) 545-6853
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5011 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double

; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 196..4788
 US-08-461-384B-3

Query Match 27.2%; Score 1227.6; DB 3; Length 5011;
 Best Local Similarity 55.8%; Pred. No. 4e-281;
 Matches 2538; Conservative 0; Mismatches 1934; Indels 80; Gaps

QY	36	GGTCTGGACACAGAGAGCCTGAACCTCGCGCCACACGCTGCTGAGCCTGTCCTCT	95
DB	237	GCTCTGGGACTGGATGACCTGGATACACAGACACCCGACTTCACCAAGGCTTTCA	296
QY	96	GAGAACAGAGAGGGTCTGGGTACCCGCCATGTACCTCTGGGTCTTTGGTCCCATCTACCT	155
DB	297	GAACAGGTCCTCGTGGGTGCTTTTACCTCTGGGCTGTTTCCCTCTCTACTT	356
QY	156	CCTCTTCATCCACACAGAGCGGGCTACCTCGGATGTCGCCACTCTTCAAGCCAA	215
DB	357	CCTCTATCTCTCCGACATGACGAGGCTACATTCAGATGACACCTCTCAACAAAACCAA	416
QY	216	GATGTGCTTGATTCGCCCTCATATGCTGTGTACCTCCAGCGTGGCTGCTCTTG	275
DB	417	ACTGCTTGGATTTTCTGCTGTGATCTGCTGGGAGACCTCTTCTACTCTTCTTG	476
QY	276	GAANAATCCAAAGGAGCGCTGAGGCCGCCAGAAATTCCTTCAATCTCTACTGTGGCT	335
DB	477	GGAAGAAGTGGGCAATATTCCTGGCCCACTGTTTGGTGGTCAAGCCAACTCTCTTGG	536
QY	336	CACCAAGATGCTTCGAGTCTTCTGATTTACACACGAGAGAGAAAGGGAGTCCAGTC	395
DB	537	CATCACCAGGCTGCTGTACTCTTTTAAATTCAGTGGAGAGAGAGGAGTTTCAAGTC	596
QY	396	ATCTGAGTGTCTTGTGTTACTGCTCTCTGCTTGTCTTGTTCGACAGTACCAACCTGC	455
DB	597	TTCAAGGATCATGCTCACTTTCTGGCTGGTACCTAGTGTGCTAGCCATCTCTGAG	656
QY	456	CCAGCAG-----GCCCTGGAGCGGGCTTCAGAGCGACCTGTCCGCCACCTGTG	506
DB	657	ATCCAAAATATGACAGCCTTAAAGAGAGATGCCAGGTGGACCTGTTTCGTGACATAC	716
QY	507	CACCTACCTATGCTCTCTGCTGTGGTGGCAGATGCTGCTGCTGCTGGCGATCA	566
DB	717	TTCTACGTCTACTTTTCCCTTACTCATTCAGCTGCTGCTGCTGCTGCTGCTGCTG	776
QY	567	ACCCCTCTTCTCCCTGAAGACCCCGACAGTCTAACCCCTGTCCAGAGACTGGGGCAG	626
DB	777	CTCACCCCTGTCTCGGAACCATCCAGACCTTATCCCTGCCAGAGTCCAGCGCTTC	836
QY	627	CTTCCCTCCAAAGCAGCTTCTGCTGGTGGTCTTCTGCTGCTGCTGCTGCTGCTGCT	686
DB	837	CTTCTGTCGAGGATCATCCTCTGCTGGATCACAGGTTGATTGTCGGGGCTACCGCA	896
QY	687	GCCACTGAGACCAAGAGACCTCTGCTGGAGAGAAACTCTCAGAGAACTTGT	746
DB	897	GCCCTGGAGGCGATGACCTCTGCTCTTAAACAGGAGGACGCTCGGAACAGTCTGT	956
QY	747	TTCCCGGCTTGAAGAGGAGTGGATGAGAACCGC-----AGTCGACCCCGGAGCACA	802
DB	957	GCCTGTTTGGTAAAGACTGGAAGAGGATGCGCCAGACTAGGAACGACCCGGTGA	1016
QY	803	AGGCAATAGCAATTTAAAGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	849
DB	1017	GCTGTGTACTCTTCAAGGATCTCTGCCAGCCGAAAGAGAGTTTCAAGGTGGATGCG	1076
QY	850	-----GAGACCGAGCCCTTCTAGGCAAGAGGACCCAGTGGCGCCCTGCTGT	899
DB	1077	TGAGGAGTGGAGGCTTTGATGCTCAAGTCCCTCCAGAGGAGTGGAAACCCCTCTGT	1136
QY	900	GAAGCCATCTGGCAGGTGTTCCATCTTACTTCTCTCTGCTGGAGCCCTCAGCCTCAT	959

DB	1137	TAGGTGTTATACAGACACCTTTGGGCCCTACTTCTCTCATGAGCTTCTTCTCAAGGCCAT	1196
QY	960	CAGTGATGCTTTCAGGTTCACTGTCCCAAGCTGCTCAGGCTTTTCTCTGGAGTTATTGG	1019
DB	1197	CCACGACCTGATGATGTTTTTCCGGCGCAGATCTTAAAGTTGCTCATCAAGTTCTGTA	1256
QY	1020	TGATCCCAAGCCTCCAGCCTGGAGGGCTACCTCTCCGCGTGTGATGTTCTCTCAGC	1079
DB	1257	TGACAGAAAGCCCGCAGACTGGCAGGGCTACTTCTACACCGTGTGCTGTGTTGCTACTG	1316
QY	1080	CTCCCTGCAAAACGCTGTTTTCAGCAGCAGAAACATGTACAGCTCAAGTGGCGCAGATG	1139
DB	1317	CTGCTGACAGCCTCGTGTGCTGACAGTACTTCCACATCTGCTTCTGCTGCTGCTGCTG	1376
QY	1140	GTTGCGGTGGGCCATCACTGGCTGTGTACAGAAAGTCTTGGCTCTGTCCAGCGGCTC	1199
DB	1377	GATCAAGACCGCTGCTATTTGGGCTGTCTATCGGAAGGCCCTGGTGATCAACCAATTG	1436
QY	1200	CAGAAAGCCAGTGGGTGGTGTGCTGCTCAATCTGGTGTCCGTTGAGCTGACGCGGCT	1259
DB	1437	CAGAAATCTTCCACCGTGGGGAGATTTGCAACCTCATGCTGTGGACGCTCAGAGGTT	1496
QY	1260	GACCGAGAGGCTCTCTACCTCAACGGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1319
DB	1497	CATGGACTGGCCACGTACATTAACATGATGCTGTCAGCCCCCTGCAAGTCACTCTTGC	1556
QY	1320	CTTCTGCTATCTGTCAGCTCCTGGGGCCCTCCGGCCCTCACTGCCATCGCTGCTTCTCT	1379
DB	1557	TCTCTACCTCTGCTGCTGAATCTGGGCCCTTCCGCTCTGCTGCTGCTGCTGCTGCTG	1616
QY	1380	GAGCTCTCTCTCAATTTCTCATCTCAAGAAAGAAACCAACCATCAGGAGGAGCA	1439
DB	1617	CCTCATGGTGGCGTCAATGCTGTGATGGGATGAAGACCAAGACGATCAGTGGGCCCA	1676
QY	1440	AATGAGCAGAAAGGACTCACGGGACGGCTCAGCAGCTCTATCTCAGGAACCTGGAAGAC	1499
DB	1677	CATGAAGACAAAGACAATCGGATCAAGCTGATGAAGAAATCTCAATGGATCAAGT	1736
QY	1500	CATCAAGTTCCATGGCTGGAGGAGGCTTTCTGGACAGAGTCTTGGGCATTCGAGGCCA	1559
DB	1737	GCTAAAGCTTTATGCTGGAGCTGGCATTTCAAGAGCAAGGTGCTGGCCATCAGGAGGA	1796
QY	1560	GGAGTGGGCGCTTGGGACCTCCGGCCCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTG	1619
DB	1797	GGAGCTGAAGTGTCTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1856
QY	1620	AGTGTCTACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1679
DB	1857	CTGACGCGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1916
QY	1680	TGCTA---TGAATGACAGAAAGCCTTTTGTGATCTCAGAGTCTTCAACATCTCTCAACA	1736
DB	1917	CAACATCTCTGGATGCCAGACAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1796
QY	1737	GCGCAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1796
DB	1977	TCCCTGAAATCTCTCCCATGCTCATCAGACGATCGTGCAGCGAGTGTCTCTCTCTCAA	2036
QY	1797	CGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1856
DB	2037	ACGCTGAGGATCTTCTCTCCATGAGGAGTGGAACTTGACAGCATCAGCGACGCGCC	2096
QY	1857	CTCTGGAAGCGTGGCGGAGGATTTGATCATAACATACAGTGGCCACTTTCGCTGGTC	1916
DB	2097	TGTCAAAAGAGCGGGGCGACGAAACAGCATACCGTGAGGAATGCCACATTCACCTGGGC	2156
QY	1917	CCAGGAAAGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1976
DB	2157	CAGGAGCGACCTTCCACACATGAATGGCATCCTTCTTCCATCCCGAAGGCTCTTGGT	2216
QY	1977	GGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2036
DB	2217	GGCGTGTGGGCCAGGTGGGCTGCGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2276

QY 2037 GCTGTCAAAGGTGAGGGTTCGTGACATCGACGGTCTGTGGCTACGTGCCCCAGGA 2096
DB 2277 GATGGACAAAGTGGAGGGACGCTGGTATCAAGGGTCCGTGGCTATGTGCCACAGCA 2336
QY 2097 GGGCTGGGTGCAGAACACCTCTGTGGTAGAGAAATGTGTCTCGGGCAGGAGCTGGACCC 2156
DB 2337 GGGCTGGATTCAAGATATCTCTCCAGAAACATCTTTTGGATGTCACTGGAGGA 2396
QY 2157 ACCCTGGCTGGAGAGTACTAGAACCTGTGGCCCTCGAGCCAGATGTGGACAGCTTCCC 2216
DB 2397 ACCATATTACAGGTCCTGTATACAGGCTGTGCCCTCTCCAGACCTGGAAATCCTGCC 2456
QY 2217 TGAGGAATCCACATTCATTTGGGAGCAGGCAATCAATCTCTCCGGAGGCCAGAGCA 2276
DB 2457 CAGTGGGGATTCGGACAGAGATGGCGAGAGGGCGTGAACCTGTCTGGGGACAGAGCA 2516
QY 2277 GCGGCTGAGCCTGGCCCGGCTGTATACAGAAAGGCAGCTGTGTACCTGTGGATGACCC 2336
DB 2517 GCGGCTGAGCCTGGCCCGGCTGTACTCAACGCTGACATTTACCTCTTCGATGATCC 2576
QY 2337 CTTGGGCGCCTGGATGCCACGCTTGCCAGCATGTCTTCAACCAAGTCAATTTGGGCGCTGG 2396
DB 2577 CCTCTCAGAGTGGATGCCCATTTGGGAAACACATCTTTGAAATGTGATTGGCCCCAA 2636
QY 2397 TGGGCTACTCCAGGAACAACAGGATTCGTGTGACCCAGCAGCTCCACATCTGCCCCCA 2456
DB 2637 GGGGATGCTGAAGAACAAAGACGGGATCTTGGTCAACACAGCATGAGTACTTGGCGCA 2696
QY 2457 GGGTATTGGATCATAGTCTGCAAAATGGGCCATCGCAGATGGTTCCTTACCAGGA 2516
DB 2697 GGTGGAGCTCATCTGCTATGATGGCGCAAGATCTGTGATGGCTTCCCTACCAGGA 2756
QY 2517 GCTTCTGACAGGAAGGGCCCTCTGCTGTCTTCTGGATCAAGCCAGACGACGAGGA 2776
DB 2757 GCTGCTGCTGACAGCGCCCTTCG-CTGAGTTCTGCTGCTACCTATGTCAGCAGCAGC 2815
QY 2577 TAGAGGAGGAGAGAAACAGAACTGGGACGACCAAGCAAGCCAGAGCCAGCCTCTGC 2636
DB 2816 AGGAGAGGATGAGAGGAAGAGGGGTACGCGGCTGTCAGGGTCCAGGAAGGAAGCAA 2875
QY 2637 AGCAGAGGCGCGAGCTTAGACGCGAGAGGTCCATCAAGTCACTGCTGAGAG- 2691
DB 2876 AGCAATGGAGATGGCATCTGTCAGCAGCAGTGCAGGGAAGCACTGCAGAGACGC 2935
QY 2692 -----GACCGTACCCTTCCAGAACCCAG- 2716
DB 2936 TCAGCAGCTCCTCTCTATAGTGGGACATCAGCAGGCAACCAACAGCACCGCAGAAC 2995
QY 2717 CAGAGTTCTCTGGATGACCTGACAGGCGAGGATGGCCAGCAAGAAAGACAGATCC 2776
DB 2996 TGCAGAAAGCTGAGGCCAAGAGGAGAGACCTGGAAAGCTGATGGAGGCTGACAAAGCGC 3055
QY 2777 AATACGCGAGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGTGGCGTGGGACACCCCC 2836
DB 3056 AGACAGGCGAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCA 3115
QY 2837 TCTGCTCTACGACATCTTCTCTCTCTGTCGCGAGCAAGTGGGCTCTTCTGCGGGGCT 2896
DB 3116 TCTCTCTCTCAGCATCTTCTCTTTATGTGTAAACATGTGTCTGCGGCTGGCTTCCAACT 3175
QY 2897 ACTGGCTGAGCCTGGCGGAGACCTCTCAGTAGTGGGACAGACACCGCAGCC 2956
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QY 2957 TGCCTGGCGGATCTTTCGGGCTCCTCGGCTGTCTCAAGCAATTTGGGCTTTTGGCTTCCA 3016
DB 3236 TCCGGCTGAGCCTATGAGCCCTGGCATTTTCAACAGGGGATCGCGGCTTTGGCTACT 3295
QY 3017 TGGCTGGGTGCTCTAGGTGGGCGCGGCGATCCAGGTTGCTTTCCAGAGGCTCTCTGT 3076
DB 3296 CCATGGCGGTGCTCATCGGGGGGATCTTGGCTTCCCGCTCTCTGACAGTGGACCTGCTGC

QY 3077 GGGATGTGGTGGATCTCCCATCAGCTTCTTTGAGGGGACACCCATTTGCTACCTGCTAA 3136
DB 3356 ACAGCATCTCGGGTCAACCCATGAGCTTCTTTGAGCGGACCCCGAGTGGAACTGTTGA 3415
QY 3137 ACCGCTTCTCCAAAGAGACAGACAGCTGACGTGGACATTTCCAGACAACTCCCGTCCC 3196
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RESULT 6

US-08-141-893-1

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; Sequence 1, Application US/08141893
; Patent No. 5489519
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141.893
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923; 08/029,340
; FILING DATE: 27-OCT-1992; 8-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: POI-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5149
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-141-893-1

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Query Match 27.1%; Score 1222.8; DB 1; Length 5011;
Best Local Similarity 55.7%; Pred. No. 5.5e-280;

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QY	336	CACACGATGAGCTTCGAGTGTCTGATTCACACGAGAGAAAGAGGAGTCCAGTC	395							
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QY	396	ATCTGGAGTGTCTTTGTTTACTGGCTTCTCTCTTTTCTTCCAGCTACCAACGCTGC	455							
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Db 4136 ATGTCAGCATCAATGGGGAGAGAGGTCGGCATCGTGGGGGCGGAGGAGTGGGAAGT 4195
QY 3917 CTTCCCTGGCAGTGGCTGTCTGGGCTCCAGGAGGAGCTGAGGCTGGGATCTGGATCG 3976
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QY 3977 AGGGGTCCCAATGTCACGCTGGGCTGCACACTGCGCTCCAGGATCAGCATCATCC 4036
Db 4256 ATGGGATCAACATGCCAAGATCGGCTGCAGGACCTCCGCTTCAAGATCAACCATCATCC 4315
QY 4037 CCCAGAGCCCATCTGTCTCCCTGCTCTCTCGGATGAACCTGACCTGCTGTCAGGAGC 4096
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QY 4157 GCTCGCGGCGAGTGTGAGTACAGTGTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 4216
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QY 4217 AGAAGAGCTCTGTGTCTGGCAGCTGCCCTTCTCCGGAAGACCCAGATCTCATCTCG 4276
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QY 4277 ACGAGGCTACTCTGCTGGTGGACCTGGCAGGAGCTGAGATGACGAGGCTGCTCGGCA 4336

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RESULT 7

US-08-463-092B-1
; Sequence 1, Application US/08463092B
; Patent No. 576880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deesley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

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	Query Match	27.1%; Score 1222.8; DB 1; Length 5011;
	Best Local Similarity	55.7%; Pred. No. 5.5e-280;
	Matches 2535; Conservative	0; Mismatches 1937; Indels 80; Gaps
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QY	156	CCTCTTCATCACCAACAGCGCGGGCTACCTCCGAGTGTCCCCACTCTTCAAAGCCAA 215
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QY	803	AGSCAATACGATTTTAAAGGAAGCGGCAGTGGCATGAAGCTTCCA-----849
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DB 2397 ACCATATTACAGGTCGATGATAGAGCGCTGTGCCCTCTCCAGACCTTGAATCCTGCC 2456
QY 2217 TGAGGGAATCACACTTCAATTTGGGAGACAGGATGAATCTCTCCGAGGCCAGAA 2276
DB 2457 CAGTGGGATCGGACAGAGATTTGGCAGAAAGCGGTGAACCTGTCTGGGGGACAGAA 2516
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QY 2397 TGGGTACTCCAGGGAACACAGGATTTCTGTGAGCAGGACATCCACATCTCTGCCCA 2456
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QY 3377 ACATGGCTGAGAGCTTCCAGGCGACACAGTGTCTCGGCAATTCGGAATTCGGAACCCAG 3436
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QY 3437 TTGTGGCTCAGAACAAATGCTCGGTAGATGAAGCCAGAGGATCATTTCCCGGACTGG 3496
DB 3716 TCATCCACACAGAGTGAAGGTGGACGAGAACCCAGAGGCTATTTACCCAGCATCG 3775
QY 3497 TGGCTGACAGGTGGCTTGGCGCAATGTGGAGCTCTCTGGGAATGCGCTGGTGTTCGAG 3556
DB 3776 TGGCCAAACAGTGGCTGGCGCTGGAGTGTGGGCAACTGCATGCTGTCTGTTG 3835
QY 3557 CGCGCACGCTGTCTGTGTGAGCAAGCCCACTCAAGTCTGTCGCTGCTGGGCTCTCTCTG 3616
DB 3836 CTGCGCTGTTTGGGTGATCTCCAGGCACAGCTCAAGTCTGCTGGCTTGGTGGGCTCTC 3895
QY 3617 TCTCTGCTGCCCTCAGGTGACCCAGACACTGCAGTGGTGTTCGCAACTGCAGAGACC 3676
DB 3896 TGTCTTACTCATTTGAGGTCACACGCTACTTGAACCTGGTGTTCGATGTCTATCTGAAA 3955
QY 3677 TAGAAGACAGCATCTGTGCTGAGGCGGATGACGAGCTATGCTCGAGCCCAAGAGG 3736
DB 3956 TGGAAACCAACATCTGTGGCGTGGAGAGCTCAAGAGATTTTCAGAGACTGAGAAGAGG 4015
QY 3737 CTCCCTGAGGCTGCCACATGTGACGTACAGCCCCCTCGGCTCAGGGCGGCGAGATCG 3796
DB 4016 CGCCCTGGCAATTCAGGAGACACGCTCCGCCAGCAGCTGGCCCCAGGTGGGCGGAGTGG 4075
QY 3797 AGTTCCGGGACTTTGGGCTAAGATCCGACCTGAGTCCCGCTGGCTGCTGCGAGGCTGT 3856
DB 4076 AATTCCGGAATCTGCTGCTGCTACCGAGAGGACCTGGACTTCTGTTCTCAGGCACATCA 4135
QY 3857 COTTCAGATCCACGAGGAGAGAGTGGGATCTGTTGGCAGGACCGGGCGAGGAAAGT 3916
DB 4136 ATGTCAAGATCAATGGGGAGAAAGTCCGATCGTGGGCGGACGGAGCTGGGAAAGT 4195
QY 3917 CTTCTCTGCGAGTGGGCTGTGGGCTCCAGGAGGACGCTGAGGCTGGGATCTGGATCG 3976
DB 4196 GTCCTCTGACCTGGGCTTATTCGATCAAGAGTCTCCGAAAGGAGATCATCATCG 4255
QY 3977 AGGGGTGCCCCATTTGCCAGTGGGCTGCACACACTGCGCTCCAGGATCAGCATATCC 4036
DB 4256 ATGGCATCAACATGCCAAGATCGGCTGCAGACCTCGCTCTCAAGATCAACCTATCC 4315
QY 4037 CCCAGACCCCATCTGTTCCCTGCTCTCTCGGATGAACCTCGACCTGCTGCGAGGAC 4096
DB 4316 CCCAGGACCTGTTTGTGTTTTCGGGTTCCTCCGAATGAACCTGGACCCATTCAGCCAGT 4375
QY 4097 ACTCGGAGGCTATCTGGGCGAGCCCTGGAGACGCTGAGCTCAAGGCTTGGTGGCCA 4156
DB 4376 ACTCGGATGAAGAGTGTGGAGCTGCGAGCTGGCCACCTGAAAGGACTTCGTGTCTAG 4435
QY 4157 GCTCCCGGCGCAGCTGCAGTAAAGTGTGCTGACCGAGGCGGAGGACCTGAGGCTGGCC 4216
DB 4436 CCGTCTCTGACAGCTAGACCATGAATGTCAGAGGCGGGGAGAACCTCAGTGTCTGGGC 4495
QY 4217 AGAAACAGCTCTGCTGTGGCAGCTGCGCTTCTCCGGAAGACCCAGATCTCTATCTCTGG 4276

Db 4496 AGCGCCAGCTTGTGTGCTAGCCCGGCGCTGTGAGGAAGAGAGATCTTGTGTGG 4555
Qy 4277 ACGAGGCTACTGCTGCGGTGACCTGGCAGGAGCTGCAGATGAGGCCATGCTCGGGA 4336
Db 4556 ATGAGGACACGGCAGCGCTGACCTGGAAACGGAGACCTCATCCAGTCCACCATCCGGA 4615
Qy 4337 GCTGGTTTGACAGTGACTGTGCTGCCATTGGCCACCGCTGCGCTCCGCTGATGGACT 4396
Db 4616 CACAGTTCGAGGACTGCACCTGCTCACCATCGCCACCGCTCAACACCATCATGGACT 4675
Qy 4397 GTGCCCGGTTCTGTCATGACAAAGGGCAGGTGGCAGAGAGGGCAGCCCGGCCAGC 4456
Db 4676 ACACAAAGGCTGATGCTCTTGACAAAGGAGAAATCCAGGAGTACGGCCGCCATCGGACC 4735
Qy 4457 TGCTGGCCCAAGGGCTGTTTACAGACTGGCCCGAGGAGTACGGCTGTGT 4508
Db 4736 TCCTGCAGCAGAGAGTCTTTTCTACAGCATGGCCAAAGACGGCGCTTGGT 4787

RESULT 8

US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 582875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQ1-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-462-109A-1

Query Match 27.1%; Score 1222.8; DB 2; Length 5011;
Best Local Similarity 55.7%; Pred. No. 5.5e-280;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;
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Db 237 GCTCTGGGACTGGAATGTACGTGGAAATACACGAACCCCGACTTCACCAAGTGTCTTCA 296
Qy 96 GAGAAGACAGAGGGTCTGGGTACCCCGCTTACCTCTGGTCTTGGTCTTGGTCTTACCT 155
Db 297 GAACAGGCTCTGCTGCTGGTGTCTTGTACCTCTGGGCTGTGCTTCCCTCTTACTT 356
Qy 156 CTTCTTATCCACACACATGCGGGGTACCTTCGGATGTCCCGACTCTTCAAGCCAA 215
Db 357 CCTCTATCTCTCCGACATGACCGAGGTACATTCAGATGACACCTCTCAACAAACCAA 416
Qy 216 GATGTGTGTGATTCGCCCTCATAGTCTGTGTACTCCAGGTGGTGTGCTCTTTG 275
Db 417 AACTGCTTGGGATTTTGTCTGTGGATCTGTCTGGGAGACCTCTTCTACTCTTCTG 476
Qy 276 GAAATCCAAACAGGGAACGCTGAGGCCCGCAGAAATTCCTCATTCATCTCTACTGTGGCT 335
Db 477 GGAAGAGAGTGGGCAATATCTGCGCCCGAGTGTCTGGTCTGAGCCCACTCTCTTGG 536
Qy 336 CACCAGATGAGCTTGGCAGTGTTCCTGATTCACACCGAGAGGAAAGAGTCCAGTC 395
Db 537 CATCACCAGCTGTGCTACCTTTTAAATTCAGCTGGAGAGGAGGAGGAGTTCAGTC 596
Qy 396 ATCTGAGTGTGTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 455
Db 597 TTCAGGATCATGCTCACTTTCTGGTGTAGCCCTAGTGTGTGCTGCTGCTGCTGCTGCTG 656
Qy 456 CCAGCAG-----GCCTCGGAGCGGCTTCAGAGCGAGCCCTGTCGCCACCTGTC 506
Db 657 ATCCAAATATGACAGCCTTAAAGAGATGCCAGGTGGAGCTGTTCTGTGACATCAC 716
Qy 507 CACTACCTATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 566
Db 717 TTTCTACGCTCTACTTTTCCCTCTTACTATTTCAGCTGCTGCTGCTGCTGCTGCTGCTG 776
Qy 567 ACCCCCTCTTCCCTGAGACCCCGCAGCTCTAACCCCTGTCCAGAGACTGGGCGAC 826
Db 777 CTCACCCCTGTTCTCGGAAACCATCCAGACCTTATCCCTGCCAGAGTCCAGCGCTTC 836
Qy 627 CTTCCCTCCAAAGCCAGCTTCTGTGGGTTCCTGCGCTGCTGCGAGGGATACAGGAG 886
Db 837 CTTCTGTGAGGATCACCTTCTGTGGATCACAGGTTGATGTCGGGGGTACCGCCA 896
Qy 687 GCCACTGAGACCAAAAGACCTCTGTGCTGGGAGAGAAAACCTCTCAGAGAACTTGT 746
Db 897 GCGCTGGAGGCGAGTACCTCTGCTTAAACAGAGGAGACGCTCGGAACAAGTCTGT 956
Qy 747 TCCCGGCTTGAAGAGGAGTGTGATGAGGAAACCGC-----AGTCAGCCCGGAGGACCA 802
Db 957 GCCTGTTTGGTAAAGAACTGGAAGAGGATGCCCAAGACTAGGAAGCAGCAGCGGTGAA 1016
Qy 803 AGGCAATAGCATTTAAAGGAAAGCGGCGGCTGATGAGGCTCA----- 849
Db 1017 GGTGTGTACTCTCCAGGATCTGCCAGCGGCAAGAGAGTTCCAGGTGGATGCGGAA 1076
Qy 850 -----GAGACCGAGCCCTTCTACGGCAAGAGGAGGAGCCAGTGGCGCCACTGCT 899
Db 1077 TCAGGAGGTGGAGGCTTGTATCGTCAAGTCCCGCAGAGGAGTGGAAACCCCTCTCTGT 1136
Qy 900 GAAGCCATCTGGAGGTGTCCATTCTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 959
Db 1137 TAAGGTGTATACAAGACCTTTTGGGCCCTTACTTCTCTATGAGCTTCTTCTTCAAGGCCAT 1196
Qy 960 CAGTGTGTCTTCAAGTTTCACTGTCCCAAGCTGTCCAGCCCTTTTCTGGAGTTTATTGG 1019
Db 1197 CCAGCAGCTGATGATGTTTTCGGCGCGCCAGATCTTAAAGTTGCTCATCAAGTTCGTGAA 1256

Db 3416 ACCGCTTCTCCAGAGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTTCATCAAGATGT 3475
QY 3197 TGCTGATGATAGCCCTTTGGACTCTCTGGAGGTACAGCTGGTGGTGGCAATGGGTATCCCCAC 3256
Db 3476 TCATGGGCTCCCTGTTCAACGTCTATGGTGTCTGATCGTATCTCTGTGTGCGCACGCCCA 3535
QY 3257 TGGCCACTGTGGCCACTCTGCTCCACTGTTTCTCTCTACGCTGGGTTCAGAGCCCTGTATG 3316
Db 3536 TCGCGCGCATCATATCCCGGCCCTTGGCCCTCATCTACTTCTCGTCAGAGGTTCTACG 3595
QY 3317 TGGTTAGTCTATGACAGTGTAGAGCTTGGAGTCCAGCAGTACTCTGCTCTCTGCTGCC 3376
Db 3596 TGGCTTCTCTCCGAGCTGAAGCGCTCGAGTGGTCCAGCGCTCCCGGCTCTATTC 3655
QY 3377 ACATGGCTGTAGACGTTCCAGGGCAGCAGATGGTGGTCCGGGCATTCGGAACCCAGCCGCC 3436
Db 3656 ATTTCAACGAGACCTTGTGGGGGTGAGCGTCAATTCGAGCCTTCGAGGAGCAGGAGCGCT 3715
QY 3437 TTGTGGCTCAGAACATCTCGCTAGATGAAGCCAGAGATCAGTTTCCCGGACTGG 3496
Db 3716 TCATCCACCAGAGTGAAGTGGAGTGGAGAGAACAGAGGCTATTTACCCAGCATCG 3775
QY 3497 TGGCTGACAGTGGCTTGGGCCAATGTGGAGCTCTCTGGGAATGGCTGTGTGTTGCGAG 3556
Db 3776 TGGCCACAGTGGTGGCTGGCTGGGTGGAGTGTGGGCACTGATCGTTCTGTGTTG 3835
QY 3557 CCGCCAGTGTGTGCTGTAGCAAGCCACCTCAGTGTGGCTCTGTGGGCTTCTCTG 3616
Db 3836 CTGCGCTGTTTGGCGTGTATCTCCAGGCACAGCCTCAGTGTGGCTTGTGGGCTCTCAG 3895
QY 3617 TCTCTGCTGCCCTCAGGTGACCCAGACACTGCACTGGTGTGTCGCAACTGGACAGCC 3676
Db 3896 TGTCTTACTATTCAGGTCACCACTGACTTGAATGGCTGGTTCGATGTCATCTGAAA 3955
QY 3677 TAGAAGACAGATCGTGTCAAGTGGAGGGATGCAAGTACTGCTGCGACGCCCAAGAGG 3736
Db 3956 TGGAAACCAACATCGTGGCGTGGAGAGCTCAAGAGTATTCAGAGACTCAGAGAGG 4015
QY 3737 CTCCTGGAGCTGCCACATGTGCAGCTCAGCCGCCCTGCGCTCAGGGGGGCGAGATCG 3796
Db 4016 CGCCCTGGCAAAATCCAGGAGACAGCTGCCGCCAGCAGCTGGCCCGAGTGGCGGAGTGG 4075
QY 3797 AGTTCCGGGACTTTGGCTTAAGATGCGAGCTGAGCTGCCCTGCTGGCTGTGCGAGGCGTGT 3856
Db 4076 AATTCGGAACTACTGCTGCTGCTTACGAGGAGCTGGAGCTTCTGTTCTCAGGCACATCA 4135
QY 3857 CTTTAAAGATCCAGCAGGAGAGAGTGGGCTATGTTGGCAGGACCGCGGCGAGGAGT 3916
Db 4136 ATGTACAGATCAATGGGGAGAGAGTGGCATCTGTTGGGCGACCGGAGCTGGGAGT 4195
QY 3917 CTCCTCGGCGAGTGGGCTGCTGGGCTCCAGAGGAGCAGTGGGTTGGATCTGGATCG 3976
Db 4196 CGTCCCTGACCTGGGCTTATTTCCGATCAACAGTCTGCCGAAGAGAGATCATCTCG 4255
QY 3977 ACGGGTCCCATGTCACGCTGGGCTGCACACACTGCGCTCAGGATCAGCATATCC 4036
Db 4256 ATGGCATCAACATGCGCAAGATGGCTGCGCATGCAAGCTCCGCTTCAAGATCACCATATCC 4315
QY 4037 CCAGGAGCCCATCTGTTCCCTGGCTCTCTGGGATGAACCTCGACCTGTGTCAGGAGC 4096
Db 4316 CCCAGGACCTGTTTGTGTTTGGTTCCTCCGATGAACCTGGACCCCATTCAGCCAGT 4375
QY 4097 ACTGGACGAGGCTATCTGGGCGCCCTGGAGAGCGGTGAGCTCAAGCCCTTGGTGCCCA 4156
Db 4376 ACTCGATGAAGAAGTCTGGACGCTCCCTGGAGTGGGCCACCTGAAGGACTTCTGTCTAG 4435
QY 4157 GCCTGCGCGCCAGCTCAGTACAGTGTCTGACCGAGGCGGAGGACTGAGCGTGGCC 4216
Db 4436 CCCTTCTGCAAGCTAGACCATGAATGTGCAAGAGCGGGGAGAACTCAGTGTCCGGC 4495
QY 4217 AGAAACAGCTCTCTGTCTGGCAGCTGCCCTTCTCCGGAAGACCCAGATCTCTATCTCG 4276
Db 4496 AGCCCGAGCTTGTGTGCTAGCCGGGCCCTGCTGAGGAAGACGAAGATCTCTGTGTGG 4555

QY 4277 ACAGGCTACTCTGCTGCGTGGACCCCTGGCCAGCGAGTGTGAGATGTCAGAGCCATGCTCGGA 4336
Db 4556 ATGAGCGCCAGCGACCGTGGACCTGGAAACGAGCAGACCTCATCCAGTCCACCATCCGA 4615
QY 4337 GCTGCTTTGCACAGTGCCTGCTGCTGCCCATTTGCCACCGCTGCGCTCGGTGATGACT 4396
Db 4616 CACAGTTCGAGACTGCACCGCTCTCACCATCGCCACCGGCTCAACACCATCATGACT 4675
QY 4397 GTGCGCGGCTTCTGCTCATGACAAAGGGGCGAGTGGCAGAGCGGCGCCGCCAGC 4456
Db 4676 ACACAGGGTGTATCTCTTGGACAAAGAGAAATCCAGGAGTACGGCGCCCATCGGACC 4735
QY 4457 TGCTGCCCGCAGAGGCGCTGTTTACAGACTGGCCCGCAGGATCAGGCTGTT 4508
Db 4736 TCCTGACGAGAGGCTCTTTTCTACAGATGGCCAAAGACCGCGCTTGGT 4787

RESULT 9

US-08-460-907B-1
; Sequence 1, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

QY	2037	GCTCTCAAAGGTGGAGGGGTTCTGTAGCATCGAGGGGTCTGTGGCCCTACGCTGGCCCCAGGA	2096
Db	2277	GATGGCAAAAGTGGAGGGCACGTGGCTATCAAGGGCTCCGTGGCCCTATGTGGCCACAGCA	2336
QY	2097	GGCTGGGTCCAGAACACTCTGTGTGTAGAGAATGTGTCTTCGGGCAGAGCTGGACCC	2156
Db	2337	GGCTGTGATTTCAGAAATGTTCTCTCCGAGAAAACATCCTTTTGTGGATGTCTCAGCTGGAGGA	2396
QY	2157	ACCTTGCTGGAGAGAGTACTAGAAGCCTCTGCCCTGACCGCAGATGTGCACAGCTTCCC	2216
Db	2397	ACCATATTACAGTCCGTGTATCAGCGCTGTGCCCTCTCCACAGACTGGAAATCTGTGCC	2456
QY	2217	TGAGGAATCCACACTTCATNTGGGAGCAGGCATGAATCTCTCCGGAGCCACAGAAGCA	2276
Db	2457	CAGTGGGATCGGACAGAGATTGGCGAGAAGGCGTGAACCTGCTCTGGGGACAGAAGCA	2516
QY	2277	GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGACAGCTGTACTCTCTGCTGGATGACCC	2336
Db	2517	GCGGTGTAGCCTGGCCCGGGCGGTGTACTCCAACGCTGACATTTAGCTCTTCGATGATCC	2576
QY	2337	CCTGGCGGCCCTGGATGCCACACCTTGGCCAGCATGTCTTCAACAGGTGATTTGGGCTTGG	2396
Db	2577	CCTCTCAGCAGTGGATGCCCATGTGGGAACACATCTTTGAAATGTGATTGGCCCCCAA	2636
QY	2397	TGGGCTACTCCAGGGMAACACGGAATCTCGTGCAGCACGCACTCCACATCTCGTCCCCA	2456
Db	2637	GGGGATGCTGAAGAACAGACGCGGATCTTGGTCAACGCACGATGAGCTACTTGCCTGCA	2696
QY	2457	GGCTGATTGGATCATAGTCTGGCAANTGGGCCATCGCAGAGATGGGTTCTTACAGGA	2516
Db	2697	GGTGGACGTCACTCATCGTCAATGAGTGGCGGCAAGATCTCTGAGATGGGCTCTCTACCA	2756
QY	2517	GCTTCTGCAGAGAAAGGGGGCCCTCGTGTGTCTCTCGGATCAAGCCAGACAGACGAGGA	2576
Db	2757	GCTGCTGGCTCGAGACGGCGCCTTCG-CTGAGTTCCTGCTACCTATGCCAGCAGACGC	2815
QY	2577	TAGAGGAAGAGGAACAGAACCTTGGGACCAAGCAAGACCCAGAGGACCTCTCTCC	2636
Db	2816	AGGACAGGATGCAGAGGAGAACGGGGTCAACGGGCTCAGCGGTCACGGGAAGGAAGCAA	2875
QY	2637	AGCAGGAGGCCCGAGCTTAGACGGCAGAGGTCCATCAAGTCAGTCCCTGTAGAG- ----	2691
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QY	2692	-----GACCGTTACCACCTTCAGAAAGCCCA- --	2716
Db	2936	TCAGCAGCTCCTCCTCTATAGTGGGACATCAGCAGGACCCACACAGACCCGACAGAC	2995
QY	2717	CAGAGGTTCTCTGTATGACCTGACAGGCGAGGATGGCCACGACAGAAAGGACAGATCC	2776
Db	2996	TGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTTGAAGCTGATGAGGCTGACAAAGGCGC	3055
QY	2777	AATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCCTACTCGTGGCTGGGCACCCCC	2836
Db	3056	AGACAGGCGAGGTCAAGCTTTCGGTGTACTGGGACTACATGAAGGCCATCGGACTTTCA	3115
QY	2837	TCTGCTCTACGCACCTCTTCCTCTTCCTCTGCCAGCAAGTGGCCCTCTCTGCCGGGCT	2896
Db	3116	TCTCCTCTCTCAGCATCTCTCTTTTCATGTGTGTAACCATGTGTGCGGCTGGCTTCCA	3175
QY	2897	ACTGCTCAGCCTGTGGCGGACGACCTCTCAGTAGTGGGAGGAGGAGGACGAGGACGCC	2956
Db	3176	ATTGGCTCAGGCTCTGAGACTGATGACCCCATCGTCAACGGGACTCAGGAGCAGACGAAG	3235
QY	2957	TGCGTGGCGGGATCTTCGGGCTCTTCGGCTGTCTCAAGCCATTTGGGCTGTGTGCTCCA	3016
Db	3236	TCCGGCTCAGCGTCTATGGAGCCCTTGGGCATTTTCAAGGGATGCCCGTGTGTGGCTACT	3295
QY	3017	TGGCTTGGCGGTCTCTTAGGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTTCCTGT	3076
Db	3296	CCATGGCGGTGTCCATCGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGCACCTGTCTGC	3355
QY	3077	GGATGTGTGGATCTCCCATACAGTTCTTTTGAGCGGACACCCATTTGGTCACCTGTCTAA	3136

Db	3356	ACAGCATCCTGGCGTCA	CCCCATGAGCTTCTTTGAGCGGACCCCGAGTGGGAACCTTGGTGA	3415
QY	3137	ACGCGTTCTTCCAAAGGAGACAGACACGGTTGACCTGGACATTC	CCAGACAAACTCCGGTCCC	3196
Db	3416	ACGCGTTCTTCCAAAGGAGCTG	GACACAGTGACATCCCATGATCCCGGAGGTTCATCAAGATGT	3475
QY	3197	TGCTGATGTAGCGCTTTGGACTCCTGGAGGTGACGCTGGTGGTGGGAGTGGGTACGCCAC	3256	
Db	3476	TCATTGGGCTCCCTGTTC	CAAGCTCATTTGGTGCCGTGCATTCGTTATCCTGCTGGCCACGCGCCA	3535
QY	3257	TGGCCACTGTGGCATCTCCCACTGT	TTTCTCCTCTACGCTGGGTTTCAGAGCGCTGTATG	3316
Db	3536	TGCGCGCATCATCATC	CCCCCGCTTGGCCCTCATCTTACTTTCTTCGTGCAGAGGTTCTTACG	3595
QY	3317	TGSTTAGCTTATGCCAGCTGAGACGGTTGGAGTTCAGCCAGCTACTCGTGTCTGTCTGTCCC	3376	
Db	3596	TGCGTTCTCCCGSAGCTGA	AGCGCCTCGAGTCTGCTCAGCGCTCCCGCGTCTATTC	3655
QY	3377	ACATGGGTGAGACGTTCC	AGGGCAGCACAGTGTGTCGGGCATTTCCGAACCCAGGCGCCCT	3436
Db	3656	ATTTCAACGAGACCTTGT	TGGGGTCAAGCGCTATTTCAGCGCTTCGAGGAGGAGGACGCT	3715
QY	3437	TTCTGGCTCAGAACATGCT	CGCGTATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG	3496
Db	3716	TCATTCACCAAGAGTAGCT	GAAGGTGGACGAGAACCAAGAGGCGCTATTATCCCCAGCATCG	3775
QY	3497	TGCGTGCACAGTGGCTT	TCGGCCAAATGTGAGCTCCTGGGGAATGCGCTGGTGTTCGCAG	3556
Db	3776	TGSCCAACAGGTGCGT	TGGCGCTGGAGTGTGTGGCAACTGCATCTGTCTCTTTG	3835
QY	3557	CCGCCAGGTGTGCTGTG	TGAGAAAGCCCACTCAGTCTGGCCTCGTGGGCTTCTCTG	3616
Db	3836	CTGCCCTGTTTGGGTGATCT	CCAGGCACAGCCTCAGTCTGCTGGCTTGGTGGGCTCTCAG	3895
QY	3617	TCFCTGCTCGCTCCAGGTG	ACCCAGACACTGCAGTGGGTTGTTCCCAACTGGACAGACC	3676
Db	3896	TGTCTTACTCATTTGCAGGT	CAACCACTGTTGAATGGGTGTTTCGGATGTCTATCTGAAA	3955
QY	3677	TAGAGAACAGCATCTGT	TCAGTGGAGCGGATCGAGACTTATGCCCTGGAGCCGCCAAGAGG	3736
Db	3956	TGSAACCAACATCTGT	TGGCGCTGAGAGGCTCAGAGGATATTCAGAGACTGAGAAGGAGG	4015
QY	3737	CTCCCTGGAGGCTGCC	CACTGTGCAGCTACGCCCTTCAGGCGGGCAGAGATCG	3796
Db	4016	CGCCTTGGCAATTC	CAGGAGACACGTCCGCCACAGAGCTGGCCCGCAGGTGGGCCGAGTGG	4075
QY	3797	AGTTCGGGACATTTGGCT	TAAGATGCCGACCTGAGCTCCCGCTGGCTGTGCAGGGCGGTGT	3856
Db	4076	AAATTCGGAACTACTGCT	TGCGCTACCGAGAGGACTTGACATTCCTTCTCAGGCACTCA	4135
QY	3857	CGTTTAAAGATCCACG	CAGGAGAAAGTTGGGCATGCTTGGCAGGACCCGGGCGAGGAAGT	3916
Db	4136	ATGTCACGATCAAT	GGGGAGAAAAGTCTGGCATCTGGGGCGGACGGAGCTGGGAAGT	4195
QY	3917	CCTCCCTGGCCAGTGGGT	GTCTGCGGCTCCAGAGGCAGCTGAGGGTGGGATCTGGATCG	3976
Db	4196	CGTCTCTGACCTTGGGCT	TATTTCCGATCAACGAGCTCTGCCAAGGAGAGATCATCATCG	4255
QY	3977	ACGGGGTCCCCATTTCC	CCACGTGGGGCTGCACACACTGGCTCCAGGATCAGCATCATCC	4036
Db	4256	ATGGCATCAACATCG	CAAGATCGGCGCTCGAGACCTCCCGTTCAAGATCACCATCATCC	4315
QY	4037	CCAGGACCCCATCTCT	CTCTGCGGATGAACCTCGACCTGCTGCAGGAGC	4096
Db	4316	CCAGGACCCCTGTTT	GTGTTTCGGGTTCCCTCCGAATGAACCTGGACCCATTCAGCCAGT	4375
QY	4097	ACTCGGACGAGCTATCT	GGCGAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCA	4156
Db	4376	ACTCGGATGAAGAACT	CTGGAGTCTCCCTGGAGCTGGCCCACTGAAGGACTTCGTGTCTAG	4435
QY	4157	GCCTCCCGGCGAGCT	GCAGTACAAGTGTGTGACCGGAGGACCTGAGGCTGGGCC	4216

Db 4436 CCCTTCTGACAAAGCTAGACCATGATGTGCAGAAAGCGGGGAGAACCTCAGTGTGCGGC 4495
QY 4217 AGAAACAGCTCTGTCTGTGGCAGCTGCGCTTCTCCGGAGACCCAGATCTCATCTGG 4276
Db 4496 AGGCCAGCTGTGTGCTAGCCCGGGCCCTGCTGAGGAGAGCAAGATCTTGTGTGG 4555
QY 4277 ACAGAGCTACTGTGCTGCGTGGACCTTGGCAGCAGGCTGCAGATGCAGAGGCCATGCTCGGA 4336
Db 4556 ATGAGGCCAGCAGCGCTGGACCTGGAACGAGACGACCTCATCAGTCCACCATCGGA 4615
QY 4337 GCTGGTTTGCAGATGCACTGTGCTGCCCATTTGCCACCCGCTGCGCTCGTGATGACT 4396
Db 4616 CACAGTTCGAGGACTGACCGCTCTCACCATCGCCACCGGCTCAACACCATGGAAT 4675
QY 4397 GTGCCGGGTTCTGTCATGAGGAGGCGAGGTGCGCAGAGCGCGCGGCCAGC 4456
Db 4676 ACAAGGGGTGATGCTTGTGGCAAGAGGAATCCAGAGTACGCGGCCCATCGGACC 4735
QY 4457 TGTGCCCCAGAAAGGCTGTGTTTACAGACTGGCCCGAGGAGTCAGGCTGGT 4508
Db 4736 TCCTGCGCAGAGAGGTCTTTTCTACAGCATGCGCAAGACGCGGCTGGT 4787

RESULT 10

US-08-463-179A-1
; Sequence 1, Application US/08463179A
; Patent No. 6001563
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,179A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 196..4788
US-08-463-179A-1
Query Match 27.1%; Score 1222.8; DB 3; Length 5011;
Best Local Similarity 55.7%; Pred. No. 5.5e-280;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;
QY 36 GGCTGGAAACACACAGAGCCTGAAACCTGGCGCCACACAGCCTGCTGAGCCCTGCTTCCT 95
Db 237 GCTCTGGGACTGGAATGTACGTGGAATACACAGCAACCCGAGCTTCACCAAGTCTTTCA 296
QY 96 GAGAAACAGCAGGGGTCTGGGTACCCCATGTACTCTGGTCTCTGGTCCCTACCTCTACCT 155
Db 297 GAACAGGTCTCTGCTGGGTGCTGTTTTTACCTCTGGGCTGTTTCCCTCTTACTT 356
QY 156 CTTCTTATCCACACACATGCGGGGCTACCTCCGGATGTCCTCCACTCTTCAAGCAA 215
Db 357 CTTCTATCTCCCGACATGACCGAGGCTACATTACAGTACACCTCTCAACAAACCAA 416
QY 216 GATGCTGCTTGGATTCGCCCTCATAGTCTCTGTACCTCCAGCGTGTGCTGCTCTTTG 275
Db 417 AACTGCTTGGGATTTTGTCTGGAATGCTGCTGGGACAGCCTCTTCTACTCTTTCTG 476
QY 276 GAAATCCAAACAGGGAACGCTGAGGCCCCAGAAATCTCTCATCTCTACTGTGTGCT 335
Db 477 GGAAGAAGTCTGGGCATATCTCTGGCCCAAGTGTCTGTGTCAGCCCACTCTTTGGG 536
QY 336 CACCACATGAGCTTCGCACTGTTCTCTGATTCACACGAGAGGAAAGGAGTCCAGTC 395
Db 537 CATCACACGCTCTGCTACCTTTTAAATCAGTGGAGGAGGAGGAGTTCAGTC 596
QY 396 ATCTGAGTGTCTGTTGGTGTCTGCTGCTTCTGCTTGTCTGCTGCTGCTGCTGCTGCTG 455
Db 597 TACAGGATCATGCTCACTTTCTGGTGTGAGCCCTAGTGTGCTGCTGCTGCTGCTGCTG 656
QY 456 CCAGCAG-----GCCTCCGGAGCGGCTTCCAGAGCAGACCTCTCCGCCACCTGTC 506
Db 657 ATCCAAATATGACAGCCTTAAAGAGGATGCCAGTGGACCTGTTCTGTCATCATC 716
QY 507 CACTTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
Db 717 TTTCTACGCTACTTTTCTCCCTTACTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
QY 567 ACCCCCTCTCTCCCTGAAGACCCCGCAGCAGTCTTAACCCCTGCTCCAGAGACTGGGCG 626
Db 777 CTACCCCTGTTCTCGGAACCATCCAGACCTTAATCCCTGCCAGAGTCCAGCGCTTC 836
QY 627 CTTCCTCCAAAGCCACGTTCTGCTGGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
Db 837 CTTCTGTCGAGGATCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 896
QY 687 GCACTGAGACCAAAAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746
Db 897 GCCCTTGGAGGCGAGTCACTCTGCTGCTTAAACAAAGGAGGACACGCTCGGAACAGTCT 956
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Db 957 GCTGTTTGGTAAAGAACTGGGAAGAGGAATGCGCAAGACTAGGAAGCAGCGCGGTGAA 1016
QY 803 AGCAATAGCATTTAAAGAAAGGCGGAGTGGCATGAAGGCTCCA----- 849
Db 1017 GGTGTGTACTCTCCAGAGTCTGCCAGCCGCGAAGAGAGTTCGAAGTGGATCGAA 1076
QY 850 -----GAGACGAGCCCTTCTACGGCAAGAGGAGGAGGAGTGGCGCCACTGCT 899
Db 1077 TGAGGAGGTGGAGGCTTGTATCGTCAAGTCCCAACAGAGGAGTGGAAACCCCTCTCTGT 1136
QY 900 GAAGCCATCTGCGAGGTGTTCAATCTTACCTTCTCCCTGGGACCCCTCAGCTCATCAT 959
Db 1137 TAAGGTGTTATACAGACCTTTGGGCGCTTCTTCTCATAGCTTCTTCTTCAAGGCCAT 1196
QY 960 CAGTGATGCTTTCAGGTTCACTGTCGCCAAGCTGCTCAGCCTTTTCTGAGTTTATTGG 1019

Db 1197 CCAGCCTGATGATGTTTTCCGGCCGACAGATCTTAAAGTTGCTCATCAAGTTTCGTGAA 1256
QY 1020 TGATCCAAAGCCTCCAGCCTGGAAAGGCTACCTCTCGCGTGTGATGTTCTCTCAGC 1079
Db 1257 TGACAAAGAGCCCGCCAGACTGGCAGGCTACTTCTACACCGTGTGCTGTGTGTCACCTGC 1316
QY 1080 CTGCTCCAAACGCTGTTTTCAGCAGCAGAACATGTACAGGCTCAAGTGCAGCAGATGAG 1139
Db 1317 CTGCTGCAGACCTCGTGTGTGACCAAGTACTTCCACATCTGCTTCAGTGGCATGAG 1376
QY 1140 GTTGGGCTCGGCCATCACTGGCCTGFTGTACAGAAAGTCTGSCCTCTGCCAGCGCTC 1199
Db 1377 GATCAAGACCGCTGTCTATTGGGCTGTCTATCGGAAGCCCTGGTGATCAACCAATTCAGC 1436
QY 1200 CAGAAAGCCAGTCCGCTGGGTGATGTGGTCAATCTGGTGTCCGTGCAAGTGCAGCGGCT 1259
Db 1437 CAGAAATCTCCACGCTCGGGAGATGTCAACCTCATCTGTGTGACGCTCAGAGGTT 1496
QY 1260 GACCGAGAGCGTCTCTTACCTCAACGGGCTGTGGCTGCCCTCTGCTGTGGATCGTGGTCTG 1319
Db 1497 CATGGACTTGGCCACGTACATTAACATGATCTGGTACGCCCTCTGCAAGTCACTCTTGC 1556
QY 1320 CTTCGCTATCTCTGGCAGCTCTGGGGCCCTCGGCCCTCACTGCCATCGCTGTCTTCTCT 1379
Db 1557 TCTCTACCTCTCTGGCTGAATCTGGGCCCTTCGGTCTGGAGTGGCGGTGATGGT 1616
QY 1380 GAGCCTCTCTCTGATTTCTTATCTATCTCAAGAAAGAACACCATCAGAGGAGCA 1439
Db 1617 CCTCATGGTCCCGCTCAATCTGTGTGGCGATGAAGACAAAGACGATCAGGTGGCCCA 1676
QY 1440 AATGAGCGAAGAGCTACGCGCACCGCTCACAGCTCTATCTCTAGGAACTCGAAGAC 1499
Db 1677 CATGAAGACAAGACAATCGGATCAAGCTGATGAACGAATTCATCGGATCAAGT 1736
QY 1500 CATCAAGTTCATGGCTGGAGGAGGAGCTTTCTGGACAGAGTCTGGGCAATCCGAGGCCA 1559
Db 1737 GCTAAAGCTTTATGCTGGAGCTGGCATTCGAAGGACAAGGTGCTGCCATCAGCGCAGGA 1796
QY 1560 GGAGCTGGGGCTTGGGACCTCGGCCCTCTCTCTCTGCTGCTGTGCTCTTCCA 1619
Db 1797 GGAGCTGAAGGTGCTGAAGAGTCTGCTCTACCTCTGACGCGTGGGCACTTCACTCGGT 1856
QY 1620 AGTGTCTACATTTCTGCTGCACTGTGTGTTGTGCTCCACACTGTGCTGGCCGGAGAA 1679
Db 1857 CTGACGCCCTTTCTGTGSCCTTTGTGCACATTTGCGCTACGTGACCAATGACGAGAA 1916
QY 1680 TGCTA---TGAATGACAGAAAGCTTTGTGACTCTCAGAGTCTCAACATPCCTCAACAA 1736
Db 1917 CAACATCTCTGGATGCCAGACAGCCTCTGCTTTGGCCCTTGTCAACATCCTCCGGTT 1976
QY 1737 GGCCAGGCTTTCTGCCCTTCTCCATCCACTCTCTGCTCCAGGCCCGGTGCTTTGA 1796
Db 1977 TCCCTTGACATTTCTCCCATGTCTATCAGACGATCGTGCAGCGGAGTGTCTCCCTCAA 2036
QY 1797 CCGCTGTGGTCACTCTCTGCTGGAAGAGTTGACCTGGTGTGCTAGACTCAAGTTC 1856
Db 2037 ACGCCGTGAGGATCTTTCTCTCCATGAGGAGCTGGAACTGACAGATCAGGAGCGGCC 2096
QY 1857 CTCTGGAAGCGCTGCGGGAAGGATTCATPCACCATACAGAGTCCACCTTCCGCTGGTC 1916
Db 2097 TGTCAAAGACGGGGGGGACGAACAGCATCACCGTGAGGAATGCCACATTCACCTGGGC 2156
QY 1917 CCAGGAAGCCCTCCCTGCTCCACAGATAAACCTCAGCGTGGCCCGGCTGTCTGCT 1976
Db 2157 CAGGAGGACCCCTCCACACTGAATGGCATACCTTCTCCATCCCGGAAGGTGCTTTGGT 2216
QY 1977 GGTGTGTGCTGCTGAGTGGGGCAGGAAAGTCTCTCTGCTGTGCGCCCTCTTGGGGA 2036
Db 2217 GGCCGTGGGGCCAGGTGGGCTGCGGAAGTGTCTCCCTGCTCTCAGCCCTCTTGGCTGA 2276
QY 2037 GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGTGTGGCTTACGTGCCCGCAGGA 2096
Db 2277 GATGGACAAAGTGGAGGGACGCTATCAAGGGCTCGGTGGCTATGTGCCACAGCA 2336

QY 2097 GGCCTGGTGCAGAACACCTCTGTGGTAGAATGTGTCTTCGGGAGGAGCTGGACCC 2156
Db 2337 GGCCTGGATTGAGATGATCTCTCCGAGAAACATCTCTTTTGGATGTGACGTGGAGGA 2396
QY 2157 ACCCTGGCTGGAGAGAGTACTAGAACCTGTGCCCTGCAGCCAGCATGTGGACAGCTTCC 2216
Db 2397 ACCATATTACAGTCCGTGATACAGCCCTGTGCCCTCTCTCCAGACCTTGGAAATCTTCC 2456
QY 2217 TGAGGGAATCCACACTTCAATTGGGAGCAGGCAATGAATCTCTCCGAGGCGCAGGA 2276
Db 2457 CAGTGGGATCGGACAGAGATTGGCAGAGGCGTGAACCTGTCTGGGGGACACAGGA 2516
QY 2277 GCGCTGAGCTGGCCCGGCTGTATACAGAAAGCAGCTGTGTACCTGCTGGATGAOCC 2336
Db 2517 GCGCTGAGCCTGGCCCGGCTGTATCCAACTGACATTTACCTTCTCGATGATCC 2576
QY 2337 CTTGGCGCCTGGATGCCAGCTGTGGCAGCATCTCTCAACAGGTCATTTGGGCCCTGG 2396
Db 2577 CTTCTACAGTGGATGCCATGTGGGAAACACATCTTTGAAATGTGATTTGGGCCCAA 2636
QY 2397 TGGCTACTTCCAGGGAACAACACGGATTCTGTGACGACGCACTTCCACATCTTCCCA 2456
Db 2637 GGGATGCTGAAGAACAGACGCGGATCTGTGTACGACACACATGAGCTACTTGGCCGA 2696
QY 2457 GCCTGATTGGATCATAGTGTGTGGCAATGGGCCATCGCAGAGATGGGTTCCTACAGGA 2516
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QY 2517 GCTTCTGACAGGAGGGGCGCTCTGTCTCTCTGATCAAGCCCAAGGACCTCTCTC 2576
Db 2757 GCTGCTGCTCGAGCGGCGCTTGG-CTGAGTCTCTGCTACCTATGCGCAGCAGAGC 2815
QY 2577 TAGAGGAAGGAGAAACAGAACTTGGGACCAAGGACCCCAAGGACCTCTCTC 2636
Db 2816 AGGAGCAGGATGACAGAGGAACGGGTACGGGGTCCAGGAGGAGGA 2875
QY 2637 AGGAGGAGGCGCGAGCTTACAGCGGAGAGTCCATCAAGTCAAGTCCCTGAGAAG- 2691
Db 2876 AGCAATGGAGAAATGGCATGTGTGACGGACAGTGTGAGGGAAGCACTGACAGACAGC 2935
QY 2692 -----GACCTTACACTTCAAGAGCCCGA- 2716
Db 2936 TCAGCAGCTCTCTCTCTATAGTGGGACATCAGCAGGCCACCAACAGACCCGAGAAC 2995
QY 2717 CAGAGTTCCTCTGATGACCTTACAGGCGAGGATGCCAGCAGGAAGGACAGCAGCTCC 2776
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Db 3116 TCTCTCTCTCAGCATCTTCTTTCTGATGTAACTGTGTCCGCTGCTTCCACT 3175
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Db 3176 ATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCAGACAGAA 3235
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Db 3236 TCCGGCTGAGGCTCTATGGAGCCCTTGGGCAATTTCAAAAGGATGCGCGCTGTGTGGCTACT 3295
QY 3017 TGGCTGGGCTCTCTAGTGGGCGCGGCTCAGGCTCTCTTCCAGAGGCTCTCTGT 3076
Db 3296 CCATGGCGGTCTCCATCGGGGGGATCTTGGCTTCCGCTGTCTGACGTGACCTTGTGC 3355
QY 3077 GGGATGTGGTCTCTCCATCAGCTTCTTTGAGCGGACACCCATTTGGTCTGCTGTAA 3136
Db 3356 ACACCATCTCGGTCACCCCATGAGCTTCTTTGAGCGGACCCCGCAGTGGGAACTGTGTA 3415

Qy	3137	ACCCCTTCTCAAGGACACAGACACAGCTTGGACGTGGACATATCCACAGACAAATCTCCGGTCCC	3139
Db	3416	ACCCCTTCTCAAGGAGCTGGACACAGTGGACTCCATGATATCCAGGAGGTATCAAGATGT	3475
Qy	3197	TGCTGATGTAGGCTTTTGGACATCCCTGGAGGTACAGCTGGTGGCAGTACCCAC	3256
Db	3476	TCATGGGCTCCCTGTTCAACGTCATTTGGTGCCTGCTGATCTCTGCTGGCCACGCCA	3535
Qy	3257	TGGCCACTGTGGCCATCTCCGCCACTGTTTCTCTACGCTGGGTTTCAGAGCCCTGTATG	3316
Db	3536	TGCGCGCCATCATCATCCCGCCCTTGGCCTCATCTACTTCTTCCAGAGGTTCTACG	3595
Qy	3317	TGGTTAGCTCATGCCAGCTGAGACGGTTGGAGTGCAGCAGTACTCTGTCTGTCTGCC	3376
Db	3596	TGGCTTCTCCCGGCAGCTGAAGCGCCTCGATGCGTTCAGCGCTCCCGGTCTATTCCC	3655
Qy	3377	ACATGGCTGAGAGTTTCCAGGGCAGCACAGTGGTCCGGSCATTCGGAACCCAGGCCCT	3436
Db	3656	ATTTCAACGAGACTTGTCTGGGGTTCAGGCTCATTTCTGAGCCCTTCGAGAGCAGGAGCGCT	3715
Qy	3437	TTGTGGCTCAGAAACAATGCTCGCGTAGATGAAGCCACAGAGTACAGTTTCCCGCGACTGG	3496
Db	3716	TCATCCACAGATGACTTGAAGTGGAGGACCAAGAGCCCTATTACCCAGATCG	3775
Qy	3497	TGGCTGACAGGTGGCTTTCGGGCCAATGTGGAGTCTCTGGGGAATGGCTGGTGTTCAG	3556
Db	3776	TGGCCAAAGTGGCTGGCCGTGCGCTGGAGTGTGGGCAACTGCATCGTTCTGTTTG	3835
Qy	3557	CCGCCAGCTGTGCTGTGACGAAAGCCCACTCAGTGTCTGGCTCGTGGGCTTCTCTG	3616
Db	3836	CTGCCCTGTTTGGCGGTGATCTCCAGGCACAGCCTCAGTGTGGCTTGGTGGGCTCTCAG	3895
Qy	3617	TCCTGTCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTTCGAACCTGGACAGACC	3676
Db	3896	TGCTTACTCATGTGAGGTCACCACTACTTGAACCTGCTGGTTCGATGTCTATCTGAAA	3955
Qy	3677	TAGAACACAGCATCTGTTCAGTGGAGCGGATGCAGGACTATGCTTGACGCCCAAGSAGG	3736
Db	3956	TGAAACCAACATCTGTGGCGTGGAGAGGCTCAAGAGGATATTCAGAGACTGAGAAGSAGG	4015
Qy	3737	CTCCCTGGAGGCTGCCACATGTGCAGCTCAGCCCTCGCCTCAGGGCGGCGAGATCG	3796
Db	4016	CGCCCTGGCAATCCAGSAGACACCTCCGCCACAGCTGCGCCACAGGTGGGCGGAGTGG	4075
Qy	3797	AGTTCGGGACTTTTGGGCTTAAGATCCGACCTTGAGCTCCCGCTGGCTGTGCAGGGGCTGT	3856
Db	4076	AATTCCGGAACACTGCTCTGCCTACCCAGAGGACCTGGACTTCGTTCTCAGGCACATCA	4135
Qy	3857	CCTTCAAGATCCACGACGAGAGAAAGTTGGGATCTGTTGGCAGGACCGGGCAGGGAAGT	3916
Db	4136	ATGTACGATCAATATGGGGAGAAAAGTTCCGATCTGTGGGCGCAGCGGAGCTGGGAAGT	4195
Qy	3917	CTTCCTTGCCAGCTGGGCTGTCTGGGCTCCAGGAGGACGCTGAGGTTGGATCTGGATCG	3976
Db	4196	CGTCCCTGACCTGGGCTTATTTCGGATCAACAGTCTGCCGAAGSAGAGATCATCATCG	4255
Qy	3977	ACGGGCTCCCACTTGCCACGTGGGGCTGCACACACTCGCTCCAGATCAGCATCATCC	4036
Db	4256	ATGGCATCAACATCCCAAGATCGGCTTGCAGCACCCTCCGCTTCAAGATCACCATATCC	4315
Qy	4037	CCAGGACCCCATCTCTGTTCCCTGTGCTCTCTCGGATGAACCTCGACCTCTCTCGAGGAC	4096
Db	4316	CCGAGGACCTGTTTGTGTTTTCGGGTTCCCTCCGAATGAACCTTGGACCCATTCAGCCAGT	4375
Qy	4097	ACTCGACAGGCTATCTGGGACGCCCTTGAGAGCGGTGCAGCTCAAGCCTTGGTGGCCA	4156
Db	4376	ACTCGGATGAAGAAGCTGTGAGCTGCCCTGGAGCTGGGCCACCTCAAGACTTCTGTCTCAG	4435
Qy	4157	GCTTCCCGGCGAGCTGCAGTACAGTCTGTCTGACCGGAGGAGGACCTCAGCGTGGGCC	4216
Db	4436	CCCTTCTGACAAAGCTAGACCATGAATGTGCAGAAGCGGGAGAACCTCAGTGTCTGGGC	4495
Qy	4217	AGAAACAGCTCTCTGTCTTGGCAGCTGCCCTTCTCCGGAAGACCCAGATCCTCATCTCTGG	4276

Db	4496	AGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAGACGAAGATCCTTGTGTGG	4555
Qy	4277	ACGAGGCTACTGCTCCGCTGGACCCCTGGCAGAGCTGCAGATGCAGGCCATGCTCGGGA	4336
Db	4556	ATGAGGCCACGCAGCCGTGGACCTGGAAACGAGACCTCATCCAGTCACCACTCCGA	4615
Qy	4337	GCTGCTTTGCACAGTGCACTGTGCTGCCATTGTGCCACCGCTGCCTCGTGATGGACT	4396
Db	4616	CACAGTTCGAGGACTGCACCGTCTCCACCATGCCCAACGGCTACACCATCATGGACT	4675
Qy	4397	GTGCCCGGGTTCGTGTCATGGACAGGGCGAGTGGCAGAGCGAGCGCCGCCAGC	4456
Db	4676	ACACAAGGGTGTGCTCTTGGACAAGGAGAAATCAGGAGTACGGCGCCCCATCGGACC	4735
Qy	4457	TGCTGGCCACAGAGGGCCCTGTTTTACAGACTGCCCCAGGAGTACAGCCCTGGT	4508
Db	4736	TCCTGCACGACAGAGGTCTTTTCTACAGCATGCCAAAGACGCCGGCTGGT	4787

RESULT 11
 US-08-461-384B-1
 : Sequence 1, Application US/08461384B
 : Patent No. 6025473
 : GENERAL INFORMATION:
 : APPLICANT: Cole, Susan P.C.
 : APPLICANT: Deesly, Roger G.
 : TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
 : STREET: Queen's University at Kingston
 : CITY: Kingston
 : STATE: Ontario
 : COUNTRY: CANADA
 : ZIP: K7L 3N6
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: ASCII text
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/461,384B
 : FILING DATE: 05-JUN-95
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/966,923
 : FILING DATE: 27-OCT-1992
 : APPLICATION NUMBER: 08/029,340
 : FILING DATE: 8-MAR-1993
 : APPLICATION NUMBER: 08/141,893
 : FILING DATE: 26-OCT-1993
 : APPLICATION NUMBER: 08/407,207
 : FILING DATE: 20-MAR-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Steeg, Carol Miernicki
 : REGISTRATION NUMBER: 39,539
 : REFERENCE/DOCKET NUMBER: Q1547
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (613) 545-2342
 : TELEFAX: (613) 545-6853
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5011 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: CDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 196..4788
 : US-08-461-384B-1

Query Match	Score 1222.8	DB 3	Length 5011
27.18			

Best Local Similarity 55.7%; Pred. No. 5.5e-280;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;

[illegible]

QY 2157 ACCCTGGCTGGAGAGAGTACTAAGAACCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC 2216
DB 2397 ACCATATTACAGGTCGGTGATACAGCCCTGTGCCCTTCCCAGACCTGAAATCTCGCC 2456
QY 2217 TGAGGGAATCCACACTTCAATTTGGGAGCAGGCGCATGAATCTCTCCGGAGGCCAGAAGA 2276
DB 2457 CAGTGGGATCGACAGAGATTGGCGAGAAGGCGTGAACCTGTCTGGGGGACAGAGCA 2516
QY 2277 GCGGCTAGCCTGGCCCGGCTGTATACAGAAAGGACGTGTACTCTGCTGTGATGACCC 2336
DB 2517 GCGGCTAGCCTGGCCCGGCGGTGTACTTCCAAACGTGACATTTACCTCTCGATGATCC 2576
QY 2337 CCTGCGGCCCTGGATGCCACGTTGGCCAGCATGCTTCAACCAGGTCTATGGGCTGG 2396
DB 2577 CTTCTAGCAGTGGATGGCCATGTGGAAACACATCTTTGAAATGTGATTTGGCCCCAA 2636
QY 2397 TGGGCTACTCCAGGGAACAACAGGATTTCTCGTAGCCACGCACTCCACATCTCTGCCCA 2456
DB 2637 GGGGATGCTGAAGAACAAGACGCGGATCTTGTACGCCACAGCATGAGCTACTTGC CGCA 2696
QY 2457 GCGTATTTGGATAGTGTCTGGCAATGGGGCCATPCGCAGAGATGGGTCTTACCAGGA 2516
DB 2697 GGTGAAGCTCATCATCGTCTATGAGTGGCGGCAAGATCTCTGAGATGGGCTCTTACCAGGA 2756
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QY 2897 ACTGGCTAGCCTGTGGGCGGACGACCTTGCAGTAGGTGGGCGAGCAGCGAGCGAGCC 2956
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DB 3296 CCATGCGGCTGTCATCGGGGGATCTTGGCTTCCGCTGTCTGACGTGGACCTGCTGC 3355
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QY 3137 ACCGTTCTCCAAAGGACAGACAGGTTGACGTGGACATTCAGACAAACTCCGCTCC 3196
DB 3416 ACCGTTCTCCAAAGGAGTGGACAGACTGCACTTCCATGATCCCGGAGGTGATCAAGATGT 3475

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QY 3257 TGCGCACTGTGGCCACTCTCCCTACCTGTTCCTCTACGCTGGTGTTCAGAGCCTGTATG 3316
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QY 3317 TGGTTAGCTCATCCAGCTGAGACGCTTGGAGTCAGCCAGTACTCTGTCTGTCTGCTCC 3376
DB 3596 TGGCTTCCCTCCCGCAGCTGAAGCGCTCGAGTGGTTCAGCGCTGCCCGCTTATTC 3655
QY 3377 ACATGCTGAGAGCTTCCAGGCGAGCAGTGTTCGGGATTCGGAACCCAGGCCCT 3436
DB 3656 ATTTCAACGAGACTTGTGGGGTTCAGCGTCTTCAGGCTTTCAGGAGCAGAGGCGCT 3715
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RESULT 13

US-08-463-092B-5
Sequence 5, Application US/08463092B
Patent No. 5768880
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 6 4589
US-08-463-092B-5

Query Match

26.4%; Score 1189.8; DB 1; Length 5889;

Best Local Similarity 55.4%; Pred. No. 3.8e-272;
Matches 2516; Conservative 0; Mismatches 1952; Indels 75; Gaps 8;

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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1429 TTCTCATGCTACCTTAATGCTGTGATGGCCATGAAGACCAAGACTTACCAGGTGGCAC 1488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1439 AAATGAGCAGAAAGACTCACGGGCACGCTCACAGCTCTATCTCTCAGGAACCTCAAGA 1498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1489 ACATGAAGAGCAAGAACACCGAATCAAGCTGATGAACGAGATCTCAATGGGATCAAG 1548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1499 CCATCAAGTTCATGCTGGGAGGAGCCCTTCTTGACAGAGTCTCTGGGATCCGAGGCC 1558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1549 TCTCAAGCTGTACGCTGGGAGCTGGCCTTCCAGGACAAAGTATGAGCATCAGGACAG 1608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1559 AGGAGCTGGGCGCTTGGCGACTCCGCGCTCTCTTCTGTGTGCTGGTGTCTCTTCC 1618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1609 AGGAGCTCAAGTGTGTAAGAAATCTGCCTACCTGCGCAGCTGTAGGCACATTCACGTGG 1668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1619 AAGTGTACATTTCTGGTGCAGCTGGTGTGCTGTCTGCTGTC---CACACTCTGGTGCGCG 1675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1669 TGTGCACACCTTCTGCTGGGCGCTGTCAACCTTGTCTGTTGTGACTGTGGATGAGA 1728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1676 AGAATGCTATGAATGCAGAAAGCCTTGTGACTCTCAAGTCTCAACATCTCAACAT 1735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1729 GAAATATCTAGATGCAAAAGACCTTGTGTCCCTAGCCCTGTTCAATATCTGCGCT 1788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1736 AGGCGCCAGGCTTCTGCGCTTCTCCATCCACTCTCCAGGCCCGGGTGTCTTTG 1795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1789 TCCCACTCAACATCTCGCCATGGTTATCAGCAGCATTTGTGACAGGCGCGCTGTCCCTCA 1848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1796 ACCGTCTGTCACTTCTCTGCTGGAAGAAGTTGACCTGTGTGCTGTAGACTCAAGTT 1855
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Db 1849 AGCGTCTCAGGATTTTCTGCTCATGAGGAGCTGGAGCCAGACATTTAGCGGAGGT 1908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1856 CCTCTGGAAGCGCTCGCGGAAGATTGATCACCATACACAGTGCACCTTCGCGCTGGT 1915
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Qy 1976 TGGCTGTGTGCTGCTGAGTGGGGGAGGAAAGTCTTCCCTGTGTCCGCCCTCTCTTGGGG 2035
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Db 2026 TGGCGTGTGTGGGCGCAGGTAGGTGCGGGAAGTCACTCTGTGTGTCAGCCCTGCTGGCTG 2085
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Qy 2036 AGCTGTCAAAAGTGGAGGGGTTCTGTGAGCATCGAGGTGCTGTGGCTACGTGCCCCAGG 2095
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Db 2086 AGATGGAAGGTGGAGGAGCATGTGACTCTCAAGGGCTCGGTGGCTACGTGCCCCAGC 2145
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Db 2146 AGGCTGTGATTCAGATGACTCTCTCCGAGAGAACATACTGTTTGGGACACCCCTTCAGG 2205
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QY	2156	CACCCCTGGCTGGAGAGTACTAGAAAGCCTGTGCCCTGCAGCCAGATGTGACAGCTTCC	2211
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QY	2216	CTGAGGGAATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCCGGAGGCCAAGC	2275
DB	2266	CCAGTGGGACCCACACAGAGATCGGTGAGAAGGGTGAACCTGTCAAGGGGCCAGAGC	2325
QY	2276	ACGGCTGAGCTGGCCCGGGCTGTATACAGAAGACGCTGTGTACCTGTCTGGATGACC	2335
DB	2326	ACGGTGTGAGCTGGCCCGGGCTGTGTATCTCTAACTCTGACATCTACCTCTTTGTATGACC	2385
QY	2336	CCCTGGGSCCCTGGATGCCACGTTGGCCAGCATGTCTTACACAGGTCTATTTGGSCCTG	2395
DB	2386	CCCTCTGGCTGTGATGCACATGTTTGGGAAGCACATCTTGAAGAAGTGTGTGGTCCCA	2445
QY	2396	GTGGGCTACTCCAGGGAACAACACGGATTTCTGTCAGCCAGCAGCTCCACATCCTGCCCC	2455
DB	2446	TGGGCTCTACTGAAGAACAAGACACGGATCCTGGTCACCATGGTATCAGTCACTGCCCC	2505
QY	2456	AGGCTGATTTGATCATAGTGTGGCAATTTGGGCCATCGCAGAGATGGGTTCCTACCAAG	2515
DB	2506	AAATGGATGTCAATCTGTATGATGAGTGGCGCAAGATCTCAGAGATGGGTCTTATCAGG	2565
QY	2516	AGCTTCTGACAGGAAGGGGGCCCTGCTGTCTCTG-----GATC	2557
DB	2566	AGCTGCTAGACCGGATGGGCTTCTGCTGAGTTCCTGCGACCTATGCCAAGCTGAGC	2625
QY	2558	AAAGCAGACAGCCAGAGATAGAGAGAGGAAGAAACAGAACTGGGACCGACCAAGG	2617
DB	2626	AGGACCTGGCTCGAGGATGACAGTGTCTAGTGTTCAGGGAAGAGTCAAGACCGGTG	2685
QY	2618	ACCCAGAGGCACCTCTCGACGAGGAGGCCCGAGCTTAGACGCGAGAGTCCATCAAGT	2677
DB	2686	AAATGGGATGCTGTGACACAGACCGTAGGAAAGCACCTGCAGAGGCACTCAGCAACT	2745
QY	2678	CAGTCCCTGAGAAGACCGTACCACCTTCAGAAGCCAGACAGAGTTCTCTGTGGATGACC	2737
DB	2746	CGTCTTCCACAGTGGGGATACGCCAGCAACACAGCAGCATAGCCGAACCTGCAGAAG	2805
QY	2738	CT-----GACAGGGCAGGATGGCCAGCAGGAAGACAGCATCCAAATACGGCAGGG	2788
DB	2806	CTGGAGCTAAGGAGGAGAGCTGGAGCTTAATGGAAGCAGACAGCCCAAGACGGCAGG	2865
QY	2789	TGAAGGCACAGTGCACCTGGCCTACCTGCGTGGCGTGGGCACCCCTCTCGCTCAGC	2848
DB	2866	TGCAGCTGTCACTGTGGAACATACATGAAGGCCATTGGCCTCTTCATCACTTCTTGA	2925
QY	2849	CACCTTCTCTTCTCTGCCAGCAAGTGGCTCTCTTTCGCGGGGCTACTGGCTGAGCC	2908
DB	2926	GTATCTCTCTTTCTGTGCAACCATGATCTGCACCTGGCCTCTAACTATTGGCTGAGCC	2985
QY	2909	TGTGGCGGAGCACCTCCAGTAGG---TGGSACAGACAGCAGCAGCCCTGCGGTGGCG	2965
DB	2986	TCTGACAGATGACCCCTCTGTTCAATGGAGCTACGCGAACAGGAATTTTCGGCTGA	3045
QY	2966	GGATCTTCGGCTCTCGGCTGTCTCCAGGCATTGGGTGCTTGGCTCCATGGCTGCGG	3025
DB	3046	GTGCTATGGGCTTTGGGCATCTTGAAGGTGCAACAATTTTGGCTACTCCATGGCTG	3105
QY	3026	TGCTCTAGTGGGCGCGGATCCAGGTGTCTCTTCCAGAGGCTCTGTGGGATGTGG	3085
DB	3106	TGTCATCTGGGGCATCTTTGCTCCCTCGCTTGCATCTGACCTGTGATATAAATGTTTC	3165
QY	3086	TGCGATCTCCCATCAGCTTCTTTCAGCGGACACCCATTTGGTCACCTGCTAAACCGCTCT	3145
DB	3166	TTCGATCACCATGATTTCTTCGAGCGGTACACCCAGTGGGAACCTAGTGAACCGATTCT	3225
QY	3146	CAAGGACACAGACACGCTTACGTGGACATTTCCAGACAAACTCCGGTCCCTGCTGATGT	3205
DB	3226	CAAGGACCTGGACACATGCACTCCATGATATCCCGCAGGTCAATCAAGATGTTCAATGGGTT	3285

QY	3206	ACGCCCTTTGGACATCCTTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCACTGGCCACTG	3265
Db	3286	CACCTTTTCAGTGTTCATTGGAGCTGTGCATCATCATCTACTTGGCCAGCCCATTTGCCGCAG	3345
QY	3266	TGGCCATCTGCCACATGTTTCTCCTACGCTGGGTTCAGAGCCCTGATGTGGTTAGCT	3325
Db	3346	TCATCATCCCACTTTGGGTCGTGGTTTACTTCTTTGTCAGAGGTTCTATGTGGCTTTCCT	3405
QY	3326	CATGCCAGCTGAGACGCTTTGGAGTCAAGCCAGCTACTCGTCTGTCTGCCATCCACATGGCTG	3385
Db	3406	CAAGACAACGTGAAGCCGCTGGAGTCTGTTCAGCCGTTCCCTCTGTACTCACACTTCAATG	3465
QY	3386	AGACGTTTCAGGGCAGCAGTGTCTCCGGCATTCGAAACCCAGGCCCTTTGTGGCTC	3445
Db	3466	AGACCTGTGGGGAGTCAGTGTCTATCCCTGCTTTTGAGGAGCAGAGCGCTTCATTCAAC	3525
QY	3446	AGAAACAATGCTCGCTAGATGAAAGCCAGAGGATCAGTTTCCGCGACCTGGTGGCTGACA	3505
Db	3526	AGAGTGACCTGAAAGTAGATGAGAACCAAGAGCCCTACTACCCACGATTTGTGGCCAAACA	3585
QY	3506	GCTGGCTTTCGGCCCAATGTGGAGCTCCTGGGAATGGCCCTGTGTTTGCAGCCGCCACGT	3565
Db	3586	GATGGCTTCTGCTGSCCTTGAGTGTGTGGCAACTGCATTGTGCTGTTTGTGCTCCCTCT	3645
QY	3566	GTGCTGTGCTGAGCAAGCCACCTCAGTGTCTGGCCCTCGTGGGCTTCCTGTGCTCTGTGCTG	3625
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QY	3626	CCCTCCAGTGCACCCAGACACATGCAGTGGGTTCCTCGCAACTGGACAGACCTAGAGACA	3685
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QY	3686	GCATCGTGTCACTGGAGCGGATGCGAGCTATCGCTTGGACGCCCAAGAGGCTCCCTCGGA	3745
Db	3766	ACATTTGTGCGCATGGAGAGACTAAGGAGTATCTGAAACAGAGAGGAGCTCCTTGGC	3825
QY	3746	GGCTGCCACATGTGCAGCTAGCCCCCTCGGCTCAGGGCGGGAGATCGAGTTCGGG	3805
Db	3826	AAATCCAGGAACAGCTCCACCAGCAGCCTGGCCCATTCAGGCCGTGTAGATTTCCGG	3885
QY	3806	ACTTTTGGGCTAAGATGCCACCTGAGCTCCCGCTGCTGTGAGGGCGTGTCTCTCAAGA	3865
Db	3886	ATTACTGCTGAGGTATCGAAGACATTGGACTTGGTCTCTAAGCAACATAAATGTCAACA	3945
QY	3866	TCCACGAGGAGAGAGTGGGCATCTGTTGGCAGGACCCGGGCGAGGAACTCCTCCCTGG	3925
Db	3946	TTGAGGGTGGAGAAAGGTGGGTATTGTAGTCTGTACGGGAGCTGGGAAATCATCTCTCA	4005
QY	3926	CCAGTGGGCTGTCTGGCTTCCAGGAGGACGTGTAGGGTGGGATCTGGATCGACGGGGTCC	3985
Db	4006	CCCTGGGTTTGTTCGGGATCAATGATCTGCAGAGGGGAGATCATCATTTGATGGGGTCA	4065
QY	3986	CCATTGCCACGTGGGGTGCACACATCGCGTCCAGGATCAGCATATCCCCCAGGACC	4045
Db	4066	ACATGCCAAGATCGGCTGCAACACCTTCGCGCTTCAAGATCACCATCATTTCCACAGGATC	4125
QY	4046	CCATCTGTCTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGCACTCGGACG	4105
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QY	4106	AGGCTATCTGGCGACCTTGGAGCGGTGCAGCTCAAAAGCCTTGGTGGCCAGCTGCCCG	4165
Db	4186	AAGAGTCTGGATGTCCTGGAGCTTGTCTACCTAAAGGGCTTTGTGTGTCAGCCTTGGCTG	4245
QY	4166	GCCAGCTCAGTACAAGTGTCTGACCCGAGGGCAGGACCTGAGCTGGGCGCAGAAACAC	4225
Db	4246	ACAAGCTGAACCATAGTGTGCGAAGGTGGAGAAACCTGAGTGTGGGGCAGCGACACG	4305
QY	4226	TCCCTGTCTGSCAGCTGCCCTTCTCCGGAACACCCAGATCCTCATCTCTGGACGAGGCTA	4285
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Db 4366 CCGCAGCTGTGACCTAGACAGATAACCTTATCCAGTCCACCATCCGGACCGAGTTG 4425
QY 4346 CACAGTGCACTGTGCTGCCATGCCCCACCGCTGCGCTCGGTGATGGACTGTGCCCGG 4405
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QY 4466 AGAAGGGCCTGTTTACAGACTGGCCAGGAGTCAAGGCTGCTGGT 4508
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RESULT 14

US-08-462-109A-5

; Sequence 5, Application US/08462109A

; Patent No. 582875

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Delevy, Roger G.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING

; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,109A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/966,923

; FILING DATE: 27-OCT-1992

; APPLICATION NUMBER: 08/029,340

; FILING DATE: 8-MAR-1993

; APPLICATION NUMBER: 08/141,893

; FILING DATE: 26-OCT-1993

; APPLICATION NUMBER: 08/407,207

; FILING DATE: 20-MAR-1995

; ATTORNEY/AGENT INFORMATION:

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; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5889 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 6 4589

US-08-462-109A-5

Query Match

Best Local Similarity 26.4%; Score 1189.6; DB 2; Length 5889;

Matches 2516; Conservative 0; Mismatches 1952; Indels 75; Gaps 8;

QY 38 TCTGGAAACACAGACAGACGCTGAACCTGCCGCCACACGCTGCTGAGCGTGTGCTTCTGTA 97
Db 49 TCTGGGACCTGAATGTACATATGGCAGACACACACCGGAGCTTTACCAAGTGTCTTTCAGA 108
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Db 109 ACAGGTCTTCACATGGGTGCTTGTTCACCTCTGCTGCTGCTTCCCTCTTCTTCT 168
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QY 218 TGGTGTCTGATTCGCGCTCATAGTCTGTGTACTCCAGGTGGCTGTCTCTTCTTGA 277
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QY 278 AAATCCAAACAGGAACGCTGAGGCCCGCAGAAATTCCTCATTCATCTACTGTGGCTCA 337
Db 289 AAAGAGTCAGGAGAGTCTCGGAGCCCGGTGTACTGGTCAGCCCAACACTGCTGGGCA 348
QY 338 CCAGATGAGCTTCGCAAGTGTTCCTGATTCACACCGAGAGGAGGAGGAGTCCAGTCAT 397
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Db 529 TCTATCTGTACTTACCTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
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DB 1669 TGTGCACACCTTTCTCTGGTGGCCCTGTCAACCTTTGCTGTCTGTGACCTGTGATGAGA 1728
QY 1676 AGAATGCTATGAATCAGAGAAAGCCCTTGTGACTCTCAAGTCTCAACATCTCTCAACA 1735
DB 1729 GAAATATCTAGATGCAAGAAAGCCCTTGTGTCCCTAGCCCTGTCAATATCTTGGCT 1788
QY 1736 AGGCCAGGCTTCTCTGCTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1795
DB 1789 TCCCACTCAACATCTCTGCT 1848
QY 1796 ACGCTCTGCT 1855
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DB 1909 CGATCAAGAGTGGAGAAGGA ---ATPAGATCACTGTGAAGATGCAACCTTCACTTGGG 1965
QY 1916 CCAGGAAAGCCCT 1975
DB 1966 CCAGGGTGAACCTCCACATGAATGGCATCACCTTCTCTCTCTCTCTCTCTCTCTCTCT 2025
QY 1976 TGGCTGTCT 2035
DB 2026 TGGCGTGTGGCCAGGTAGGCTGCGGGAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2085
QY 2036 AGCTGTCAAAGTGGAGGGTGTGTGATCATCAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 2095
DB 2086 AGATGACAAGTGGAGGACATGTGACTCTCAAGGGCTCCGTGGCTACGTGCCCCAGC 2145
QY 2096 AGGCTGGTGGCAGACACCTCTGTGTGATGAGAAATGTCTCTCTCTCTCTCTCTCTCTCTCT 2155
DB 2146 AGGCTGGATTCAGATGACTCTCTCCGAGAGAAACATACTGTCTGGGCAACCCCTCTCAG 2205
QY 2156 CACCCTGGGAGAGAGTACTAGAAGCCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2215

DB 2206 AAAATTAATAAGCAGCTATGGAAGCCTGTGCCCTTCTCCAGATTTGGAAATCCTGC 2265
QY 2216 CTGAGGGAATCCACTTCAATTTGGGAGCAGGAGGATGAATCTCTCCGAGGCCAGAAGC 2275
DB 2266 CCAGTGGGACCGCACAGAGATCGGTGAGAAGGTGTGAACCTGTTCAGGGGCCAGAAGC 2325
QY 2276 AGCGCTGAGCTGCCCGGGCTGTATACAGAAAGGAGCTGTGTACCTGTCTGGATGACC 2335
DB 2326 AGCGTGTGAGCTGGCCGGGCTGTACTCTAACTCTGACATCTACCTCTTTGATGACC 2385
QY 2336 CCTCGGCGCTGTGATGCCACGTTGGCCAGCATGTCTTCAACAGGTCATTTGGCCCTG 2395
DB 2386 CCTCTCGCTGTGATGCACATGTTGGAGACATCTTTGAGAAGTGGTGGTCCCA 2445
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DB 2446 TGGCCTACTGAAGAAACAGACACGATCTTGGTCAACCATGATACAGTACCTGCCCC 2505
QY 2456 AGGCTGATGATCATGTGCTGGCAATTTGGGCCATCGCAGAGATGGTTCCTACCAAG 2515
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DB 2566 AGCTGTAGCCGGATGGGCCCTTCTGTGATTTCTCTGCGCACCTATGCCAACGCTGAGC 2625
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DB 2626 AGGACCTGGCCTCGAGGATGACAGTGTCTGTTTCTAGGAGAGGATCAAGCCGGTGG 2685
QY 2618 ACCCCAGAGGACCTCTGTCAGGAGGAGGCCCTGTAGCGCGAGAGTCCATCAAGT 2677
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QY 2678 CAGTCCCTGAGAAGGACCGTACCACTTCCAGAGGCCACAGAGAGTTCCTCTGGATGACC 2737
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DB 2806 CTGAGCTAAGGAGGAGACGTTGGAAGCTAATGGAAGCAGACAGGCCACAGAGGCGAG 2865
QY 2789 TGAAGGCCACAGTGCACCTGCGCTTACCTGCGTGGCGGACACCCCTCTGCTCTCTACG 2848
DB 2866 TGCAGCTGTCACTGTGTAACATACATGAAGGCCATTTGGCTCTTCTATCACCCTCTTGA 2925
QY 2849 CACTCTTCTCTCTCTGTCAGCAAGTGGCTCTCTCTGCGGGGCTACTGGCTGAGCC 2908
DB 2926 GTATCTTCTCTCTGTCNAACCTGTATCTGCACTGGCCCTCTAACTATTGGCTGAGCC 2985
QY 2909 TGTGGCGGAGCAGCCCTGCAGTAGG ---TGGGCGACAGCAGCAGCAGCCCTGCTGGCG 2965
DB 2986 TCTGCAGAGATGACCCCTTGTCTCAATGGACTCAGGCCGACAGAGAAATTTTCGGCTGA 3045
QY 2966 GGATCTTCGGCTCTCTGCTGCTCTCAAGCCATTTGGCTGTTCCTCTCAAGTGGCTGGG 3025
DB 3046 GTGTCTATGGGCTCTGGGCACTCTTGAAGGTGCAAGCAATATTGGCTACTCTCCATGGCTG 3105
QY 3026 TGTCTCTAGTGGGCGCCGCGCATCTGCTTCTCCAGAGGCTCTCTGTTGGGATGTTG 3085
DB 3106 TGTCCATCGGGGATCTTTGGCTCTCCGCTGCTGTCACCTGGACCTGCTATACAAATGTTCT 3165
QY 3086 TGGCATCTCCATCAGCTTCTTTGAGCGGACACCATTTGGTCACTGCTAAACCGCTCTCT 3145
DB 3166 TTCGATCAACCATGAGTTTCTTCGAGGCTACACCCAGTGGGAACTTAGTGAACCGATCTCT 3225
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DB 3226 CCAAGGAGCTGGACAGAGTGGACTCCATGATCCCGCAGGTCATCAAGATGTTTATGGTT 3285
QY 3206 ACGCCTTGTGACTCTCTGGAGGTGAGCTGTTGGTGGCAGTGGCTACCCCACTGCCACTG 3265

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Qy 3386 AGACGTTCCAGGCGAGCAGAGTGTGCGGGCATTCGAAACCCAGCCGCCCTTTGGGCTC 3445
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Db 3826 AATCCAGGAAACAGCTCCACCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3885
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Qy 3866 TCCACGAGAGAGAAAGTGGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3925
Db 3946 TTGAGGTGAGAAAGTGGGTATTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4005
Qy 3926 CCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3985
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Qy 4286 CTGCT 4345
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RESULT 15

US-08-460-907B-5
; Sequence 5, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6 4589

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Job time : 146.919 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:00:25 ; Search time 563.826 Seconds
(without alignments)
18009.573 Million cell updates/sec

Title: US-09-647-140A-7

Perfect score: 4509

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11	4487.4	99.5	4511	22	AAZ30081	Human ATP-binding
12	3030	67.2	4980	24	AAZ30081	Rat sequence diffe
13	3007.2	66.7	4980	22	AAZ30081	Mouse ATP-binding
14	1229.2	27.3	5011	21	AAZ30081	Human ATP-binding
15	1229.2	27.3	5011	21	AAZ30081	Prostate cancer-as
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26	1222.8	27.1	5011	21	AAZ30081	Human MRP variant
27	1222.8	27.1	5011	21	AAZ30081	Human MRP variant
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34	1106	24.5	4885	17	AAZ30081	Human MRP variant
35	1076.8	23.9	1612	18	AAZ30081	Human MRP variant
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38	1052.8	23.3	5193	24	AAZ30081	Human MRP variant
39	1045	23.2	4864	17	AAZ30081	Human MRP variant
40	1039	23.0	4762	18	AAZ30081	Human MRP variant
41	977.2	21.7	4423	17	AAZ30081	Human MRP variant
42	967.6	21.5	4834	17	AAZ30081	Human MRP variant
43	760.8	16.9	4669	17	AAZ30081	Human MRP variant
44	721	16.0	4864	21	AAZ30081	Human MRP variant
45	713	15.8	5300	24	AAZ30081	Human MRP variant

ALIGNMENTS

RESULT 1
ID AAZ30081 standard; cDNA: 4509 BP.
AC AAZ30081;
XX AAZ30081 (first entry)
DT 26-JAN-2000
DE cDNA encoding a human MRP-related ABC transporter designated MOAT-E.
XX Human; MRP-related ABC transporter; MOAT protein; MOAT-E;
KW MOAT mediated transport; anticancer drug sensitivity;
KW transporter mediated cellular efflux; anticancer; ss.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..4509
FT /*tag= a
FT /*product= "MOAT-E"
FT /transl_except= (pos: 3645..3647, aa: Ala)
FT /transl_except= (pos: 3820..3822, aa: Tyr)
FT /transl_except= (pos: 3859..3861, aa: Leu)
FT /transl_except= (pos: 4363..4365, aa: Leu)
FT /note= "MPR-related ABC transporter; no stop codon given"
XX WO9949735-A1.
XX 07-OCT-1999.
XX 26-MAR-1999; 99WO-US06644.

XX 27-MAR-1998; 98US-0079759.
PR 03-AUG-1998; 98US-0095153.
XX (FOXC-) FOX CHASE CANCER CENT.
XX Kruh G, Lee K, Belinsky M, Bain L;
XX WPI, 1999-610812/52.
DR P-PSDB; AAY43544.
XX New transporter gene useful for screening for anti-cancer drugs -
PS Claim 34; Page 143-144; 153pp; English.
XX The present sequence encodes a human MPR-related ABC transporter (MOAT)
CC protein, designated MOAT-E. The protein comprises a multi-domain
CC structure including a tandem repeat of nucleotide binding folds
CC appended C-terminal to a hydrophobic domain, having Walker A and B ATP
CC binding sites and several potential membrane spanning domains. The MOAT
CC nucleic acids are useful for screening a test compound for inhibition of
CC MOAT mediated transport, indicated by restoration of anticancer drug
CC sensitivity, which in turn causes a reduction of transporter mediated
CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
CC probes to detect the presence or expression of genes encoding MOAT
CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
CC MOAT proteins.
XX
SQ Sequence 4509 BP; 833 A; 1385 C; 1353 G; 938 T; 0 other;
Query Match 100.0%; Score 4509; DB 20; Length 4509;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGCGCGCGCTGTGACCCCTGCGCGGGCAGGGGTCTGGAACACAGACAGAGCTGAA 60
Qy 61 CTTGCGCGCACAGCCTGCTGAGCCTGTGCTTCTTCCAGACAGAGGGGTCTGGGTACCC 120
Db 61 CTTGCGCGCACAGCCTGCTGAGCCTGTGCTTCTTCCAGACAGAGGGGTCTGGGTACCC 120
Qy 121 CCCATGTACCTCTGGTCTTGGTCCCATCTACCTCCCTTTCATCCACACCATGGCGGG 180
Db 121 CCCATGTACCTCTGGTCTTGGTCCCATCTACCTCCCTTTCATCCACACCATGGCGGG 180
Qy 181 GGCTACCTCCGGATGCCCACTCTTAAAGCAAGATGGCTGGATTCGCCCTCATATA 240
Db 181 GGCTACCTCCGGATGCCCACTCTTAAAGCAAGATGGCTGGATTCGCCCTCATATA 240
Qy 241 GTCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTTGGAAATCCACAGGACGCTGAG 300
Db 241 GTCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTTGGAAATCCACAGGACGCTGAG 300
Qy 301 GCCCAGAAATTCCTCATTCATCTACTGTGGCTTCACACAGATGAGCTTCGCACTGTC 360
Db 301 GCCCAGAAATTCCTCATTCATCTACTGTGGCTTCACACAGATGAGCTTCGCACTGTC 360
Qy 361 CTGATTCACCGAGAGAAAGGAGTCCAGTCACTGAGTGTCTGTTGGTTACTGG 420
Db 361 CTGATTCACCGAGAGAAAGGAGTCCAGTCACTGAGTGTCTGTTGGTTACTGG 420
Qy 421 CTTCTCTGCTTTGCTTCCAGCTACCAACGCTGCCAGCAGGCTCCGGACGGGCTTC 480
Db 421 CTTCTCTGCTTTGCTTCCAGCTACCAACGCTGCCAGCAGGCTCCGGACGGGCTTC 480
Qy 481 CAGAGCGACCTGTCCGCACTGTCCACCTACCTATGCTGTCTCTGTGTGGTGCACAG 540
Db 481 CAGAGCGACCTGTCCGCACTGTCCACCTACCTATGCTGTCTCTGTGTGGTGCACAG 540
Qy 541 TTTGTGCTGCTGCTGCCGCGGATCAACCCCTCTTCCCTGAAGACCCCGCAGTCT 600
Db 541 TTTGTGCTGCTGCTGCCGCGGATCAACCCCTCTTCCCTGAAGACCCCGCAGTCT 600

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Qy 661 GGCTGTGTCTGGAGGGATACAGGAGCCACTGAGACCAAAAGACCTCTGGTCCCTTGGG 720
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Qy 721 AGAGAAACTCTCTCAGAAACTTGTTCCTGGGCTTGAAAGAGGAGTGGATGAGAAACCG 780
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Db 841 AAGGCTCCAGACCCGAGCCCTTCTTACGCAAGAGAGGAGCCAGTGGCCGCCACTGCTG 900
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Qy 961 AGTGATGTCTTCTCAGGTTTCACTGTCCCAAGCTGCTCAGCCTTTTCTGGAGTGTATTGGT 1020
Db 961 AGTGATGTCTTCTCAGGTTTCACTGTCCCAAGCTGCTCAGCCTTTTCTGGAGTGTATTGGT 1020
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Db 1381 AGCCTCCTCCTCTGAAATTTCTTCTATCTCCAGAAAGAACCCACCATCAGAGGAGGACAA 1440
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QY	1741	CAGGCTTTCTCCCTTCTCCATCCACTCCCTGCTCCAGSCCCGGGTGCTCTTGACCGT	1800
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QY	1801	CTGGTCACTTCTCTGCTGCGTGAAGAAGTTGACCCCTGGTGTGCTAGACTCAAGTTCCTCT	1860
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QY	1921	GAAGCCCTCCCTGCTCCACAGATAAACCTCACGGTCCGCCAGGGCTGTCTGCTGGCT	1980
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QY	1981	GTGTGCGGTCCAGTGGGGGAGGAAAGTCTCCCTGCTGTCGCCCTCCTTGGGGAGCTG	2040
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QY	2101	TGGGTGCAGAACACCTCTGTGTGACAGAAATGTCTCTCGGCGAGAGCTGGACCCACCC	2160
Db	2101	TGGGTGCAGAACACCTCTGTGTGACAGAAATGTCTCTCGGCGAGAGCTGGACCCACCC	2160
QY	2161	TGGCTGGAGAGTAGTACTAGAAGCCCTTGCCCTCGAGCCAGATGTGGACAGTTCCTCTGAG	2220
Db	2161	TGGCTGGAGAGTAGTACTAGAAGCCCTTGCCCTCGAGCCAGATGTGGACAGTTCCTCTGAG	2220
QY	2221	GGATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAACGAGCGG	2280
Db	2221	GGATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAACGAGCGG	2280
QY	2281	CTGAGCTGGCCCGGGCTGTATACAGAAGGACGCTGTGTACTCTGTGGATGACCCCTCG	2340
Db	2281	CTGAGCTGGCCCGGGCTGTATACAGAAGGACGCTGTGTACTCTGTGGATGACCCCTCG	2340
QY	2341	CGGGCTTGGATGCCACGTTTGGCCAGGATGTCTTCAACAGGTCATTTGGGCTGTGTGGG	2400
Db	2341	CGGGCTTGGATGCCACGTTTGGCCAGGATGTCTTCAACAGGTCATTTGGGCTGTGTGGG	2400
QY	2401	CTACTCAGGGAACAAACAGGATTTCTGTGAGCAGCAGCACTCCACATCTGCCCCAGGCT	2460
Db	2401	CTACTCAGGGAACAAACAGGATTTCTGTGAGCAGCAGCACTCCACATCTGCCCCAGGCT	2460
QY	2461	GATTGGATCATAGTCTCGSAAATGGGGCCATCGCAGAGATGGTTCCTACAGGAGCTT	2520
Db	2461	GATTGGATCATAGTCTCGSAAATGGGGCCATCGCAGAGATGGTTCCTACAGGAGCTT	2520
QY	2521	CTCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGATCAAGCCAGACAGCAGCAGGATAGA	2580
Db	2521	CTCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGATCAAGCCAGACAGCAGCAGGATAGA	2580
QY	2581	GGAGAGGAGAAACAGAACTTGGGACACAGCAACCAAGGCCCCAGAGGCACCTCTCGAGGC	2640
Db	2581	GGAGAGGAGAAACAGAACTTGGGACACAGCAACCAAGGCCCCAGAGGCACCTCTCGAGGC	2640
QY	2641	AGGAGGCCGAGCTTAGACGCGAGAGGTCCATCAGTCACTCCCTGAGNAGGACCGTACC	2700
Db	2641	AGGAGGCCGAGCTTAGACGCGAGAGGTCCATCAGTCACTCCCTGAGNAGGACCGTACC	2700
QY	2701	ACTTCAGAAAGCCACAGAGAGTTCTCTGTGATGACCTTGACAGGGCAGGATGGCCAGCA	2760
Db	2701	ACTTCAGAAAGCCACAGAGAGTTCTCTGTGATGACCTTGACAGGGCAGGATGGCCAGCA	2760
QY	2761	GGAAAGGACAGCATCCAATAGCGAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT	2820

Db	2761		GGAAAGGACAGCATCCAATACGCGCAGGGTGAAGGGCCACAGTGCACCTGGCCTACCTGCGT	2820
Qy	2821		GCGTGGGACACCCCTCTGCCTCTACGCACCTTCTCCTCTTCTCTCTGCCAGCAAGTGGCC	2880
Db	2821		GCGTGGGACACCCCTCTGCCTCTACGCACCTTCTCCTCTTCTCTCTGCCAGCAAGTGGCC	2880
Qy	2881		TCCTTCTGCGGGGCTACTGGCTGAGCCCTGTGGCGGACGACCCCTGCAGTAGTGGGCGAG	2940
Db	2881		TCCTTCTGCGGGGCTACTGGCTGAGCCCTGTGGCGGACGACCCCTGCAGTAGTGGGCGAG	2940
Qy	2941		CAGACGACGCGACCCCTGCGTGGCGGGATCTTTCGGGCTCCTTCGGGCTCTTCCAAGCCATT	3000
Db	2941		CAGACGACGCGACCCCTGCGTGGCGGGATCTTTCGGGCTCCTTCGGGCTCTTCCAAGCCATT	3000
Qy	3001		GGGCTCTTTGGCTTCCATGCGCTGGGCTGCTCTTTCAGTGGGGCCCGGGCATCCAGTTGCTC	3060
Db	3001		GGGCTCTTTGGCTTCCATGCGCTGGGCTGCTCTTTCAGTGGGGCCCGGGCATCCAGTTGCTC	3060
Qy	3061		TTTCAGAGGCTCTCTGTGGGATGTGTGGCGATCTCCCATCAGCTTCTTTCAGCGGACACCC	3120
Db	3061		TTTCAGAGGCTCTCTGTGGGATGTGTGGCGATCTCCCATCAGCTTCTTTCAGCGGACACCC	3120
Qy	3121		ATTGTCTACCTGCTTAACCGCTTCTCCAAGGACAGACACAGGTTGACGTGGACATTCCA	3180
Db	3121		ATTGTCTACCTGCTTAACCGCTTCTCCAAGGACAGACACAGGTTGACGTGGACATTCCA	3180
Qy	3181		GACAACTCCGGTCCCTGCTGATGTACGGCTTTTGGACTCCTGGAGTGCAGCTTGGTG	3240
Db	3181		GACAACTCCGGTCCCTGCTGATGTACGGCTTTTGGACTCCTGGAGTGCAGCTTGGTG	3240
Qy	3241		GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTGCCACTGTTCTCTCTACGCTGGG	3300
Db	3241		GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTGCCACTGTTCTCTCTACGCTGGG	3300
Qy	3301		TTTCAGAGGCTGTATGTGGTTAGTCTATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC	3360
Db	3301		TTTCAGAGGCTGTATGTGGTTAGTCTATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC	3360
Qy	3361		TCGCTGTCTGTCTCCCATGCGCTGAGACGTTTCCAGGGCAGACAGTGTCTGGGCAATTC	3420
Db	3361		TCGCTGTCTGTCTCCCATGCGCTGAGACGTTTCCAGGGCAGACAGTGTCTGGGCAATTC	3420
Qy	3421		CGAACCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCTAGATGAAAGCCAGAGGATC	3480
Db	3421		CGAACCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCTAGATGAAAGCCAGAGGATC	3480
Qy	3481		AGTTTCCCGCGACTGGTGGCTGACAGTGGCTTTCGGGCCAATGTGGAGTCTCTGGGGAAT	3540
Db	3481		AGTTTCCCGCGACTGGTGGCTGACAGTGGCTTTCGGGCCAATGTGGAGTCTCTGGGGAAT	3540
Qy	3541		GSCCTGGTGTTCGACGCCGCGACGTTGCTGTGTGAGCAAGCCACCTCAGTGTCTGGC	3600
Db	3541		GSCCTGGTGTTCGACGCCGCGACGTTGCTGTGTGAGCAAGCCACCTCAGTGTCTGGC	3600
Qy	3601		CTCGTGGGCTTCTCTGTCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTGTT	3660
Db	3601		CTCGTGGGCTTCTCTGTCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTGTT	3660
Qy	3661		CGCAACTGACAGACCTAGAGAACAGCATGTGTCTCAGTGGAGCGGATGCAGGACTATGCC	3720
Db	3661		CGCAACTGACAGACCTAGAGAACAGCATGTGTCTCAGTGGAGCGGATGCAGGACTATGCC	3720
Qy	3721		TGGACGCCCAAGGAGGCTCCCTGGAGGTCGCCACATGTGCAGTGCAGCCCTCGGCT	3780
Db	3721		TGGACGCCCAAGGAGGCTCCCTGGAGGTCGCCACATGTGTGCAGTGCAGCCCTCGGCT	3780
Qy	3781		CAGGCGGGCAGATCAGTTCGGGACTTTTGGGCTTAAGATCCGACCTCAGCTCCCGCTG	3840
Db	3781		CAGGCGGGCAGATCAGTTCGGGACTTTTGGGCTTAAGATCCGACCTCAGCTCCCGCTG	3840
Qy	3841		GCTGTGCAGGGGCTGTCTTCAAGATCCACGCAAGGAGAAAGTGGGCAATCGTTGGCAGG	3900

1021 GATCCAAAGCTCCAGCCTGGAAGGCTACCTCTCGCGTCTGATGTTCTCTCAGCC 1080
1021 GATCCAAAGCTCCAGCCTGGAAGGCTACCTCTCGCGTCTGATGTTCTCTCAGCC 1080
1081 TGCCTGCAAAAGCTGTTTGAAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
1081 TGCCTGCAAAAGCTGTTTGAAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
1141 TTGGGCTCGGCCATCAGTGGCTGTGTGTACAGAAAGTTCCTGGCTGTCTCAGCGGCTCC 1200
1141 TTGGGCTCGGCCATCAGTGGCTGTGTGTACAGAAAGTTCCTGGCTGTCTCAGCGGCTCC 1200
1201 AGAAGGCGAGTGGCGGTGATGTGTCTCAATCTGGTGTCCGTGGAGCTGCAGCGGCTG 1260
1201 AGAAGGCGAGTGGCGGTGATGTGTCTCAATCTGGTGTCCGTGGAGCTGCAGCGGCTG 1260
1261 ACCGAGAGGCTCTACTCTCAACGGGCTGTGGCTGTCTCGTCTGGATCTGCTCTGC 1320
1261 ACCGAGAGGCTCTACTCTCAACGGGCTGTGGCTGTCTCGTCTGGATCTGCTCTGC 1320
1321 TTCGTCTATCTGCGAGCTCTCGGGGCTCCCGGCTCACTGCCATCGCTGTCTTCCTG 1380
1321 TTCGTCTATCTGCGAGCTCTCGGGGCTCCCGGCTCACTGCCATCGCTGTCTTCCTG 1380
1381 AGCCTCTCCCTCTCAATTTCTTCTATCTCCAAAGAAAGAACCCATCAGGAGGACAA 1440
1381 AGCCTCTCCCTCTCAATTTCTTCTATCTCCAAAGAAAGAACCCATCAGGAGGACAA 1440
1441 ATGAGGCGAAGGACTACGGGCGAGGCTCACAGCTCTATCTCAGGAATCTCAGAGACC 1500
1441 ATGAGGCGAAGGACTACGGGCGAGGCTCACAGCTCTATCTCAGGAATCTCAGAGACC 1500
1501 ATCAAGTTCCATGCTGGAGGAGGCTTTCTGGACAGAGTCTGGGATCCGAGGCGCAG 1560
1501 ATCAAGTTCCATGCTGGAGGAGGCTTTCTGGACAGAGTCTGGGATCCGAGGCGCAG 1560
1561 GAGCTGGGCGCTTCGGGACCTCCGGGCTCTCTTCTCTGTCTGTCTGTCTGTCTTCAA 1620
1561 GAGCTGGGCGCTTCGGGACCTCCGGGCTCTCTTCTCTGTCTGTCTGTCTGTCTTCAA 1620
1621 GTGTCTACATTTCTGGTGGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
1621 GTGTCTACATTTCTGGTGGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
1681 GCTATGAATGAGAAAGCCTTTGTGACTCTCAGACTCTCAAGTCTCAAGTCTCAAGAGGCC 1740
1681 GCTATGAATGAGAAAGCCTTTGTGACTCTCAGACTCTCAAGTCTCAAGTCTCAAGAGGCC 1740
1741 CAGGCTTTCTGCTGCTTCTCCATCCACTCCCTCTGTCAGGCGCGGCTGTCTTGAACCT 1800
1741 CAGGCTTTCTGCTGCTTCTCCATCCACTCCCTCTGTCAGGCGCGGCTGTCTTGAACCT 1800
1801 CTGCTACCTTCTGCTGCTGGAAGTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
1801 CTGCTACCTTCTGCTGCTGGAAGTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
1861 GGAAGCGTCCGCGGAGGATTTGCATCACCATTACAGAGTGCCACCTTCGCTTGGTCCCA 1920
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1921 GAAAGCCTCTCTGCTCCACAGAAATAAAGCTTCAGGCTGCGGCGGCTGTCTGTGGCT 1980
1921 GAAAGCCTCTCTGCTCCACAGAAATAAAGCTTCAGGCTGCGGCGGCTGTCTGTGGCT 1980
1981 GTTGTGCTGCTGCTGCTGGAAGTGTCTCTCTGCTGTCTGCTGCTGCTGCTGCTGCTG 2040
1981 GTTGTGCTGCTGCTGCTGGAAGTGTCTCTCTGCTGTCTGCTGCTGCTGCTGCTGCTG 2040
2041 TCAAAGGTGGAGGCTTCTGTGAGCATCCAGGCTGTGTGGCTTACGTGCCCGAGAGGCC 2100
2041 TCAAAGGTGGAGGCTTCTGTGAGCATCCAGGCTGTGTGGCTTACGTGCCCGAGAGGCC 2100
2101 TGGGTGCAGAACCTCTGT 2160

2101 TGGGTGCAGAACACCTCTGT 2160
2161 TGGGTGCAGAACACCTCTGT 2160
2161 TGGGTGCAGAACACCTCTGT 2220
2161 TGGGTGCAGAACACCTCTGT 2220
2221 GGAATCCACACTTCAATTTGGGAGCAGGATCAATCTCTCCGAGGCGCAGAGCAGCGG 2280
2221 GGAATCCACACTTCAATTTGGGAGCAGGATCAATCTCTCCGAGGCGCAGAGCAGCGG 2280
2281 CTGAGCCTTGCCCGGCTGTATACAAAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
2281 CTGAGCCTTGCCCGGCTGTATACAAAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
2341 GGGGCTCTGGATGCTCCAGCTGTGGCAGCATGTCTTCAACAGGCTCATTTGGGCTGTGTGG 2400
2341 GGGGCTCTGGATGCTCCAGCTGTGGCAGCATGTCTTCAACAGGCTCATTTGGGCTGTGTGG 2400
2401 CTACTCCAGGAGACACAGGATTCGTGACGCGACGCTCCACATCTCTGCCCGAGGCT 2460
2401 CTACTCCAGGAGACACAGGATTCGTGACGCGACGCTCCACATCTCTGCCCGAGGCT 2460
2461 GATTGATCATAGTGTGCAAAATGGGCCATCGCAGAGATGGTTCCTTACAGGAGCTT 2520
2461 GATTGATCATAGTGTGCAAAATGGGCCATCGCAGAGATGGTTCCTTACAGGAGCTT 2520
2521 CTGCAGAGAAAGGGGCTCTGCTGTCTTCTGATCAAGCCAGACAGCAGGAGATAGA 2580
2521 CTGCAGAGAAAGGGGCTCTGCTGTCTTCTGATCAAGCCAGACAGCAGGAGATAGA 2580
2581 GGAGAGGAGAAACAGAACTGGGACAGCACCAGGACCCAGAGGACCTCTGCGAGGC 2640
2581 GGAGAGGAGAAACAGAACTGGGACAGCACCAGGACCCAGAGGACCTCTGCGAGGC 2640
2641 AGGAGCCCGAGCTTAGAGCGGAGAGGTCCATCAAGTCTAGTCTCTGAGAAAGCCTGAC 2700
2641 AGGAGCCCGAGCTTAGAGCGGAGAGGTCCATCAAGTCTAGTCTCTGAGAAAGCCTGAC 2700
2701 ACTTCAGAGCCAGACAGAGGTTCTCTGGATGACCTCTGACAGGCGAGGATGCCAGCA 2760
2701 ACTTCAGAGCCAGACAGAGGTTCTCTGGATGACCTCTGACAGGCGAGGATGCCAGCA 2760
2761 GGAAGGACAGATCCAAATACGCGGAGGTGAAGCCACAGTGCACCTGGCTTACCTCGCT 2820
2761 GGAAGGACAGATCCAAATACGCGGAGGTGAAGCCACAGTGCACCTGGCTTACCTCGCT 2820
2821 GCGGTGGGACACCCCTCTGCTCTTACGCACTCTTCTCTCTCTGCGGCTGCTCTCAAGGCT 2880
2821 GCGGTGGGACACCCCTCTGCTCTTACGCACTCTTCTCTCTCTGCGGCTGCTCTCAAGGCT 2880
2881 TCGTCTGCGGGGCTTACTGGCTGAGCTGTGGGCGGACGACCTCTGAGTGTGGGCTG 2940
2881 TCGTCTGCGGGGCTTACTGGCTGAGCTGTGGGCGGACGACCTCTGAGTGTGGGCTG 2940
2941 CAGACGCGAGCCTCTGCTGGGCTCTGCGGCTCTGCGGCTCTGCTCTCTGCGGCTGCTCT 3000
2941 CAGACGCGAGCCTCTGCTGGGCTCTGCGGCTCTGCGGCTCTGCTCTCTGCGGCTGCTCT 3000
3001 GGGCTTTTGGCTTCCATGCTGCTGGCTGCTCTAGTGGGCGGCGGCTCTGAGGCTGCTC 3060
3001 GGGCTTTTGGCTTCCATGCTGCTGGCTGCTCTAGTGGGCGGCGGCTCTGAGGCTGCTC 3060
3061 TTCCAGAGGCTCTGTGGGATGTGGTCCGATCTCCATCAGCTTCTTTGAGCGGACACCC 3120
3061 TTCCAGAGGCTCTGTGGGATGTGGTCCGATCTCCATCAGCTTCTTTGAGCGGACACCC 3120
3121 ATTGTGCTCCTGCTTAACCGCTTCTCAAGGAGACACAGCTTGTGAGCTTGTGAGCTTCCA 3180
3121 ATTGTGCTCCTGCTTAACCGCTTCTCAAGGAGACACAGCTTGTGAGCTTGTGAGCTTCCA 3180
3181 GACAAACTCCGGTCTCTGT 3240
3181 GACAAACTCCGGTCTCTGT

Db 3181 GACAACTCCGGTCCCTGCTGATGATGACGCCCTTTGGACTCCTGGAGTCAAGCTGGTGGT 3240
QY 3241 GCAGTGGCTACCCACATGCGACATGTCGGCATCTGCGACATGTTCTCCTCTACGCTGGG 3300
Db 3241 GCACTGGCTACCCACATGCGACATGTCGGCATCTGCGACATGTTCTCCTCTACGCTGGG 3300
QY 3301 TTTTCAGAGCCTGTATGTGGTTAGTCTATGCCAGCTGAGAGCGTTGGAGTCAGCCAGCTAC 3360
Db 3301 TTTTCAGAGCCTGTATGTGGTTAGTCTATGCCAGCTGAGAGCGTTGGAGTCAGCCAGCTAC 3360
QY 3361 TCGTCTGTCTGCTCCACATAGGCTGAGACGTTCCAGGGCAGACAGTGGTCCGGGCATTC 3420
Db 3361 TCGTCTGTCTGCTCCACATAGGCTGAGACGTTCCAGGGCAGACAGTGGTCCGGGCATTC 3420
QY 3421 CGAACCAGGCCCTTTGTGGCTCAGAACATGCTGCGGTAGATGAAGCCAGAGGATC 3480
Db 3421 CGAACCAGGCCCTTTGTGGCTCAGAACATGCTGCGGTAGATGAAGCCAGAGGATC 3480
QY 3481 AGTTTCCCGGACTGGTGGCTGACAGTGGCTTGGCGCAATGTGGAGCTCCTGGGGAAT 3540
Db 3481 AGTTTCCCGGACTGGTGGCTGACAGTGGCTTGGCGCAATGTGGAGCTCCTGGGGAAT 3540
QY 3541 GGCTGTGTTCGACGCCCGCACGTGTGCTGTGCTGAGCAAAACCCACCTCACTGTGTGC 3600
Db 3541 GGCTGTGTTCGACGTGCCACGTGTGCTGTGCTGAGCAAAACCCACCTCACTGTGTGC 3600
QY 3601 CTCGTGGGCTTCTGTCTCTGCTGCTCCAGGTGACCCAGACACTGCACTGGGTGGTGT 3660
Db 3601 CTCGTGGGCTTCTGTCTCTGCTGCTCCAGGTGACCCAGACACTGCACTGGGTGGTGT 3660
QY 3661 CGCACTGACAGACCTAGAGAACACATCGTGTGCTGAGTGGAGCGGATGAGGACTATGCC 3720
Db 3661 CGCACTGACAGACCTAGAGAACACATCGTGTGCTGAGTGGAGCGGATGAGGACTATGCC 3720
QY 3721 TGGACCCCAAGAGAGCTCCCTGGAGGCTGCCACATGTGAGCTCAGCCCCCTGGCCCT 3780
Db 3721 TGGACCCCAAGAGAGCTCCCTGGAGGCTGCCACATGTGAGCTCAGCCCCCTGGCCCT 3780
QY 3781 CAGGGGGGAGATCAGATTCGGGACTTTGGGCTAAGATGCGGACTGAGCTCCCGCTG 3840
Db 3781 CAGGGGGGAGATCAGATTCGGGACTTTGGGCTAAGATGCGGACTGAGCTCCCGCTG 3840
QY 3841 GCTGTGAGGGGTGCTTCAAGATCCACGAGGAGAGAGTGGGCATCGTTGGCAGG 3900
Db 3841 GCTGTGAGGGGTGCTTCAAGATCCACGAGGAGAGAGTGGGCATCGTTGGCAGG 3900
QY 3901 ACCGGGGCAGGGAAGTCTCCCTGGCCAGTGGGCTCTCGGCTCCAGGAGGAGCTGAG 3960
Db 3901 ACCGGGGCAGGGAAGTCTCCCTGGCCAGTGGGCTCTCGGCTCCAGGAGGAGCTGAG 3960
QY 3961 GGTGGATCTGATCGACGGGGTCCCATTTGCCAGTGGGGCTGCACACTGCGCTCC 4020
Db 3961 GGTGGATCTGATCGACGGGGTCCCATTTGCCAGTGGGGCTGCACACTGCGCTCC 4020
QY 4021 AGGATCAGCATCATCCCCCAGGACCCCATCTCTGTTCCCTGGCTCTCTCGGATGAACCTC 4080
Db 4021 AGGATCAGCATCATCCCCCAGGACCCCATCTCTGTTCCCTGGCTCTCTCGGATGAACCTC 4080
QY 4081 GACCTGCTCAGAGAGACTCGACAGAGGCTATCTGGGACGCCCTGGAGAGCTGAGCTC 4140
Db 4081 GACCTGCTCAGAGAGACTCGACAGAGGCTATCTGGGACGCCCTGGAGAGCTGAGCTC 4140
QY 4141 AAAGCTTTGGTGGCAGCTGCCGGCCAGCTGAGTACAAAGTGTGCTGACCGAGCGAG 4200
Db 4141 AAAGCTTTGGTGGCAGCTGCCGGCCAGCTGAGTACAAAGTGTGCTGACCGAGCGAG 4200
QY 4201 GACCTGAGGCTGGCCAGAAACAGTCTCTGTGCTGGCAGCTGCCCTTCTCCGGAGACC 4260
Db 4201 GACCTGAGGCTGGCCAGAAACAGTCTCTGTGCTGGCAGCTGCCCTTCTCCGGAGACC 4260
QY 4261 CAGATCCTCATCTCGTGGCAGGAGCTACTGCTGCGGTGGACCCCTGGCAGCGAGTGCAGATG 4320
Db 4261 CAGATCCTCATCTCGTGGCAGGAGCTACTGCTGCGGTGGACCCCTGGCAGCGAGTGCAGATG 4320

QY 4321 CAGCCCATGCTGGAGAGCTGTTGGACAGTGCATGTGTCGCCATTTGCCACCGCCTG 4380
Db 4321 CAGCCCATGCTGGAGAGCTGTTGGACAGTGCATGTGTCGCCATTTGCCACCGCCTG 4380
QY 4381 CGCTCCGCTGATGAGTGTGCGCGGTTCTGCTCATGGACAAGGGCAGGTGCCAGAGC 4440
Db 4381 CGCTCCGCTGATGAGTGTGCGCGGTTCTGCTCATGGACAAGGGCAGGTGCCAGAGC 4440
QY 4441 GGCAGCCCGGCCAGCTGCTGGCCAGAAAGGCCCTGTTTACAGACTGCCCGAGAGTCA 4500
Db 4441 GGCAGCCCGGCCAGCTGCTGGCCAGAAAGGCCCTGTTTACAGACTGCCCGAGAGTCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 3

AAD16256

ID AAD16256 standard; cDNA; 4512 BP.

XX AAD16256;

XX AC (first entry)

DT 19-NOV-2001 (first entry)

XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #1.

DE Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;

KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;

KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;

KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;

KW mutant; mutens; ss.

XX Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

CDS 1..4512

FT /*tag= a

FT /product= "Human ABCC6 (MRP6) mutant protein"

FT replace (3341, G)

FT /*tag= b

FT mutation

FT

XX WO200162977-A2.

PN

PD 30-AUG-2001.

XX

XX 23-FEB-2001; 2001WO-US05741.

XX

PR 23-FEB-2000; 2000US-0184269.

XX

XX (PXET-) PXE INT INC.

PA (UYHA-) UNIV HAWAII.

XX

PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;

XX WPI; 2001-536645/59.

DR P-PSDB; AAE09363.

XX

XX Screening presence of Pseudoxanthoma elasticum mutation useful for

PT identifying homozygotes, compound heterozygotes or carriers involves

PT determining presence of mutation in MRP6 (ABCC6) nucleic acid

XX

PS Example 2; Page -; 163pp; English.

XX

CC The invention relates to methods and compositions for diagnosing and

CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological

CC dysfunctions. The invention is useful for screening for the presence of

CC a PXE mutation. Mutations associated with PXE maps to the ATP-binding

CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated

CC protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165

CC kDa protein located in the plasma membrane containing 17 membrane-

Db	1801	 CTGTCACCTTCTCTCTGCGCTGGAAGAAGTTGACCTGTGTGCTGTAGACTCAAGTTCCTCT	1861
Qy	1861	GGAAAGCCTCGCGGGAAGGATTGCATFACATFACACAGTGCACACTTCGCGCTGTGTCCAG	1920
Db	1861	GGAAAGCCTCGCGGGAAGGATTGCATCACCATACACAGTGCACACTTCGCGCTGTGTCCAG	1920
Qy	1921	GAAGGCCCTCCCTCGCTCCACAGAAATAAACCTCACGGTGCCTCCAGGCTGTCTCTGGCT	1980
Db	1921	GAAGGCCCTCCCTCGCTCCACAGAAATAAACCTCACGGTGCCTCCAGGCTGTCTCTGGCT	1980
Qy	1981	GTGTGCGGTCCAGTGGGGCAGGGAAGTCTCTCCCTGCTGTGCGGCCCTCTCTTGGGGAGCTG	2040
Db	1981	GTGTGCGGTCCAGTGGGGCAGGGAAGTCTCTCCCTGCTGTGCGGCCCTCTCTTGGGGAGCTG	2040
Qy	2041	TCAAAGTGGAGGGTTCGTGAGCATCGAGGGTGTGTGGCTTACGTGCCCCCAGAGGCC	2100
Db	2041	TCAAAGTGGAGGGTTCGTGAGCATCGAGGGTGTGTGGCTTACGTGCCCCCAGAGGCC	2100
Qy	2101	TGGGTGCAGAACACCTCTCTGTGTAGAGAAATGTGTCTTTCGGGCAGGAGCTGGACCCACC	2160
Db	2101	TGGGTGCAGAACACCTCTCTGTGTAGAGAAATGTGTCTTTCGGGCAGGAGCTGGACCCACC	2160
Qy	2161	TGGCTGGAGAGAGTACTAGAACGCTGTGCCCTGACGCCAGATGTGGACAGTTCCCTGTAG	2220
Db	2161	TGGCTGGAGAGAGTACTAGAACGCTGTGCCCTGACGCCAGATGTGGACAGTTCCCTGTAG	2220
Qy	2221	GGAAATCCACACTTCAATTTGGGAGCAGGCGCATGAATCTCTCCGAGGCCAGACAGCGG	2280
Db	2221	GGAAATCCACACTTCAATTTGGGAGCAGGCGCATGAATCTCTCCGAGGCCAGACAGCGG	2280
Qy	2281	CTGAGCCTGSCCGGCGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCTG	2340
Db	2281	CTGAGCCTGSCCGGCGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCTG	2340
Qy	2341	CGCGCCTTGGATGCCACGCTTGGCCAGCATGTCTTTCACACAGGTCTATTGGCCCTGGTGGG	2400
Db	2341	CGCGCCTTGGATGCCACGCTTGGCCAGCATGTCTTTCACACAGGTCTATTGGCCCTGGTGGG	2400
Qy	2401	CTACTCCAGGGAACAACCGGATTCCTGTGAGCGACGCACATCCACATCTGCCCCAGGCT	2460
Db	2401	CTACTCCAGGGAACAACCGGATTCCTGTGAGCGACGCACATCCACATCTGCCCCAGGCT	2460
Qy	2461	GATTGGATCATAGTGTGTCGCAATGGGCCATTCGCAGAGATGGGTTCCTACCAAGAGCTT	2520
Db	2461	GATTGGATCATAGTGTGTCGCAATGGGCCATTCGCAGAGATGGGTTCCTACCAAGAGCTT	2520
Qy	2521	CTGCAGAGGAAGGGGCCCTCGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA	2580
Db	2521	CTGCAGAGGAAGGGGCCCTCGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA	2580
Qy	2581	GGAGAAGGAGAAACAGAACTCGGGACAGCACCAAGGACCCAGAGCACCTCTGCAGGC	2640
Db	2581	GGAGAAGGAGAAACAGAACTCGGGACAGCACCAAGGACCCAGAGCACCTCTGCAGGC	2640
Qy	2641	AGGAGGCCGAGGCTTAGCGCAGAGGTCCTATCAAGTCAGTCCCTGAGAAGACCGTACC	2700
Db	2641	AGGAGGCCGAGGCTTAGCGCAGAGGTCCTATCAAGTCAGTCCCTGAGAAGACCGTACC	2700
Qy	2701	ACTTCAGAGCCCCAGACAGGTTTCTCTGGATGACCTTGACGGGCAGAGTGGCCAGCA	2760
Db	2701	ACTTCAGAGCCCCAGACAGGTTTCTCTGGATGACCTTGACGGGCAGAGTGGCCAGCA	2760
Qy	2761	GGAAAGGACAGCATCCAATTACGGCAGGTTGAAGGCCACAGTGCACCTTACCTTCGCT	2820
Db	2761	GGAAAGGACAGCATCCAATTACGGCAGGTTGAAGGCCACAGTGCACCTTACCTTCGCT	2820
Qy	2821	GCGTGGGGCACCCCTCTGCGCTCTACGCACTTCTTCCTTCTTCCCTGCCAGCAAGTGCC	2880
Db	2821	GCGTGGGGCACCCCTCTGCGCTCTACGCACTTCTTCCTTCTTCCCTGCCAGCAAGTGCC	2880
Qy	2881	TCCTTCTGCGGGGCTACTGCGTGTAGCCCTGTGGCGGACAGACCTGTGAGTGGGCAG	2940

Db	2881	TCTTCTGCGGGGTACTGGCTGAGCCTGTGGCGGACGACCCTGCAGTAGTGTCG	2940
Qy	2941	CAGACGACGACGCCCTCGTGGCGGATCTTCGGGCTCCTCGSGCTCTCCCAAGCATTT	3000
Db	2941	CAGACGACGACGCCCTCGTGGCGGATCTTCGGGCTCCTCGSGCTCTCCCAAGCATTT	3000
Qy	3001	GGGCTGTTTTGCCCTCCAATGGCTGCGGTGCTCTTAGTGGGGCCCGGCATCCAGTGTGCTC	3060
Db	3001	GGGCTGTTTTGCCCTCCAATGGCTGCGGTGCTCTTAGTGGGGCCCGGCATCCAGTGTGCTC	3060
Qy	3061	TTCCAGAGGCTCGTGTGGGATGTGTGGGATCTCCCATCAGCTTCTTTGAGCGGACACCC	3120
Db	3061	TTCCAGAGGCTCGTGTGGGATGTGTGGGATCTCCCATCAGCTTCTTTGAGCGGACACCC	3120
Qy	3121	ATTGGTCACTCGTAACCGCTTCTCCAAGGACAGACACGGTTGAGCTTCTTTGAGCGGACATTC	3180
Db	3121	ATTGGTCACTCGTAACCGCTTCTCCAAGGACAGACACGGTTGAGCTTCTTTGAGCGGACATTC	3180
Qy	3181	GACAACTCCGGTCCCTGCTGATGTACGGCTTTTGAGCTCCTGGAGCTCAGCCTTGGTGGTG	3240
Db	3181	GACAACTCCGGTCCCTGCTGATGTACGGCTTTTGAGCTCCTGGAGCTCAGCCTTGGTGGTG	3240
Qy	3241	GGAGTGGCTACCCCACATGGCTGAGAGCTTCCAGGGCAGCACACTGGTCCGGGCAATTC	3300
Db	3241	GGAGTGGCTACCCCACATGGCTGAGAGCTTCCAGGGCAGCACACTGGTCCGGGCAATTC	3300
Qy	3301	TTTCAGAGCTGTATGTGGTTAGCTCATGCCAGCTGAGAGCTTGCAGTCAGCCAGCTAC	3360
Db	3301	TTTCAGAGCTGTATGTGGTTAGCTCATGCCAGCTGAGAGCTTGCAGTCAGCCAGCTAC	3360
Qy	3361	TGCTGTCTGCTCCACATGGCTGAGAGCTTCCAGGGCAGCACACTGGTCCGGGCAATTC	3420
Db	3361	TGCTGTCTGCTCCACATGGCTGAGAGCTTCCAGGGCAGCACACTGGTCCGGGCAATTC	3420
Qy	3421	CGAACCCAGGCCCTTTTGTGGCTCAGAACATGTCTCGGTAGATGAAGCCAGAGGATC	3480
Db	3421	CGAACCCAGGCCCTTTTGTGGCTCAGAACATGTCTCGGTAGATGAAGCCAGAGGATC	3480
Qy	3481	AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGGCCCAAATGTGGAGCTCTCTGGGGAAT	3540
Db	3481	AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGGCCCAAATGTGGAGCTCTCTGGGGAAT	3540
Qy	3541	GGCTGGTGTTCGACGCCACGTGTGTGTCTGTCTGAGCAAAAGCCCCACCTCAGTGTCTGGC	3600
Db	3541	GGCTGGTGTTCGACGTCCACGTGTGTGTCTGAGCAAAAGCCCCACCTCAGTGTCTGGC	3600
Qy	3601	CTCTGGGGCTTCTGTCTCTGTCTGTCCTGAGGTGACCCAGACACTGCAGTGGGTGTGT	3660
Db	3601	CTCTGGGGCTTCTGTCTCTGTCTGTCCTGAGGTGACCCAGACACTGCAGTGGGTGTGT	3660
Qy	3661	CGCACTGGACAGACTGAGAACAGCATCTGCTCAGTGGAGCGGATGACGAGCTATGCC	3720
Db	3661	CGCACTGGACAGACTGAGAACAGCATCTGCTCAGTGGAGCGGATGACGAGCTATGCC	3720
Qy	3721	TGGACGCCAAGGAGSCTCCCTGGAGGCTGCCACATGTGCAGCTCAGCGCCCCCTGGCCT	3780
Db	3721	TGGACGCCAAGGAGSCTCCCTGGAGGCTGCCACATGTGCAGCTCAGCGCCCCCTGGCCT	3780
Qy	3781	CAGGGGGGCAGATCGAGTTCGGGAGCTTTGGGCTTAAGATGCGGACCTGAGCTCCCGCTG	3840
Db	3781	CAGGGGGGCAGATCGAGTTCGGGAGCTTTGGGCTTAAGATGCGGACCTGAGCTCCCGCTG	3840
Qy	3841	GCCTGTGAGGGCTGTCTCTCAAGATCCACGAGGAGAAGGTGGGCATCGTTGGCAGG	3900
Db	3841	GCCTGTGAGGGCTGTCTCTCAAGATPCACGAGGAGAAGGTGGGCATCGTTGGCAGG	3900
Qy	3901	ACCGGGGACGGAAGTCTCTCCCTGGCCAGTGGGCTCTCGGGCTCCAGGAGGCAGCTGAG	3960
Db	3901	ACCGGGGACGGAAGTCTCTCTCCCTGGCCAGTGGGCTCTCGGGCTCCAGGAGGCAGCTGAG	3960
Qy	3961	GGTGGATCTGTATCGAGGGGTGCCCATTTGCCACGTGGGGCTGCACACTGCGCTCC	4020
Db	3961	GGTGGATCTGTATCGAGGGGTGCCCATTTGCCACGTGGGGCTGCACACTGCGCTCC	4020

[illegible]

QY	3721	TGGACGCCCAAGAGAGGCTCCCTGGAGGGCTGCCACATGTGCAGCTCAGCCCCCTGGCCCT	3780
Db	3721	TGGACGCCCAAGAGAGGCTCCCTGGAGGGCTGCCACATGTGCAGCTCAGCCCCCTGGCCCT	3780
QY	3781	CAGGGCGGCAGATCAGATTCCGGGACTTTGGGCTAAGATGCCGACTGAGCTCCGGCTG	3840
Db	3781	CAGGGCGGCAGATCAGATTCCGGGACTTTGGGCTAAGATACCAGACTGAGCTCCGGCTG	3840
QY	3841	GCTGTGCAGGGGTGTCCTTCAAGATCCACGCAGGAGAGAAGTGGSCATCGTTGGCAGG	3900
Db	3841	GCTGTGCAGGGGTGTCCTTCAAGATCCACGCAGGAGAGAGAAGTGGGATCGTTGGCAGG	3900
QY	3901	ACCGGGGCAGGGAAGTCTCCCTGGCCAGTGGGCTGCTGGGGTCCAGGAGGAGCTGAG	3960
Db	3901	ACCGGGGCAGGGAAGTCTCCCTGGCCAGTGGGCTGCTGGGGTCCAGGAGGAGCTGAG	3960
QY	3961	GGTGGGATCTGGATCGACGGGTCCCCATTGCCACGTGGGGCTGCACACACTGGCGCTCC	4020
Db	3961	GGTGGGATCTGGATCGACGGGTCCCCATTGCCACGTGGGGCTGCACACACTGGCGCTCC	4020
QY	4021	AGGATCAGCATCATCCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGGATGAACCTC	4080
Db	4021	AGGATCAGCATCATCCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGGATGAACCTC	4080
QY	4081	GACCTGCTCAGAGAGCACTCGGACGAGGCTATTCTGGGCAGCCCTGGAGACGGTGCAGCTC	4140
Db	4081	GACCTGCTCAGAGAGCACTCGGACGAGGCTATTCTGGGCAGCCCTGGAGACGGTGCAGCTC	4140
QY	4141	AAAGCCTTGGTGCCAGCTCGCCGGCCAGCTCAGTACAAAGTGTCTGACCCAGGCGAG	4200
Db	4141	AAAGCCTTGGTGCCAGCTCGCCGGCCAGCTCAGTACAAAGTGTCTGACCCAGGCGAG	4200
QY	4201	GACCTGAGCGTGGGCAGAAACAGCTCCTGTGTCTGGCAGCTGCCCTTCTCCGGAAGACC	4260
Db	4201	GACCTGAGCGTGGGCAGAAACAGCTCCTGTGTCTGGCAGCTGCCCTTCTCCGGAAGACC	4260
QY	4261	CAGATCCTCATCTCGACGAGGCTACTGCTCGCTGGACCCCTGGCAGGAGCTGCAGATG	4320
Db	4261	CAGATCCTCATCTCGACGAGGCTACTGCTCGCTGGACCCCTGGCAGGAGCTGCAGATG	4320
QY	4321	CAGGCCATGCTCGGAGCTGGTTTGCACAGTGCACATGTGTGTCGCCATTTGCCACCCGCTG	4380
Db	4321	CAGGCCATGCTCGGAGCTGGTTTGCACAGTGCACATGTGTGTCGCCATTTGCCACCCGCTG	4380
QY	4381	CGCTCCGTGATGACATGTGCCCGGGTTCTGGTTCATGGACAAGGGGAGGTGGCAGAGAC	4440
Db	4381	CGCTCCGTGATGACATGTGCCCGGGTTCTGGTTCATGGACAAGGGGAGGTGGCAGAGAC	4440
QY	4441	GGCAGCCGGGCCAGCTGCTGGCCCAAGAGGGGCTGTTTTACAGACTGGCCCCAGGAGTCA	4500
Db	4441	GGCAGCCGGGCCAGCTGCTGGCCCAAGAGGGGCTGTTTTACAGACTGGCCCCAGGAGTCA	4500
QY	4501	GGCCTGGTC 4509	
Db	4501	GGCCTGGTC 4509	

RESULT 5

AAD16258
ID AAD16258 standard; cDNA; 4512 BP.

AC AAD16258;

DT	19-NOV-2001	(first entry)
----	-------------	---------------

DE Human ATP-binding cassette transporter ABCB6 (MRP6) mutant cDNA #3.

Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;	KW
Multidrug Resistance-associated protein 6; macular degeneration; ABCG6;	KW
ATP-binding cassette transporter; arterial insufficiency; chromosome 16	KW
Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;	KW
mutant; mteuin; ss.	KW

Db 3361 TCGTCTGCTGCCACATAGGCTGAGACGTTCCAGGGCAGCAGTGGTCCGGGCATTC 3420
 Qy 3421 CGAACCCAGCCCTTTTGGCTCAGAACATGCTCGCTAGATGAAGCCAGAGGATC 3480
 Db 3421 TGAACCCAGCCCTTTTGGCTCAGAACATGCTCGCTAGATGAAGCCAGAGGATC 3480
 Qy 3481 AGTTTCCCGGACTGGTGGCTGACAGTGGCTTGGGCCAATGTGGAGCTCCTGGGGAAT 3540
 Db 3481 AGTTTCCCGGACTGGTGGCTGACAGTGGCTTGGGCCAATGTGGAGCTCCTGGGGAAT 3540
 Qy 3541 GGCTGGTGTTCAGCGCCGACGCTGCTGTGCTGAGCAAAAGCCACCTCAGTGTGGC 3600
 Db 3541 GGCTGGTGTTCAGCGCTGACGCTGCTGTGCTGAGCAAAAGCCACCTCAGTGTGGC 3600
 Qy 3601 CTGCTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
 Db 3601 CTGCTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
 Qy 3661 CGCACTGGACAGCTAGAGAACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
 Db 3661 CGCACTGGACAGCTAGAGAACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
 Qy 3721 TGGACGCCAAGGAGGCTCCCTGAGGCTGCCACATGTGACGTCAGCCGCTGCTGCTGCT 3780
 Db 3721 TGGACGCCAAGGAGGCTCCCTGAGGCTGCCACATGTGACGTCAGCCGCTGCTGCTGCT 3780
 Qy 3781 CAGGGGGGAGATGAGATTCGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTG 3840
 Db 3781 CAGGGGGGAGATGAGATTCGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTG 3840
 Qy 3841 GCTGTGAGGGCTGCTTCCAGATCCAGGAGGAGAGAGTGGGCTGCTGCTGCTGCTGCT 3900
 Db 3841 GCTGTGAGGGCTGCTTCCAGATCCAGGAGGAGAGAGTGGGCTGCTGCTGCTGCTGCT 3900
 Qy 3901 ACCGGGGGAGGAGGCTCCCTGAGGCTGCCACATGTGACGTCAGCCGCTGCTGCTGCTGCT 3960
 Db 3901 ACCGGGGGAGGAGGCTCCCTGAGGCTGCCACATGTGACGTCAGCCGCTGCTGCTGCTGCT 3960
 Qy 3961 GGTGGATCTGATGACAGGGGCTCCCATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 4020
 Db 3961 GGTGGATCTGATGACAGGGGCTCCCATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 4020
 Qy 4021 AGGATCAGCATATCCCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4080
 Db 4021 AGGATCAGCATATCCCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4080
 Qy 4081 GACCTGCTCAGGAGCACTCGGAGGCTTATCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4140
 Db 4081 GACCTGCTCAGGAGCACTCGGAGGCTTATCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4140
 Qy 4141 AAGACCTTGGTGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4200
 Db 4141 AAGACCTTGGTGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4200
 Qy 4201 GACCTGAGGCTGGGCGAGAACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4260
 Db 4201 GACCTGAGGCTGGGCGAGAACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4260
 Qy 4261 CAGATCTCATCTGACGAGGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4320
 Db 4261 CAGATCTCATCTGACGAGGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4320
 Qy 4321 CAGGCCATGCTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4380
 Db 4321 CAGGCCATGCTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4380
 Qy 4381 CGCTCGTATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4440
 Db 4381 CGCTCGTATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4440
 Qy 4441 GGCAGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500

Db 4441 GGCAGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
 Qy 4501 GGCCTGGTC 4509
 Db 4501 GGCCTGGTC 4509
 RESULT 6
 AAD16260
 ID AAD16260 standard; cDNA; 4512 BP.
 XX AAD16260;
 XX AC AC
 XX 19-NOV-2001 (first entry)
 XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #5.
 XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
 XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
 XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
 XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
 XX mutant; mutein; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX
 Key Location/Qualifiers
 CDS 1..4512
 FT /*tag= a
 FT /product= "Human ABCC6 (MRP6) mutant protein"
 FT mutation replace (3892, G)
 FT /*tag= b
 XX
 XX WO200162977-A2.
 XX
 XX 30-AUG-2001.
 XX
 XX 23-FEB-2001; 2001WO-US05741.
 XX
 XX 23-FEB-2000; 2000US-0184269.
 XX
 XX (PXEI-) PXE INT INC.
 XX (UYHA-) UNIV HAWAII.
 XX
 XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
 WPI; 2001-536645/59.
 P-PSDB; AAE09367.
 Screening presence of Pseudoxanthoma elasticum mutation useful for
 identifying homozygotes, compound heterozygotes or carriers involves
 determining presence of mutation in MRP6 (ABCC6) nucleic acid -
 Example 2; Page -; 163pp; English.
 The invention relates to methods and compositions for diagnosing and
 treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
 dysfunctions. The invention is useful for screening for the presence of
 a PXE mutation. Mutations associated with PXE maps to the ATP-binding
 cassette transporter ABCC6 (MRP6-Multidrug Resistance associated
 protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165
 kDa protein located in the plasma membrane containing 17 membrane-
 spanning helices grouped into three transmembrane domains. PXE is
 inherited as an autosomal recessive phenotype or appears as a sporadic
 phenotype. PXE is a heritable disorder characterised by mineralisation of
 elastic fibers in skin, arteries and the retina, that result in dermal
 lesions with associated laxity and loss of elasticity, arterial
 insufficiency, cardiovascular disease and retinal haemorrhages leading to
 macular degeneration. The method is useful for screening a population of
 individuals in order to identify individuals with one or more PXE
 associated MRP6 alleles who are then provided with appropriate genetic
 counselling in view of the PXE status. The methods are useful for
 identifying homozygotes, compound heterozygotes or carriers and thus are

QY 1981 GTTGTGCTCCAGTGGGGGAGGGAAGTCCCTCCTGCTGTCGCCCTCTCTTGGGAGCTG 2040
DB 1981 GTTGTGCTCCAGTGGGGGAGGGAAGTCCCTCCTGCTGTCGCCCTCTCTTGGGAGCTG 2040
QY 2041 TCAAAGTGGAGGGGTTGCTGAGCATCGAGGCTGCTGCGCTACGTGCCCCAGAGGCC 2100
DB 2041 TCAAAGTGGAGGGGTTGCTGAGCATCGAGGCTGCTGCGCTACGTGCCCCAGAGGCC 2100
QY 2101 TGGGTGAGAAACACTCTGTGGTGTAGAGAAATGTGTCTCGGGCAGGAGCTGGACCAACC 2160
DB 2101 TGGGTGAGAAACACTCTGTGGTGTAGAGAAATGTGTCTCGGGCAGGAGCTGGACCAACC 2160
QY 2161 TGGGTGAGAGAGTACTAGAAAGCTGTGCCCTGCAGCAGATGTGGAGCTTCCCTGAG 2220
DB 2161 TGGGTGAGAGAGTACTAGAAAGCTGTGCCCTGCAGCAGATGTGGAGCTTCCCTGAG 2220
QY 2221 GGAATCCACACTTCAATTTGGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAAAGCAGCGG 2280
DB 2221 GGAATCCACACTTCAATTTGGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAAAGCAGCGG 2280
QY 2281 CTGAGCCTGGCCCCGGGTGTATACAGAAAGCAGCTGTGTACCTGTGGATGACCCCGTG 2340
DB 2281 CTGAGCCTGGCCCCGGGTGTATACAGAAAGCAGCTGTGTACCTGTGGATGACCCCGTG 2340
QY 2341 GCGGCCCTGGATGCCACAGTGTGGCCAGCATGTCTTCAACCAGGTCAATTGGSCCTGGTGGG 2400
DB 2341 GCGGCCCTGGATGCCACAGTGTGGCCAGCATGTCTTCAACCAGGTCAATTGGSCCTGGTGGG 2400
QY 2401 CTACTCCAGGGAACAAACACAGGATCTCTGACGACACACTCCACATCTTGCCTCAGGCT 2460
DB 2401 CTACTCCAGGGAACAAACACAGGATCTCTGACGACACACTCCACATCTTGCCTCAGGCT 2460
QY 2461 GATTGGATCATAGTGTGGCAATGGGGCATCGCAGAGATGGTTCCTACAGAGGCTT 2520
DB 2461 GATTGGATCATAGTGTGGCAATGGGGCATCGCAGAGATGGTTCCTACAGAGGCTT 2520
QY 2521 CTGCAGAGGAAGGGGCCCTCGTGTGTCTTGGATCAAGCCAGACAGCAGGAGATAGA 2580
DB 2521 CTGCAGAGGAAGGGGCCCTCGTGTGTCTTGGATCAAGCCAGACAGCAGGAGATAGA 2580
QY 2581 GGAGAGGGAACAAAGAACCTGGGACACAGCACCAAGGACCCAGAGACCTCTGCAAGC 2640
DB 2581 GGAGAGGGAACAAAGAACCTGGGACACAGCACCAAGGACCCAGAGACCTCTGCAAGC 2640
QY 2641 AGGAGCCCGAGCTTAGACCGGAGAGTCCATCAAGTCACTGCTGAGAGGACCCGTACC 2700
DB 2641 AGGAGCCCGAGCTTAGACCGGAGAGTCCATCAAGTCACTGCTGAGAGGACCCGTACC 2700
QY 2701 ACTTCAGAGCCCGACAGAGAGTTCCTCTGGATGACCCCTGACAGGGCAGGATGGCCAGCA 2760
DB 2701 ACTTCAGAGCCCGACAGAGAGTTCCTCTGGATGACCCCTGACAGGGCAGGATGGCCAGCA 2760
QY 2761 GGAAGAGCAGCATCCAAATACGGAGGGTGAAGGCCACAGTGCACCTCGGCTACCTCGCT 2820
DB 2761 GGAAGAGCAGCATCCAAATACGGAGGGTGAAGGCCACAGTGCACCTCGGCTACCTCGCT 2820
QY 2821 GCGTGGGACCCCGCTCTGCTGCTAGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
DB 2821 GCGTGGGACCCCGCTCTGCTGCTAGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
QY 2881 TCCTTCTGCGGGGCTACTGGCTGAGCCTGTGGCGGAGCAGACCCCTGCAGTAGTGGGAG 2940
DB 2881 TCCTTCTGCGGGGCTACTGGCTGAGCCTGTGGCGGAGCAGACCCCTGCAGTAGTGGGAG 2940
QY 2941 CAGACGAGCAGCCCTGCTGCTGGGGATCTTCGGGCTCTCTCGGCTCTCTTCCAAAGCCATT 3000
DB 2941 CAGACGAGCAGCCCTGCTGCTGGGGATCTTCGGGCTCTCTCGGCTCTCTTCCAAAGCCATT 3000
QY 3001 GGGCTGTTGCCCTCCATGGCTGGGTGCTCTCTAGTGGGGCCCGGGGATCCAGTTGCTC 3060
DB 3001 GGGCTGTTGCCCTCCATGGCTGGGTGCTCTCTAGTGGGGCCCGGGGATCCAGTTGCTC 3060
QY 3061 TTCCAGAGGCTCTGTGGATGTGGTGGCATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120

DB 3061 TTCCAGAGGCTCTGTGGATGTGGTGGCATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120
QY 3121 ATTGTCACTGCTTAAACCGCTTCTTCAAGGAGACAGACACGCTTGACGTGGACATTTCCA 3180
DB 3121 ATTGTCACTGCTTAAACCGCTTCTTCAAGGAGACAGACACGCTTGACGTGGACATTTCCA 3180
QY 3181 GACAACTCCGGTCCCTGCTGATGTACGGCTTTGGACTCCTTGAGGTACAGCTTGGTGGT 3240
DB 3181 GACAACTCCGGTCCCTGCTGATGTACGGCTTTGGACTCCTTGAGGTACAGCTTGGTGGT 3240
QY 3241 GCAGTGGCTACCCCACTGSCCACTGSGCCATCTCTGCGCACTGTTCTCTCTACGCTGG 3300
DB 3241 GCAGTGGCTACCCCACTGSCCACTGSGCCATCTCTGCGCACTGTTCTCTCTACGCTGG 3300
QY 3301 TTTCAGAGCCTGTATGTGTGTTAGCTCATGCCAGCTGAGACGCTTGAGTACAGCAGCTAC 3360
DB 3301 TTTCAGAGCCTGTATGTGTGTTAGCTCATGCCAGCTGAGACGCTTGAGTACAGCAGCTAC 3360
QY 3361 TCGTCTGTCTGCCATGCTGAGGCTTCCAGGGCAGCACAGTGTGCGGGCATTC 3420
DB 3361 TCGTCTGTCTGCCATGCTGAGACGCTTCCAGGGCAGCACAGTGTGCGGGCATTC 3420
QY 3421 CGAACCCAGGCCCTTGTGCTCAGAACATGCTGCGCTAGATGAAAGCCAGAGGATC 3480
DB 3421 CGAACCCAGGCCCTTGTGCTCAGAACATGCTGCGCTAGATGAAAGCCAGAGGATC 3480
QY 3481 AGTTTCCCGGACTGGTGGCTGACAGTGGCTTGGGGCAATGTGGAGCTCTCTGGGGAAT 3540
DB 3481 AGTTTCCCGGACTGGTGGCTGACAGTGGCTTGGGGCAATGTGGAGCTCTCTGGGGAAT 3540
QY 3541 GGCCTGGTGTTCAGCGCCGACAGTGTGCTGTGAGCAAAAGCCACCTCAGTGTGCTG 3600
DB 3541 GGCCTGGTGTTCAGCGCCGACAGTGTGCTGTGAGCAAAAGCCACCTCAGTGTGCTG 3600
QY 3601 CTCGTGGCTTCT 3660
DB 3601 CTCGTGGCTTCT 3660
QY 3661 CGCAACTGGACAGACTTAGAAGACATCTGTCTCAGTGGAGCGGATGAGGACTATGCC 3720
DB 3661 CGCAACTGGACAGACTTAGAAGACATCTGTCTCAGTGGAGCGGATGAGGACTATGCC 3720
QY 3721 TGGAGCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTGAGCTCAGCCCCCTGGGCT 3780
DB 3721 TGGAGCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTGAGCTCAGCCCCCTGGGCT 3780
QY 3781 CAGGCGGGCAGATCGAGTTCGGGACTTGGGGCTAAGATGCCAGCTGAGCTCCCGCTG 3840
DB 3781 CAGGCGGGCAGATCGAGTTCGGGACTTGGGGCTAAGATGCCAGCTGAGCTCCCGCTG 3840
QY 3841 GCTGTGAGGGCGTGTCTTCAAGATCCACGAGGAGAGGTTGGGCTCCAGGAGGAGG 3900
DB 3841 GCTGTGAGGGCGTGTCTTCAAGATCCACGAGGAGAGGTTGGGCTCCAGGAGGAGG 3900
QY 3901 ACCGGGCGAGGAGTCTCTCTCTGGCAGTGGGCTGCTGGGCTCCAGGAGGAGGAG 3960
DB 3901 ACCGGGCGAGGAGTCTCTCTCTGGCAGTGGGCTGCTGGGCTCCAGGAGGAGGAG 3960
QY 3961 GGTGGGATCTGGATCGAGGGGTGCCCATTTGCCAGCTGGGGCTGCACACACTGGGCTCC 4020
DB 3961 GGTGGGATCTGGATCGAGGGGTGCCCATTTGCCAGCTGGGGCTGCACACACTGGGCTCC 4020
QY 4021 AGGATCAGCATCATCCCCAGGACCCCATCTCTGTCTCTCTCTCTCTCTCTCTCTCTCT 4080
DB 4021 AGGATCAGCATCATCCCCAGGACCCCATCTCTGTCTCTCTCTCTCTCTCTCTCTCTCT 4080
QY 4081 GACCTGTGAGGAGACTCGGAGAGGCTATCTGGGAGCCCTTGGAGAGGCTGAGCTC 4140
DB 4081 GACCTGTGAGGAGACTCGGAGAGGCTATCTGGGAGCCCTTGGAGAGGCTGAGCTC 4140
QY 4141 AAAGCCTTGGTGGCAGCTGCCCGGCGAGCTGAGTACAGTGTGCTGACCGGCGGAG 4200

Db 4141 AAAGCCTTTGGTGGCCAGCCTGCGCCGCCAGCTGCAGTACAGTGTGCTGACCGAGGCGAG 4200
QY 4201 GACCTGAGCGTGGGCGAGAAACAGCTCTCTGTCTGGCACGTGCCCTTCTCGGAGAGACC 4260
Db 4201 GACCTGAGCGTGGGCGAGAAACAGCTCTCTGTCTGGCACGTGCCCTTCTCGGAGAGACC 4260
QY 4261 CAGATCCTCATCTCTGGACGAGGCTACTGCTGCCGTGGACCCCTGGCACGGAGTGCAGATG 4320
Db 4261 CAGATCCTCATCTCTGGACGAGGCTACTGCTGCCGTGGACCCCTGGCACGGAGTGCAGATG 4320
QY 4321 CAGGCGATGCTCGGAGCTGTTTGCACAGTGCACACTGTGCTGCCATATGCCACGCCCTG 4380
Db 4321 CAGGCGATGCTCGGAGCTGTTTGCACAGTGCACACTGTGCTGCCATATGCCACGCCCTG 4380
QY 4381 CGCTCCGTGATGACTGTGCGCGGTTCTGTGTCATGGACAAGGGGCGAGTGCAGAGAC 4440
Db 4381 CGCTCCGTGATGACTGTGCGCGGTTCTGTGTCATGGACAAGGGGCGAGTGCAGAGAC 4440
QY 4441 GGCAGCCCGGCCAGCTGCTGSCCCAGAGAGGCCCTGTTTACAGACTGGCCCCAGGAGTCA 4500
Db 4441 GGCAGCCCGGCCAGCTGCTGSCCCAGAGAGGCCCTGTTTACAGACTGGCCCCAGGAGTCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 7

AD16261
ID AAD16261 standard; cDNA; 4512 BP.

XX AAD16261;

XX AC

XX 19-NOV-2001 (first entry)

XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #6.

XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; mutein; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 1..4512

FT /*tag= a

FT /product= "Human ABCC6 (MRP6) mutant protein"

FT mutation replace (3904, G)

FT /*tag= b

XX WO200162977-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US05741.

XX 23-FEB-2000; 2000US-0184269.

XX (PXEI-) PXE INT INC.

XX (UYHA-) UNIV HAWAII.

XX Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;

XX WPI; 2001-536645/59.

XX P-PSDB; AAE09368.

XX Screening presence of pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid

PS Example 2; Page -; 163pp; English.

XX The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of
CC a PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated
CC protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165
CC kDa protein located in the plasma membrane containing 17 membrane-
CC spanning helices grouped into three transmembrane domains. PXE is
CC inherited as an autosomal recessive phenotype or appears as a sporadic
CC phenotype. PXE is a heritable disorder characterised by mineralisation of
CC elastic fibres in skin, arteries and the retina, that result in dermal
CC lesions with associated laxity and loss of elasticity, arterial
CC insufficiency, cardiovascular disease and retinal haemorrhages leading to
CC macular degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in an
CC amino acid change from Gly to Arg at position 1302 of MRP6 protein.
CC Note: The present sequence is not shown in the specification but is
CC derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA
CC [SED ID NO: 2] shown in page 130-137 of the specification (AAD16231).

XX Sequence 4512 BP; 836 A; 1380 C; 1353 G; 943 T; 0 other;

QY Query Match 99.8%; Score 4497.8; DB 22; Length 4512;

Db Best Local Similarity 99.8%; Pred. No. 0;

QY Matches 4502; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGCTCTGAGCCCTGCGGGGCGAGGGGTCTGGAACACAGAGACGCTGAA 60

Db 1 ATGGCGCGCGCTCTGAGCCCTGCGGGGCGAGGGGTCTGGAACACAGAGACGCTGAA 60

QY 61 CTGCGCGCCACACAGCTGCTGAGCCCTGCTCTCTGAGACAGCAGGGGTCTGGGTACCC 120

Db 61 CTGCGCGCCACACAGCTGCTGAGCCCTGCTCTCTGAGACAGCAGGGGTCTGGGTACCC 120

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QY 181 GGTACTCTCGGATGTCCCCACCTCTTCAAAGCCAAAGATGTGTGGATTGCGCCCTCAT 240

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Db 361 CTGATTACACCGAGAGGAGGAGTCCAGTCACTCTGGAGTGCTGTTGGTTACTGG 420

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Qy	1801	CTGGTCACCTTCTCTGCTGGAAAGATTGACCTTGGTGTCTGTAGACTCAAGTTCTCTCT	1860
Db	1801	CTGGTCACCTTCTCTGCTGGAAAGATTGACCTTGGTGTCTGTAGACTCAAGTTCTCTCT	1860
Qy	1861	GGAAAGCGTCGCGGAAGATTGCATACACATACAGATGCCACCTTGCCTGGTCCCAG	1920
Db	1861	GGAAAGCGTCGCGGAAGATTGCATACACATACAGATGCCACCTTGCCTGGTCCCAG	1920
Qy	1921	GAAGCCCTCCCTGCTCCACAGATAAACCTCACGGTGCCTCAGGGCTGTCTGTGGCT	1980
Db	1921	GAAGCCCTCCCTGCTCCACAGATAAACCTCACGGTGCCTCAGGGCTGTCTGTGGCT	1980
Qy	1981	GTTGTGCGTCCAGTGGGGCAGGGAAGTCTCTCCCTGCTCTCGCCCTCTCTTGGGGAGCTG	2040
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RESULT 8
AADI6262
ID AADI6262 standard; cDNA; 4512 BP.
XX
AC AADI6262;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #7.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
mutant; mutein; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1.4512
FT /*tag= a
FT /product= "Human ABCC6 (MRP6) mutant protein"
FT replace (3907, G)
FT mutation
FT /*tag= b
XX
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Db 1 ATGCGCGCCTGCTGAGCCTCGCGGGCAGGGGCTCTGGAACACAGACAGCCTGAA 60
QY 61 CTTGCGGCACACAGCCTGCTGAGCCTGCTGCTTCCTGAGAACACAGAGGGGCTCTGGGTACCC 120
Db 61 CTTGCGGCACACAGCCTGCTGAGCCTGCTGCTTCCTGAGAACACAGAGGGGCTCTGGGTACCC 120
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Db 121 CCCATGTAACCTCTGGGTCTTGGTCCCATCTACCTTCCTTTCATCCACACCATGGCCGG 180
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QY 3001 GGGCTGTTGGCTCCATGGCTGGGTGCTTCTAGGTGGGGCCGGCATCCAGGTGTGCTC 3060
Db 3001 GGGCTGTTGGCTCCATGGCTGGGTGCTTCTAGGTGGGGCCGGCATCCAGGTGTGCTC 3060
QY 3061 TTCCAGAGGCTCCTGTGGGATGTGGTGGCATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120
Db 3061 TTCCAGAGGCTCCTGTGGGATGTGGTGGCATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120
QY 3121 ATTGGTCACTGTCTAAACGCTTCTCCAGGAGACAGACAGGTTGACGTGGACATTTCCA 3180
Db 3121 ATTGGTCACTGTCTAAACGCTTCTCCAGGAGACAGACAGGTTGACGTGGACATTTCCA 3180
QY 3181 GACAACTCCGTCCTGTGATGACGCTTTGGACTCTTGAGCTCCTTGAGCTCAGCTGTGGTG 3240
Db 3181 GACAACTCCGTCCTGTGATGACGCTTTGGACTCTTGAGCTCCTTGAGCTCAGCTGTGGTG 3240
QY 3241 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTCTGCCACTGTTTCTCTCTACGCTGGG 3300
|||||

Db 3241 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTGCCACTGTTTCTCTCTACGCTGGG 3300
QY 3301 TTTACAGCCCTGTATGTGTAGCTCATGCCAGCTCAGACGCTTGGAGTACAGCCAGCTAC 3360
Db 3301 TTTACAGCCCTGTATGTGTAGCTCATGCCAGCTCAGACGCTTGGAGTACAGCCAGCTAC 3360
QY 3361 TCGTCTGTCTGCTCCACATGGCTGAGAGTTCCAGGGCAGCAGTGTGTCGGGGATTTC 3420
Db 3361 TCGTCTGTCTGCTCCACATGGCTGAGAGTTCCAGGGCAGCAGTGTGTCGGGGATTTC 3420
QY 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAAATGTCTCGGTAGATGAAAGCCAGAGATC 3480
Db 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAAATGTCTCGGTAGATGAAAGCCAGAGATC 3480
QY 3481 AGTTTCCCGACCTGGTGGCTGACAGGTGGCTTGGGCCAAATGTGTGAGTCTCTGGGGAAT 3540
Db 3481 AGTTTCCCGACCTGGTGGCTGACAGGTGGCTTGGGCCAAATGTGTGAGTCTCTGGGGAAT 3540
QY 3541 GGCCTGGTGTGGAGCCGCCACAGTGTGCTGTGCTGACGAAAGCCACCTCAGTGTGCTGC 3600
Db 3541 GGCCTGGTGTGGAGCCGCCACAGTGTGCTGTGCTGACGAAAGCCACCTCAGTGTGCTGC 3600
QY 3601 CTCGTGGCTTCTCTGCTCTGCTGCCCTCCAGGTGACCCAGACACTGCGAGTGGTGT 3660
Db 3601 CTCGTGGCTTCTCTGCTCTGCTGCCCTCCAGGTGACCCAGACACTGCGAGTGGTGT 3660
QY 3661 CGCAACTGGACAGACCTTAGAAACAGCATCTGTCTGAGTGGAGCGGATGAGGACTATGCC 3720
Db 3661 CGCAACTGGACAGACCTTAGAAACAGCATCTGTCTGAGTGGAGCGGATGAGGACTATGCC 3720
QY 3721 TGGAGCCCCAAGGAGGCTCCCTGAGGCTGCCACATGTGACGCTCAGCCCCCTGGCCT 3780
Db 3721 TGGAGCCCCAAGGAGGCTCCCTGAGGCTGCCACATGTGACGCTCAGCCCCCTGGCCT 3780
QY 3781 CAGGCGGGCAGAGTCGAGTTCGGGACTTGGGCTTAAGATGCCAGCTCAGCTCCGCTG 3840
Db 3781 CAGGCGGGCAGAGTCGAGTTCGGGACTTGGGCTTAAGATGCCAGCTCAGCTCCGCTG 3840
QY 3841 GCTGTGACGGCGTGTCTTCAAGATCCACGAGGAGAAAGTGGGATCGTTGGCAGG 3900
Db 3841 GCTGTGACGGCGTGTCTTCAAGATCCACGAGGAGAAAGTGGGATCGTTGGCAGG 3900
QY 3901 ACCGGGCGAGGAAGTCTCCCTGGCCAGTGGGCTGCGGCTCCAGGAGCAGCTGAG 3960
Db 3901 ACCGGGCGAGGAAGTCTCCCTGGCCAGTGGGCTGCGGCTCCAGGAGCAGCTGAG 3960
QY 3961 GGTGGGATCTGGATCGACGGGGTCCCATTTGCCACGTGGGGCTGCACACACTGCGCTCC 4020
Db 3961 GGTGGGATCTGGATCGACGGGGTCCCATTTGCCACGTGGGGCTGCACACACTGCGCTCC 4020
QY 4021 AGGATCAGCATATCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGATGAACCTC 4080
Db 4021 AGGATCAGCATATCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGATGAACCTC 4080
QY 4081 GACCTGTGACGAGCAGCTCGGAGAGGCTATCTGGGAGCCCTTGGAGACGCTGAGCTC 4140
Db 4081 GACCTGTGACGAGCAGCTCGGAGAGGCTATCTGGGAGCCCTTGGAGACGCTGAGCTC 4140
QY 4141 AAAGCCTTGGTGGCAGCCTGCCCGGCGAGCTGACGTACAAAGTGTGCTGACGAGCGAG 4200
Db 4141 AAAGCCTTGGTGGCAGCCTGCCCGGCGAGCTGACGTACAAAGTGTGCTGACGAGCGAG 4200
QY 4201 GACCTGAGCTGGGCCAGAAACAGCTCCTGTGTCTGGCACGCTGCTCCGGAAGACC 4260
Db 4201 GACCTGAGCTGGGCCAGAAACAGCTCCTGTGTCTGGCACGCTGCTCCGGAAGACC 4260
QY 4261 CAGATCCTCATCTCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320
Db 4261 CAGATCCTCATCTCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320
QY 4321 CAGGCCATGCTCGGGAGCTGTTTGGCAGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTG 4380
Db 4321 CAGGCCATGCTCGGGAGCTGTTTGGCAGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTG 4380

Qy	4381	CGTCCGTGATGGACTGTGCCCCGGGTTCTGTGTCATGGACAAGGGGCAGGTGGCAGAGAGC	4440
Db	4381	CGCTCCGTGATGGACTGTGCCCCGGGTTCTGTGTCATGGACAAGGGGCAGGTGGCAGAGAGC	4440
Qy	4441	GGCAGCCCGGCCAGCTGCTGGCCCGACAGAGGGCCTGTTTACAGACTGGCCCCAGGAGTCA	4500
Db	4441	GGCAGCCCGGCCAGCTGCTGGCCCGACAGAGGGCCTGTTTACAGACTGGCCCCAGGAGTCA	4500
Qy	4501	GGCCTGGTTC	4509
Db	4501	GGCCTGGTTC	4509
RESULT	10		
AAID	16264		
ID	AAID16264	standard; cDNA; 4512 BP.	
XX	XX	AAID16264;	
XX	XX	19-NOV-2001 (first entry)	
XX	XX	Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #9.	
XX	XX	Human; prenatal diagnosis: dermal lesion; cardiovascular disease; MRP6;	
KW	KW	Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;	
KW	KW	ATP-binding cassette transporter; arterial insufficiency; chromosome 16;	
KW	KW	Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;	
KW	KW	mutant; muten; ss.	
XX	XX		
OS	OS	homo sapiens.	
OS	OS	Synthetic.	
XX	XX		
PH	PH	Key	
FT	FT	CDS	
FT	FT	Location/Qualifiers	
FT	FT	1..4512	
FT	FT	/tag= a	
FT	FT	/product= "Human ABCC6 (MRP6) mutant protein"	
FT	FT	replace (3961, G)	
FT	FT	/tag= b	
XX	XX		
PN	PN	W0200162977-A2.	
XX	XX		
PD	PD	30-AUG-2001.	
XX	XX		
PF	PF	23-FEB-2001; 2001WO-US05741.	
XX	XX		
PR	PR	23-FEB-2000; 2000US-0184269.	
XX	XX		
XX	XX	(PXEI-) PXE INT INC.	
PA	PA	(UYHA-) UNIV HAWAII.	
XX	XX		
PI	PI	Boyd CD, Csaszar K, Lesaux O, Urban Z, Terry S;	
XX	XX		
DR	DR	WPI; 2001-536645/59.	
DR	DR	P-PSDB; AAE09371.	
XX	XX		
PT	PT	Screening presence of Pseudoxanthoma elasticum mutation useful for	
PT	PT	identifying homozygotes, compound heterozygotes or carriers involves	
PT	PT	determining presence of mutation in MRP6 (ABCC6) nucleic acid	
XX	XX		
PS	PS	Example 2; Page -; 163pp; English.	
XX	XX		
CC	CC	The invention relates to methods and compositions for diagnosing and	
CC	CC	treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological	
CC	CC	dysfunctions. The invention is useful for screening for the presence of	
CC	CC	a PXE mutation. Mutations associated with PXE maps to the ATP-binding	
CC	CC	cassette transporter ABCC6 (MRP6-Multidrug Resistance associated	
CC	CC	protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165	
CC	CC	kDa protein located in the plasma membrane containing 17 membrane-	
CC	CC	spanning helices grouped into three transmembrane domains. PXE is	
CC	CC	inherited as an autosomal recessive phenotype or appears as a sporadic	
CC	CC	phenotype. PXE is a heritable disorder characterised by mineralisation	
CC	CC	elastic fibers in skin, arteries and the retina, that result in dermal	

QY 781 AGTGCAGCCGAGGACACACAGGCAATAGCATTTAAAGGAAGAGCGGCGAGTGGCATG 840
 Db 781 AGTGCAGCCGAGGACACACAGGCAATAGCATTTAAAGGAAGAGCGGCGAGTGGCATG 840
 QY 841 AAGGCTCCAGAGACCGAGCCCTTCCCTACGGCAAGAGGAGGAGCCAGTGGCGCCCACTGCTG 900
 Db 841 AAGGCTCCAGAGACCGAGCCCTTCCCTACGGCAAGAGGAGGAGCCAGTGGCGCCCACTGCTG 900
 QY 901 AAGGCCATCTGGCAGAGTGTTCATTTACCTTCTCTCTGGGAGCCCTCAAGCCCTCATCATC 960
 Db 901 AAGGCCATCTGGCAGAGTGTTCATTTACCTTCTCTCTGGGAGCCCTCAAGCCCTCATCATC 960
 QY 961 AATGATGTCCTTACGTTCACTGTCCTCCCAAGCTGCTCAGCCCTTTTCTGGAGTTATTTGGT 1020
 Db 961 AATGATGTCCTTACGTTCACTGTCCTCCCAAGCTGCTCAGCCCTTTTCTGGAGTTATTTGGT 1020
 QY 1021 GATCCCAAGCCTCCAGCCTGGAAGGCTTACTCTCTCGCCGTGCTGATGTTCTCTCAGCC 1080
 Db 1021 GATCCCAAGCCTCCAGCCTGGAAGGCTTACTCTCTCGCCGTGCTGATGTTCTCTCAGCC 1080
 QY 1081 TGGCTGCAACAGCTGTTGTAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
 Db 1081 TGGCTGCAACAGCTGTTGTAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
 QY 1141 TTGGGTTCGCCATCACTGGCCCTGGGTACAGAAAGTCTGCTCTGTCAGCGGCTCC 1200
 Db 1141 TTGGGTTCGCCATCACTGGCCCTGGGTACAGAAAGTCTGCTCTGTCAGCGGCTCC 1200
 QY 1201 AGAAGGCCAGTGGGTGATGTTGGTCAATCTGCTGTCGCTGGAGCTGCAGCGGCTG 1260
 Db 1201 AGAAGGCCAGTGGGTGATGTTGGTCAATCTGCTGTCGCTGGAGCTGCAGCGGCTG 1260
 QY 1261 ACCGAGAGCCTCTTACCTCAACGGGCTGTGGTGTGCTCTGCTGTGGATGCTGTGCTG 1320
 Db 1261 ACCGAGAGCCTCTTACCTCAACGGGCTGTGGTGTGCTCTGCTGTGGATGCTGTGCTG 1320
 QY 1321 TTGCTCTATCTTGGCAGCTCTTGGGCGCTCCGCGCTCACTGCTGCTGCTTCTTCTG 1380
 Db 1321 TTGCTCTATCTTGGCAGCTCTTGGGCGCTCCGCGCTCACTGCTGCTGCTTCTTCTG 1380
 QY 1381 AGCCTCTCTCTGATTTCTTCTATCTCCAAAGAAAGAACACCATCAGGAGGACAA 1440
 Db 1381 AGCCTCTCTCTGATTTCTTCTATCTCCAAAGAAAGAACACCATCAGGAGGACAA 1440
 QY 1441 ATGAGGAGAAAGACTCACGGGACGGCTCACAGCTCTATCTCAGGAACCTCGAAGACC 1500
 Db 1441 ATGAGGAGAAAGACTCACGGGACGGCTCACAGCTCTATCTCAGGAACCTCGAAGACC 1500
 QY 1501 ATCAAGTTCCATGCTGGGAGGAGCTTTCTGACAGAGTCTTGGGATCCGAGGCGCAG 1560
 Db 1501 ATCAAGTTCCATGCTGGGAGGAGCTTTCTGACAGAGTCTTGGGATCCGAGGCGCAG 1560
 QY 1561 GAGCTGGGCGCTTGGGAGCTCCGGGCTCTCTTCTGCTGCTGCTGCTGCTTCCAA 1620
 Db 1561 GAGCTGGGCGCTTGGGAGCTCCGGGCTCTCTTCTGCTGCTGCTGCTGCTTCCAA 1620
 QY 1621 GTGCTACATTTCTGGTTCGACCTGGGTGTTGCTGTGCTCAGACTCTGCTGGGCGGAGAT 1680
 Db 1621 GTGCTACATTTCTGGTTCGACCTGGGTGTTGCTGTGCTCAGACTCTGCTGGGCGGAGAT 1680
 QY 1681 GCTATGAATCGAGAAAGCTTTGTGACTCTCAGAGTCTCAGAGTCTTCAACAGGCC 1740
 Db 1681 GCTATGAATCGAGAAAGCTTTGTGACTCTCAGAGTCTCAGAGTCTTCAACAGGCC 1740
 QY 1741 CAGGCTTTCTGCTGCT 1800
 Db 1741 CAGGCTTTCTGCTGCT 1800
 QY 1801 CTGGTCACTTCTCTGCTTGGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 Db 1801 CTGGTCACTTCTCTGCTTGGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860

QY 1861 GGAAGCGCTGCGGGAAGGATTTGCATACCATACACAGTGCACACCTTCCCTGCTGCCAG 1920
 Db 1861 GGAAGCGCTGCGGGAAGGATTTGCATACCATACACAGTGCACACCTTCCCTGCTGCCAG 1920
 QY 1921 GAAAGCCCTCCCTGCTCCACAGAAATAACCTTCACGGTGCCTCCAGGGCTGTCTGCTGGCT 1980
 Db 1921 GAAAGCCCTCCCTGCTCCACAGAAATAACCTTCACGGTGCCTCCAGGGCTGTCTGCTGGCT 1980
 QY 1981 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 1981 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 QY 2041 TCAAGGTGGAGGGTTCGTGAGCATCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 Db 2041 TCAAGGTGGAGGGTTCGTGAGCATCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 QY 2101 TGGGTGCAAGAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 Db 2101 TGGGTGCAAGAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 QY 2161 TGGCTGGAGAGAGTACTAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 Db 2161 TGGCTGGAGAGAGTACTAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 QY 2221 GGAATCCACACTTCAATTTGGGAGCAGGCGATGAATCTCTCCGAGGCGCAGAGCAGCG 2280
 Db 2221 GGAATCCACACTTCAATTTGGGAGCAGGCGATGAATCTCTCCGAGGCGCAGAGCAGCG 2280
 QY 2281 CTGAGCCTTGGGCGGCTGCTATACAAAGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
 Db 2281 CTGAGCCTTGGGCGGCTGCTATACAAAGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
 QY 2341 GCGGCGCTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
 Db 2341 GCGGCGCTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
 QY 2401 CTACTCCAGGAAACAAACAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
 Db 2401 CTACTCCAGGAAACAAACAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
 QY 2461 GATTGGATCATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
 Db 2461 GATTGGATCATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
 QY 2521 CTGAGAGAGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
 Db 2521 CTGAGAGAGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
 QY 2581 GGAGAAGGAGAAACAAACAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
 Db 2581 GGAGAAGGAGAAACAAACAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
 QY 2641 AGGAGGCGCGGCTTAGACGCGAGAGGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
 Db 2641 AGGAGGCGCGGCTTAGACGCGAGAGGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
 QY 2701 ACTTCAGAAAGCCCAACAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
 Db 2701 ACTTCAGAAAGCCCAACAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
 QY 2761 GGAAGGAGCAGATCCATACGGGAGGCTGAGGCGCAGAGTGCACCTGCTGCTGCTGCTGCTGCTG 2820
 Db 2761 GGAAGGAGCAGATCCATACGGGAGGCTGAGGCGCAGAGTGCACCTGCTGCTGCTGCTGCTGCTG 2820
 QY 2821 GCGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
 Db 2821 GCGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
 QY 2881 TCCCTTCTGCGGGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 Db 2881 TCCCTTCTGCGGGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 QY 2941 CAGACGAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000


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Db 2941 CAGACGCGAGCCCTCGGTGGCGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT 3000
QY 3001 GGGCTGTTTGCCTCCATGGCTCGGTGTCTTCCAGTGGGCGCCGGGCATCCAGGTTGCTC 3060
Db 3001 GGGCTGTTTGCCTCCATGGCTCGGTGTCTTCCAGTGGGCGCCGGGCATCCAGGTTGCTC 3060
QY 3061 TTCAGAGGCTCCTGTGGATGTGGTGGATCTCCATCAGCTTCTTTGAGGGGACACCC 3120
Db 3061 TTCAGAGGCTCCTGTGGATGTGGTGGATCTCCATCAGCTTCTTTGAGGGGACACCC 3120
QY 3121 ATTGCTCACTGTCTAAACCGCTTCTCCAAAGGAGACAGACACGGTTGACGTGGACATTCCA 3180
Db 3121 ATTGCTCACTGTCTAAACCGCTTCTCCAAAGGAGACAGACACGGTTGACGTGGACATTCCA 3180
QY 3181 GACAAACTCCGGTCCCTGCTGATGATACGCTTTGGACTCCTGGAGGTACGCTGTGGTG 3240
Db 3181 GACAAACTCCGGTCCCTGCTGATGATACGCTTTGGACTCCTGGAGGTACGCTGTGGTG 3240
QY 3241 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTCGCCACTGTTCTCTACGCTGGG 3300
Db 3241 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTCGCCACTGTTCTCTACGCTGGG 3300
QY 3301 TTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC 3360
Db 3301 TTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC 3360
QY 3361 TCGTGTGTGCTGCCACATGGCTGAGAGTTCAGAGGCGAGCACAGTGGTCCGGGCATTTC 3420
Db 3361 TCGTGTGTGCTGCCACATGGCTGAGAGTTCAGAGGCGAGCACAGTGGTCCGGGCATTTC 3420
QY 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACATGCTCGGCTAGATGAAGCCAGGAGTAC 3480
Db 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACATGCTCGGCTAGATGAAGCCAGGAGTAC 3480
QY 3481 AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGGCGCAATGTGGAGCTCCTGGGGAAT 3540
Db 3481 AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGGCGCAATGTGGAGCTCCTGGGGAAT 3540
QY 3541 GGCTGTGTGTTTGCAGCCGCGACAGTGTGCTGTGAGCAAGCCACCTCAGTGTGCTGCG 3600
Db 3541 GGCTGTGTGTTTGCAGCTGCCAGTGTGCTGTGAGCAAGCCACCTCAGTGTGCTGCG 3600
QY 3601 CTCGTGGGCTTCTGTCTCTGCTGCTCCCTCCAGGTGACCCACACACTGCAGTGGTGT 3660
Db 3601 CTCGTGGGCTTCTGTCTCTGCTGCTCCCTCCAGGTGACCCACACACTGCAGTGGTGT 3660
QY 3661 CGCAACTGGACAGACTAGAGAACAGCATCGTGTGAGTGGAGCGGATGAGGACTATGCC 3720
Db 3661 CGCAACTGGACAGACTAGAGAACAGCATCGTGTGAGTGGAGCGGATGAGGACTATGCC 3720
QY 3721 TGGAGCCCAAGGAGGCTCCCTGGAGGTGCCCATGTGACAGCTCAGCCCCCTGGGCT 3780
Db 3721 TGGAGCCCAAGGAGGCTCCCTGGAGGTGCCCATGTGACAGCTCAGCCCCCTGGGCT 3780
QY 3781 CAGGCGGGCAGACTGAGTCCGGGACTTGGGCTTAAGTGCAGCTCAGCTCCGCTG 3840
Db 3781 CAGGCGGGCAGACTGAGTCCGGGACTTGGGCTTAAGTGCAGCTCAGCTCCGCTG 3840
QY 3841 GCTGTGACAGGCGTGTCTTCAAGATCCACGAGGAGAGAGTGGGATCGTTGGCAGG 3900
Db 3841 GCTGTGACAGGCGTGTCTTCAAGATCCACGAGGAGAGAGTGGGATCGTTGGCAGG 3900
QY 3901 ACCGGGCGAGGAAAGTCTCCTCGCCAGTGGGCTGTGCGGCTCCAGGAGCAGCTGAG 3960
Db 3901 ACCGGGCGAGGAAAGTCTCCTCGCCAGTGGGCTGTGCGGCTCCAGGAGCAGCTGAG 3960
QY 3961 GGTGGATCTGGATCAGCGGGTCCCAATTGCCACGTGGGCTGCACACACTGCGCTCC 4020
Db 3961 AGTGGGATCTGGATCAGCGGGTCCCAATTGCCACGTGGGCTGCACACACTGCGCTCC 4020
QY 4021 AGGATCAGCATCATCCCGCAGGACCCCATCTGTTCCCTGCTGCTCTCGGATGAACCTC 4080
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Db 4021 AGGATCAGCATCATCCCCAGGACCCCATCTCTTCCCTGGCTCTCTCGGATGAACCTC 4080
QY 4081 GACCTCTGCAGGAGCACTCGGACAGGCTATCTGGGACGCCCTTGGAGAGCGGTGCAGCTC 4140
Db 4081 GACCTCTGCAGGAGCACTCGGACAGGCTATCTGGGACGCCCTTGGAGAGCGGTGCAGCTC 4140
QY 4141 ARAAGCCTTGGTGGCCAGCCTGCCGCCAGCTGCAGTGTGCTGACCCAGGCGAG 4200
Db 4141 ARAAGCCTTGGTGGCCAGCCTGCCGCCAGCTGCAGTGTGCTGACCCAGGCGAG 4200
QY 4201 GACCTCAGCCTGGCCAGAAACAGCTCCTGTGTGGCAGCTGCCCTTCTCCGGAAGACC 4260
Db 4201 GACCTCAGCCTGGCCAGAAACAGCTCCTGTGTGGCAGCTGCCCTTCTCCGGAAGACC 4260
QY 4261 CAGATCCTCATCTCGACGAGGCTACTGTGCGGTGGACCTGGCAGCGAGCTGCAGATG 4320
Db 4261 CAGATCCTCATCTCGACGAGGCTACTGTGCGGTGGACCTGGCAGCGAGCTGCAGATG 4320
QY 4321 CAGGCCATGCTCGGAGCTGGTTGGCAGTGTGCAGTGTGCTGCCATTTGCCACCGCTG 4380
Db 4321 CAGGCCATGCTCGGAGCTGGTTGGCAGTGTGCAGTGTGCTGCCATTTGCCACCGCTG 4380
QY 4381 CGCTCCGTGATGACGTGTGCCCGGTTCTGTATGACAAAGGGGAGGTGGCAGAGAGC 4440
Db 4381 CGCTCCGTGATGACGTGTGCCCGGTTCTGTATGACAAAGGGGAGGTGGCAGAGAGC 4440
QY 4441 GGCAGCCCGGCCAGCTGTGTGGCCCGCAGAGAGGCTGTTTTACAGACTGGCCCGAGGATCA 4500
Db 4441 GGCAGCCCGGCCAGCTGTGTGGCCCGCAGAGAGGCTGTTTTACAGACTGGCCCGAGGATCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 11
AAD16259
ID AAD16259 standard; cdna; 4511 BP.
XX
XX AAD16259;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cdna #4.
XX
XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
XX mutant; mutein; ss.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200162977-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US05741.
XX
XX 23-FEB-2000; 2000US-D184269.
XX
XX (PXE-) PXE INT INC.
XX (UYHA-) UNIV HAWAII.
XX
XX Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX
XX WPI; 2001-536645/59.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
XX identifying homozygotes, compound heterozygotes or carriers involves
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid -
```


Qy	1681	GCTATGAATGCAGAGAAAGCCCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAGGCC	1740
Db	1681	GCTATGAATGCAGAGAAAGCCCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAGGCC	1740
Qy	1741	CAGGCTTTCTTGCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGCTCTTGACCTT	1800
Db	1741	CAGGCTTTCTTGCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGCTCTTGACCTT	1800
Qy	1801	CTGCTCACCTTCTCTGCTGTGGAAGAAGTTGACCTTGTGCTGATAGACTCAAGTTTCTCT	1860
Db	1801	CTGCTCACCTTCTCTGCTGTGGAAGAAGTTGACCTTGTGCTGATAGACTCAAGTTTCTCT	1860
Qy	1861	GGAAGCGCTGCCGGAAGATTTGCATACCACTACACAGTGCACACTTCGCTTGGTCCACAG	1920
Db	1861	GGAAGCGCTGCCGGAAGATTTGCATACCACTACACAGTGCACACTTCGCTTGGTCCACAG	1920
Qy	1921	GAAGCCCTCCCTGCCTCCACAGATAAACCTCACGGTGCCTCCAGGGCTGTCTGTGGCT	1980
Db	1921	GAAGCCCTCCCTGCCTCCACAGATAAACCTCACGGTGCCTCCAGGGCTGTCTGTGGCT	1980
Qy	1981	GTTGTGCGTGCAGTGGGGCAGGGAAGTCTCCCTGCTCTCCGCCCTCTCTTGGGGAGCTG	2040
Db	1981	GTTGTGCGTGCAGTGGGGCAGGGAAGTCTCCCTGCTCTCCGCCCTCTCTTGGGGAGCTG	2040
Qy	2041	TCAAAGTGGAGGGTTCTGTGAGCATCAGAGGTGCTGTGGCCCTAGCTGCCCCAGGAGGCC	2100
Db	2041	TCAAAGTGGAGGGTTCTGTGAGCATCAGAGGTGCTGTGGCCCTAGCTGCCCCAGGAGGCC	2100
Qy	2101	TGGGTGCAGACACCTCTGTGGTACAGAAATGTGTGCTTCGGGCAGGAGCTGAGCCACCC	2160
Db	2101	TGGGTGCAGACACCTCTGTGGTACAGAAATGTGTGCTTCGGGCAGGAGCTGAGCCACCC	2160
Qy	2161	TGGCTGGAGAGAGTACTAGAACCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG	2220
Db	2161	TGGCTGGAGAGAGTACTAGAACCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG	2220
Qy	2221	GGAATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAGCAGCGG	2280
Db	2221	GGAATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAGCAGCGG	2280
Qy	2281	CTGAGCCTGGCCCGGCTGTATACAGAAAGCAGCTGTCTACTGCTGGATGACCCCTTG	2340
Db	2281	CTGAGCCTGGCCCGGCTGTATACAGAAAGCAGCTGTCTACTGCTGGATGACCCCTTG	2340
Qy	2341	CGGGCCCTGGATGCCACCTTGGCCAGCATGTCTTCAACCAGGTCTAATGGGCTTGTGGG	2400
Db	2341	CGGGCCCTGGATGCCACCTTGGCCAGCATGTCTTCAACCAGGTCTAATGGGCTTGTGGG	2400
Qy	2401	CTACTCAGGGAAACAAACCGGATTTCTGTGACGACGCACTCCACATCTCTGCCCAAGCT	2460
Db	2401	CTACTCAGGGAAACAAACCGGATTTCTGTGAGCGACGCACTCCACATCTCTGCCCAAGCT	2460
Qy	2461	GATTGGATCATAGTCTGCAAAATGGGGCCATCGCAGAGATGGGTTCTTACACAGGAGCTT	2520
Db	2461	GATTGGATCATAGTCTGCAAAATGGGGCCATCGCAGAGATGGGTTCTTACACAGGAGCTT	2520
Qy	2521	CTGACAGGAAGGGGCCCTCTGTGCTTCTGTGATCAAGCCAGACAGCCAGAGATAGA	2580
Db	2521	CTGACAGGAAGGGGCCCTCTGTGCTTCTGTGATCAAGCCAGACAGCCAGAGATAGA	2580
Qy	2581	GGAGAAGGAGAAACAGAACTGGGACCAAGCAACAGGACCCAGAGGCACTCTGAGGC	2640
Db	2581	GGAGAAGGAGAAACAGAACTGGGACCAAGCAACAGGACCCAGAGGCACTCTGAGGC	2640
Qy	2641	AGGAGGCCGAGCTTTAGACGCCAGGAGTCCATCAAGTCACTCAGTAGGACCCGTACC	2700
Db	2641	AGGAGGCCGAGCTTTAGACGCCAGGAGTCCATCAAGTCACTCAGTAGGACCCGTACC	2700
Qy	2701	ACTTCAGAGCCACAGACAGAGTTCCTCTGTGATGACCTTGACAGGCGAGATGSCCAGCA	2760
Db	2701	ACTTCAGAGCCACAGACAGAGTTCCTCTGTGATGACCTTGACAGGCGAGATGSCCAGCA	2760
Qy	2761	GGAAAAGGACAGCATCCAATACGGCAGGGTGTGAAGGCCACAGTGCACCTGGCCCTACTCGCT	2820

Db	2761	GGAAAGGACAGCATCCAATACGCGACGGGTGAAGCCACACAGTGCACCTGGCCTACCTCGGT	2820
Qy	2821	GCGGTGGGACACCCCTCTGCGCTCTACGCACTCTTCTCTCTCTCTGCGGAGCAAGTGCGC	2880
Db	2821	GCGGTGGGACACCCCTCTGCGCTCTACGCACTCTTCTCTCTCTCTGCGGAGCAAGTGCGC	2880
Qy	2881	TCCTTCTGCGGGGCTACTGGCTGAGCCTGTGGCGGACACACCTGCGAGTAGGTGGGCAG	2940
Db	2881	TCCTTCTGCGGGGCTACTGGCTGAGCCTGTGGCGGACACACCTGCGAGTAGGTGGGCAG	2940
Qy	2941	CAGACGACGACCCCTCGGTGGCGGGATCTTGGGGCTCCTCGGCTCTCTCCCAAGCCATT	3000
Db	2941	CAGACGACGACCCCTCGGTGGCGGGATCTTGGGGCTCCTCGGCTCTCTCCCAAGCCATT	3000
Qy	3001	GGGCTCTTTGGCTCCCATGGCTCGGGTGCTCCTAGTGGGCGCGGGCATCCAGTTGCTC	3060
Db	3001	GGGCTCTTTGGCTCCCATGGCTCGGGTGCTCCTAGTGGGCGCGGGCATCCAGTTGCTC	3060
Qy	3061	TTCCAGAGGCTCCTGTGGATGTGGTGCATCTCCATCAGTCTTTTGAAGCGACACCC	3120
Db	3061	TTCCAGAGGCTCCTGTGGATGTGGTGCATCTCCATCAGTCTTTTGAAGCGACACCC	3120
Qy	3121	ATTGCTACCTGCTAAACCGCTTCTCCAAGGACAGACACGGTTGACGTGGACATTTCCA	3180
Db	3121	ATTGCTACCTGCTAAACCGCTTCTCCAAGGACAGACACGGTTGACGTGGACATTTCCA	3180
Qy	3181	GACAACTCGGTCCTGCTGATGTAGCCCTTTGGACTCTCGAGGTCAGCCTGGTGGT	3240
Db	3181	GACAACTCGGTCCTGCTGATGTAGCCCTTTGGACTCTCGAGGTCAGCCTGGTGGT	3240
Qy	3241	GCACTGGCTACCCACTGGCCACTGTGGCCACTCTGCCACTGTTCTCTCTACGCTGG	3300
Db	3241	GCACTGGCTACCCACTGGCCACTGTGGCCACTCTGCCACTGTTCTCTCTACGCTGG	3300
Qy	3301	TTTCAGAGCTGTATGTGGTTAGCTCATGCCAGCTGAGAGCTTGGAGTCAGCCAGCTAC	3360
Db	3301	TTTCAGAGCTGTATGTGGTTAGCTCATGCCAGCTGAGAGCTTGGAGTCAGCCAGCTAC	3360
Qy	3361	TCGCTGTCTGCTCCACATGGCTGAGACCTTCCAGGGCAGCAGTGGTCCGGGCATTC	3420
Db	3361	TCGCTGTCTGCTCCACATGGCTGAGACCTTCCAGGGCAGCAGTGGTCCGGGCATTC	3420
Qy	3421	CGAACCCAGGCCCTTTTGGGCTCAGAACATGTCTCGGTAGATGAAGCCAGAGGATC	3480
Db	3421	CGAACCCAGGCCCTTTTGGGCTCAGAACATGTCTCGGTAGATGAAGCCAGAGGATC	3480
Qy	3481	AGTTTCCCGGACTGGTGGCTGACAGGTGGCTTCCGGCCCAATGTGGAGCTCTTGGGAAT	3540
Db	3481	AGTTTCCCGGACTGGTGGCTGACAGGTGGCTTCCGGCCCAATGTGGAGCTCTTGGGAAT	3540
Qy	3541	GGCTTGGTGTTCAGCGCCGACGTGCTGTGCTGAGCAAAAGCCACCTCAGTGCCTGGC	3600
Db	3541	GGCTTGGTGTTCAGCGCTGCCAGCTGTGCTGAGCAAAAGCCACCTCAGTGCCTGGC	3600
Qy	3601	CTCGTGGCTTCTCTGTCTGTCTGCCCTCCAGTGCAGCCAGACACTGCAGTGGGTTGTT	3660
Db	3601	CTCGTGGCTTCTCTGTCTGTCTGCCCTCCAGTGCAGCCAGACACTGCAGTGGGTTGTT	3660
Qy	3661	CGCACTGGACACACCTTAGAAGACAGCATCGTGTCACTGGAGCGGATGCAGGACTATGCC	3720
Db	3661	CGCACTGGACACACCTTAGAAGACAGCATCGTGTCACTGGAGCGGATGCAGGACTATGCC	3720
Qy	3721	TGAGCCCAAGAGGCTCCTCGAGGCTGCCACATGTGCAGCTCAGCCCCCTGCGCT	3780
Db	3721	TGAGCCCAAGAGGCTCCTCGAGGCTGCCACATGTGCAGCTCAGCCCCCTGCGCT	3780
Qy	3781	CAGGGCGGCGAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTG	3840
Db	3780	CAGGGCGGCGAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTG	3839
Qy	3841	GCTGTGACAGGCGTGCTCTTCAAGATCCAGCAGGAGAGAGGTGGGCATCGTTGGCAGG	3900

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Db 3940 GCTGTGTCAGGGGCTGCTCTTCAAGATCCACGCGAGGAGAGAGTGGGCATCGTTGGCAGG 3899
QY 3901 ACCGGGCGCAGGGAAGTCTCCCTGGCGCAGTGGCTGCTGCGGTCTCCAGGAGGACAGCTGAG 3960
Db 3900 ACCGGGCGCAGGGAAGTCTCCCTGGCGCAGTGGCTGCTGCGGTCTCCAGGAGGACAGCTGAG 3959
QY 3961 GGTGGGATCTGGATCAGCAGGGGGTCCCAATTGGCCACGTGGGGCTGTCACACACTGCGCTCC 4020
Db 3960 GGTGGGATCTGGATCAGCAGGGGGTCCCAATTGGCCACGTGGGGCTGTCACACACTGCGCTCC 4019
QY 4021 AGGATCAGCATATATCCCCAGGACCCATCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4080
Db 4020 AGGATCAGCATATATCCCCAGGACCCATCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4079
QY 4081 GACCTGCTGACGAGCACTCGGACGAGGCTATCTGGGACGCCCTGGAGACGGTGCAGCTC 4140
Db 4080 GACCTGCTGACGAGCACTCGGACGAGGCTATCTGGGACGCCCTGGAGACGGTGCAGCTC 4139
QY 4141 AAGCCCTTGGTGCCAGCCTGCGCCGACGCTGCAGTACAAAGTGTGCTGACCGAGGCGAG 4200
Db 4140 AAGCCCTTGGTGCCAGCCTGCGCCGACGCTGCAGTACAAAGTGTGCTGACCGAGGCGAG 4199
QY 4201 GACCTGAGGTGGGCGAGAAACAGTCTGCTGTGCTGGCAGTGCCTTCTCCGGAAGACC 4260
Db 4200 GACCTGAGGTGGGCGAGAAACAGTCTGCTGTGCTGGCAGTGCCTTCTCCGGAAGACC 4259
QY 4261 CAGATCCTATCTGACGAGGCTACTGCTGCGTGGACCCCTGGCAGGAGTGCAGATG 4320
Db 4260 CAGATCCTATCTGACGAGGCTACTGCTGCGTGGACCCCTGGCAGGAGTGCAGATG 4319
QY 4321 CAGGCGCATGCTCGGAGCTGCTTTCACAGTGCACATGTGCTGCCATGTCGCCACCGCTG 4380
Db 4320 CAGGCGCATGCTCGGAGCTGCTTTCACAGTGCACATGTGCTGCCATGTCGCCACCGCTG 4379
QY 4381 CGCTCGTGATGACTGTGCGCGGGTTCCTGGTCAATGGACAAGGGGCAAGTGGCAGAGAGC 4440
Db 4380 CGCTCGTGATGACTGTGCGCGGGTTCCTGGTCAATGGACAAGGGGCAAGTGGCAGAGAGC 4439
QY 4441 GGCAGCGCGCGCAGCTGCTGCCAGAGAGGCGCTGTTTACAGACTGGCCCGAGGAGTCA 4500
Db 4440 GGCAGCGCGCGCAGCTGCTGCCAGAGAGGCGCTGTTTACAGACTGGCCCGAGGAGTCA 4499
QY 4501 GGCCTGGTC 4509
Db 4500 GGCCTGGTC 4508

RESULT 12
ID ABK62572
XX ABK62572 standard; cDNA; 5728 BP.
AC ABK62572;
XX ABK62572;
DT 18-JUN-2002 (first entry)
XX
DE Rat sequence differentially expressed in response to a hepatotoxin #479.
XX
KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW differential expression; centrilobular necrosis; steatosis.
XX
OS Rattus norvegicus.
XX
PN WO200210453-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US23872.
XX
PR 31-JUL-2000; 2000US-222040P.
PR 02-NOV-2000; 2000US-244880P.
PR 11-MAY-2001; 2001US-290029P.
PR 15-MAY-2001; 2001US-290645P.
PR 22-MAY-2001; 2001US-292336P.
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PR 06-JUN-2001; 2001US-295798P.
PR 13-JUN-2001; 2001US-297457P.
PR 19-JUN-2001; 2001US-298884P.
PR 09-JUL-2001; 2001US-303459P.
XX (GENE-) GENE LOGIC INC.
XX Mendrick D, Porter MW, Johnson KR, Castile AL, Elashoff MR;
PI WPI; 2002-241625/29.
XX
DR Predicting toxic effects of compounds or the progression of these toxic
XX effects by determining the changes in gene expression in tissues or
PT cells exposed to the toxin and comparing these to gene expression in
PT unexposed tissues or cells -
XX
PS Claim 1; Seq ID No 479; 239pp; English.
XX
CC The invention relates to methods for predicting toxic effects of
CC compounds or the progression of these toxic effects by determining the
CC global changes in gene expression in tissues or cells exposed to the
CC toxin and comparing these to gene expression in unexposed tissues or
CC cells. Also included are methods of predicting at least one toxic
CC effect of a compound or progression of a toxic effect, preferably the
CC hepatotoxicity of a compound, comprising detecting the level of
CC expression in a tissue or cell sample exposed to the compound of two or
CC more genes listed in the specification, where differential expression of
CC the genes is indicative of at least one toxic effect or progression.
CC The method can also be used to identify an agent which modulates the
CC toxic response and predict cellular pathways that a compound modulates
CC in a cell. The methods utilise a set of at least two probes (on a solid
CC support in kit form), where each of the probes comprises a sequence that
CC specifically hybridises to a gene listed in the specification, a computer
CC system comprising a database containing information identifying the
CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC set of genes comprising at least two genes listed in the specification,
CC and a user interface to view the information used to present information
CC identifying the expression level in a tissue or cell of at least one gene
CC listed in the specification. The method is useful for elucidating global
CC changes in gene expression and for identifying toxicity markers in
CC tissues or cell exposed to a known toxin. The genes may be used as
CC toxicity markers in drug screening and toxicity assays. The genes and
CC gene expression information may be used as diagnostic markers for the
CC prediction or identification of the physiological state of tissue or cell
CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterised by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.
XX
SQ Sequence 5728 BP; 1092 A; 1676 C; 1663 G; 1297 T; 0 other;
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Query Match 67.2%; Score 3030; DB 24; Length 5728;
Best Local Similarity 80.3%; Pred. No. 0;
Matches 3629; Conservative 0; Mismatches 850; Indels 39; Gaps 5;

QY 1 ATGCGCGCGCTGCTGAGCCCTGCGCGGCGCAGGGGCTCTGGAACACAGACAGAGCTGAA 60
Db 43 ATGCGCGCGCTGAGAGAGTCTTGGCGAGGCTGTGGAGGCTGTGGAACACAGACAGAGAG 102
QY 61 CCTGCGCGCCACACAGCCCTGCTGAGCCTGCTGCTTCTCTGAGACAGCAGGGGTCTGGGTACCC 120
Db 103 CTGTGGCCTATCATTGCTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
QY 121 CCCATGTACCTCTGGGTCTTGGTCCCATCTACCTCTCTTCTATCCACACAGCATGGCGGG 180
Db 163 CCCATGTACCTCTGGGTCTTGGCCTCATCTACCTCTCTTCTATCCATCCATCGCGCTGTC 222
QY 181 GGTACTCTCGGATGTCCTCCACTCTTCAAAGCCCAAGATGGTGTGATTCGCCCTCAT 240
Db 223 TGCTACTCTCGGATGTCCTCCGCTCTTCAAATCAAAATGAGTGTGCTGCTGCTGCTGCTGCT 282
QY 241 GTCTGTGTACCTCCAGCGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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Db 283 CTCTCTACACCTTCAACGCGGCGCTGCTCTCTGGAGGATCCACGGGGCATGCCCGAG 342
Qy 301 GCCCAGAAATCCTCATTCCTACTCTGTGGCTCACCACGATGAGCTTCCAGTGTTC 360
Db 343 GCCCAGAGCTTCTCATTCACCTTACCCTGTGGCTCACCACCATGAGCTTCCACCTTC 402
Qy 361 CTGATTCACACGAGAGAAAGAGAGTCCAGTCTATCTGGAGTGTCTGTTGGTTACTGG 420
Db 403 CTGATCCACATGGAGAGAAAGAGGGGTCCGTGCACTGGGTGTTGTTGGGTACTGG 462
Qy 421 CTCTCTCTGTTGCTTCCAGCTTACCAAGCTGCCAGAGGCTCCGGAGCGGGCTTC 480
Db 463 CTGCTCTGCTGCTGCCAGCCTACACACTGACACTGTCACAGAGGCTCCGCGAGGAGCTTC 522
Qy 481 CAGAGCGACCTGTCCGCCACTGTCCACCTACCTATGCTGTCTCTGGTGTGSCACAG 540
Db 523 GCCCAGGAGCGCCCTCCACCACTGGCCCACTACCTGTGCTGTCTGCTGGTGGCGACAG 582
Qy 541 TTGTGCTGTCTGCTGGCGGATCAACCCCTTCTTCCCTGAAGACCCCGCAGAGTCT 600
Db 583 CTGGTGTCTGTCTGTGTAGACCAAGCCACTTCTTCTCGGAAGACTCCAAAGCCATTG 642
Qy 601 AACCCCTGTCCAGAGCTTGGGAGCCTTCCCTCCAAAGCCACGTTCTGTGGGTGTTCT 660
Db 643 AATCATGTCCAGAGCGCGGCTCTTTTCCCTCCAAAGGCCATGTTCTGGTGGGCTCT 702
Qy 661 GGCCTGGTCTGGAGGGGATCAGAGGCGCACTGACACCAAGACCTCTGGTGTGCTGGG 720
Db 703 GGACTGTATGGAAGGGCTACAGGAACCTGTGGGGCCAAAGACCTCTGGTFCATTGAG 762
Qy 721 AGAGAAAACCTCTCAGAAAGAACTTGTTCCTGGCTGTAAGAGGAGTGGATGAGAAACGCG 780
Db 763 AGAGAAAACCTCTCAGAAAGAACTTGTTCCTGGCTGTAAGAGGAGTGGAGGAGAACTTC 822
Qy 781 AGTCAGCGCCGAGGAGCACAAAGCAATAGCAATTAAGAAAGGCGGCGAGTGGCATG 840
Db 823 AGTCAGCTGCGCGGGGCAC-----AAAGGGCACAGCTGGTATG 858
Qy 841 AAGGCTCAGAGACGAGCCCTCTCTACGCAAGAGGAGCGCACTGGCGCCACTGTG 900
Db 859 GGGACCCCGAGACAGAGGCTCTCTGAGCCAGAGAGGAGCGCGGGCCCGCTGCTC 918
Qy 901 AAGGCATCTGGCAGGTTCATCTTCTACCTTCCTTCCCTGGGACCCCTCAGCCTCATC 960
Db 919 AGGCTATCTGGCGTGTGTTCCGGTCCACTTCTCTGCTGGGAGCCCTCAGCCTGTCT 978
Qy 961 AGTATGTCTCAGTTCACATGTCCCAAGCTGTCCAGCTTTTCTGAGTTTATTTGGT 1020
Db 979 AGCGATGCTTTCAGGTTTGTGTTCCCAAGCTCTCTCAGTCTGTTTCTGGAGTTCATGGGC 1038
Qy 1021 GATCCCAAGCCTCCAGCCTGGAAGGCTACCTCTCCGCTGCTGCTGCTCTCAGCC 1080
Db 1039 GACCTCGAGTCTCTGGCTTGGACGGGCTGGCTCTCTGGCTGCTGCTGCTGCTGCTG 1098
Qy 1081 TGCCTGAAAGCGCTTGTGAGCAGACAGAACTGTACAGGCTCAAGGTCCCGCAGATGAG 1140
Db 1099 TGCCTACAGACACTGTTTGAACAGCAGTACATGTACAGATCAAGTCTCGAGATGAG 1158
Qy 1141 TTGGGTGCGGCATCAGTGGCCTGGTGTACAGAAAGTCTTGGCTGTCTCAGCGGCTCC 1200
Db 1159 CTGCGAACAGGCATCAGTGGCCTGGTGTACAGAAAGTCTTGGTCTCTCCAGTGGTTCC 1218
Qy 1201 AGAAGGCGCTGCGGTGGGTGATGTGCTCAATCTGGTGTCCGTGAGCTGCAGCGGCTG 1260
Db 1219 AGAAGTCCAGTGCAGAGGGAGCTGTGCTCACTGGTGTGCTGAGTGCAGTGCAGCGGCTG 1278
Qy 1261 ACCGAGAGCGCTCTACTCTCAAGGGCTGTGGCTGCTCTGCTGTGGATGCTGTCTGCTC 1320
Db 1279 GTCGAGACATCTCCACCTCAAGGGCTGTGGCTGCTCTTCTCTGTGGATCATTTGTGTG 1338
Qy 1321 TFCGTCTATCTGTGGAGCTCTCTGGGGCCCTCCGCGCTCTACTGTGCCATCGCTGTCTCTG 1380
Db 1339 TTTGTCTACCTGTGGCAGCTCTTGGGGCCCTCTGCGCTTCAGCGCGTGTCTCTCTCTG 1398

Qy 1381 AGCTCTCCTCCTCTGAATTTCTTCACTCTCAAGAAAGBAACCACTCAGAGGAGCAA 1440
Db 1399 AGCTTCTCCTCCTCCTGAATTTCTTCACTTACCAGAAGAGGAGCTTCCATCAGAGAACA 1458
Qy 1441 ATGAGCAGAAAGACTCAGGGCAGCGCTCACCAGTCTCTATCTCTCAGGAACTCGAAGACC 1500
Db 1459 ATGAGCAGAAAGGCTTCCCGAGCAGCGCTCACCAGCTCTCATGCTCAGAACTGTGAGAAC 1518
Qy 1501 ATCAAGTTCATGGCTGGGAGGAGCTTCTTGACAGAGTCTCTGGGACTCCGAGGCGCAG 1560
Db 1519 ATCAAGTTCAGGCTGGGAGTGTCTTCTGTGAGGAGCTCTCTGATATATCCGGGCGCAG 1578
Qy 1561 GAGCTGGGCGCTTGGGAGCTCCGCGCTCTCTCTCTGTGTCTGTGTCTCTCTCTCTCT 1620
Db 1579 GAGCTAGGTGGCTGAAGACCTCCGCTTCTCTCTCTGTCTCTCTCTCTCTCTCTCT 1638
Qy 1621 GTGTCTACATTTCTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1677
Db 1639 GTGTCTACATTTCTGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1698
Qy 1678 AATGTATGAATGACAGAAAGCTTGTGTGACTCTCACAGTCTCTCAACATCTCTCAACAAG 1737
Db 1699 AACGCCATGGATCGGAGAAAGGCTTGTGACGCTCAGCGTCTCAGCATCTCTTAACAAA 1758
Qy 1738 GCCCAGGCTTCTCTGCGCTTCTCCATCCACTCTCTGTCAGGCGCGGTGTCTTTGAC 1797
Db 1759 GCCCAGGCTTCTCTGCGCTTCTCTGTGCACTGCTCTGTTCAGGCTCGGGTGTCTTTGAC 1818
Qy 1798 CGTCTGTGTCTCTCTGCTGTGGAAGTGTGACCTCTGTGTCTGTGTGTGTGTGTGTGTGT 1857
Db 1819 CGCTGTGTGTCTCTGCTGTGGAAGTGTGACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1878
Qy 1858 TCTGGAAGCGCTGCGGGAGGATTCATCACCATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1917
Db 1879 TCCAGATGC---TCTCTGGAAGTTCGAATTTCTATACAAATGGCACTCTCGTGTGTGTGT 1935
Qy 1918 CAGGAAGCGCTTCTCTGCTTCCAGAAATAACCTCAGGCTGCCAGGCTGTGTGTGTGTGT 1977
Db 1936 CAGGAGAGCGCGCTTCTGCTGTGCAAGATCAGCTCAGGCTGCCAGGCTGTGTGTGTGTGT 1995
Qy 1978 GCTGT 2037
Db 1996 GCTGT 2055
Qy 2038 CTGTCAAAGTGTGGAGGGTTCGTGACATCGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2097
Db 2056 CTGTGGAAGTGTGAAGGGTCTGTGAGCAITGAGGGTTCGCTGTGTGTGTGTGTGTGTGTGT 2115
Qy 2098 GCTGTGGTGCAGAACACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2157
Db 2116 GCTGTGGTGCAGAAATCTGT 2175
Qy 2158 CCGT 2217
Db 2176 CCATGTTTGCAGGAAGTCTTAGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2235
Qy 2218 GAGGATTCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCCGGAGCGCCAGAGCAG 2277
Db 2236 GCAGGAGTTCACACCCCTAGTGGGAGCAGGGCATGAATCTTCTGTGGGGCCAGAGAGCAG 2295
Qy 2278 CGGCTGT 2337
Db 2296 CGGCTGT 2355
Qy 2338 CTGGCGGCTGT 2397
Db 2356 CTAGCAGCGCTGT 2415
Qy 2398 GGGCTACTCCAGGGAACACAGCGGATTCGTGTGAGCGGCACTCCACATCTCTGCGCCAG 2457
Db 2416 GGACTTCTCCAAAGTACGACTCGGATCTCTGTGAACACACAGCTGTGTGTGTGTGTGTGTGTGT 2475

Db 3288 TATGCTGGGTTTCAGAGCCTCTATGTGGCCACATCTTTGGCAGCTGAGACGCTAGAGTCA 3347
 QY 3352 GCCAGCTACTCGTCTCTGCTGCCACATGCTGAGACGCTTCCAGGCGACACAGTGGTC 3411
 Db 3348 GCGCGTACTCACTGCTGTGTTCCCATATGCTGCTGAGACCTTCCAGGGAAGTGTGGTGC 3407
 QY 3412 CGGGCAATCCGAACCCAGGCGCCCTTTGTGGCTCAGAAATCTCGCGTAGATGAAAGC 3471
 Db 3408 AGGGCCCTCCGGGCCAGGCGCTCTTCAGGCTCAGCAGATGCTCTCATGGATGAGAC 3467
 QY 3472 CAGAGATCAGTTTCCCGGACGCTGTGGCTGACAGTGGCTTGGCGCCAAATGTGGAGCTC 3531
 Db 3468 CAGAGGCTCAGTTTCCCGAACTGTGGCTGACAGTGGCTGGCTACTAACCTGGAGCTT 3527
 QY 3532 CTGGGGAATGGCTGTGTTTCCAGCGCCGCTGCTGTGCTGCTGAGCAAGCCACCTC 3591
 Db 3528 CTAGGGAATGGCTGTGTTTCCAGCGCCGCTGCTGTGCTGCTGAGCAAGGCTCACCTA 3587
 QY 3592 AGTGTCTGGGCTCGTGGGCTTCTGTCTCTGCTGCCCTCAGGTGACCCAGACACTGCAG 3651
 Db 3588 AGTGTCTGGGCTCGTGGGCTTCTCGGCTCTCGCTGCCCTCCAGGTGACACAGACTCTGCAG 3647
 QY 3652 TGGGTTTTCGCACTGACAGACCTAGAGACAGCATGCTGTCACTGAGCGGATGCAG 3711
 Db 3648 TGGGTGTCCGCGAGCTGAGACATCTGAGACAGCATGCTGAGCGGCTGAGCGCTGCAG 3707
 QY 3712 GACTATGCTGGAGCGCCCAAGAGGCTCCCTGAGGCTGCCACATGTCAGCTCAGCC 3771
 Db 3708 GACTAGCTCGATCCCAAGAGGCTCCCTGAGGCTGCCACATGTCAGCTCAGCC 3767
 QY 3772 CCGTGGCTCAGCGGGGCGGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAG 3831
 Db 3768 CTCTGGCTTGTGGGAGCAGATGAGTTCCGGGACTTTGGGCTCAGACACCCAGCAG 3827
 QY 3832 CTCCCGCTGGCTGTGAGGCGCTGCTTCAAGATCCAGCAGGAGAGAGTGGGCATC 3891
 Db 3828 CTGCCCCTTGTGAGGAGTGTCCCTGAAGATCCATGAGGAGAGAGTGGGCATC 3887
 QY 3892 GTTGGCAGCAGCGGGGAGGAGTCTCCCTGGCCAGTGGGCTGTGGGCTCCAGGAG 3951
 Db 3888 GTGGGAGACAGGGGCGGGAGTCTCTCTGGCTTGGGCTGTGGGCTTCAAGAG 3947
 QY 3952 GCAGCTGAGGGTGGGATCTGATGTCAGCGGGTCCCATTTGCCACGCTGGGCTGCACACA 4011
 Db 3948 GCTGCCGAGGGTAATATCTGGATCGATGGGTCCCTATCACCCATGTGGGCTGCACACA 4007
 QY 4012 CTGCGCTCAGGATCAGATCATCCCCAGGACCCCATCTGTTCCTGGCTCTCTGGG 4071
 Db 4008 CTGAGGTCCCGAATACCATCATCTCCCTCAGGACCCCTGTCTGTCCAGGCTCTCTGGG 4067
 QY 4072 ATGAACCTCGACTGTCTGAGGAGCACTCGGAGAGGCTATCTGGCAGCCCTGGAGAGC 4131
 Db 4068 ATGAACCTGAGCTGTCTCAGGAGCACACAGATGAGGCTATCTGGCAGCGCTGGAGACA 4127
 QY 4132 GTGCACTCAAGCCTTGTGTGGCAGCCTGCGCGGCGAGTCAAGTGTGCTGAC 4191
 Db 4128 GTGCACTCAAGCCTTGTGTGACAGCCTGCGCTGCGCAGTCAATGATGATGTGAGGC 4187
 QY 4192 CGAGGAGGAGCTGAGCTGTGGGCGCAGAAACAGCTCTGTGTCTGCGAGTGCCTTCTC 4251
 Db 4188 CAGGGAGATGACTGAGCTGGGTGGGTATTAACAGCTCTGTGCTGCGCAGAGCCCTTCTC 4247
 QY 4252 CGGAAGACCCAGATCTCTATCTTGGAGAGGCTACTGCTGCCGTGGACCTTGGCAGGAG 4311
 Db 4248 CGSAAACCCAGATCTCTATCTTGGAGAGGCGACTGCTCTGTGGACCCAGGAGCAG 4307
 QY 4312 CTGCACTCAGGCGCATGTCTGGGAGCTGGTTTGCAGTGTGACTGTGTGCCCATTTGCC 4371
 Db 4308 ATGCACTCAGGCGCGCTTGGAGCGCTGGTTTACACAGTGTACCTTACTGCTTATCGCT 4367
 QY 4372 CACCGCTCGGCTCCCTGTATGACTGTGCCCGGTTCTGGTATGACAGAGGGGAGGTG 4431
 Db 4368 CACCGCTCGGCTCGGCTGTGAGTGTGCCAGAGTCTTGTATGATGAGGGGAGGTG 4427

QY 4432 GCAGAGCGGACAGCCGCGCCAGCTGTGCGCCAGAGGCGCTGTTTACAGACTGGCC 4491
 Db 4428 GCAGAAAGTGGCAATCTGCTCAGCTGTGCGCCAGAAAGGCGCTGTTTACAGGCTAGCC 4487
 QY 4492 CAGAGTCAGGCGCTGG 4507
 Db 4488 CATGAGTCGGGCTCG 4503

RESULT 14
 AAZ94741
 ID AAZ94741 standard; cDNA; 5011 BP.
 XX AAZ94741;
 AC AAZ94741;
 XX 01-AUG-2000 (first entry)
 DT Human ATP binding cassette ABC1 (MRP1) cDNA.
 XX
 DE ABC1; ATP binding cassette; human; cholesterol; lipid disorder;
 XX atherosclerosis; lipid disorder; dyslipidemia; psoriasis;
 KW lupus erythematosus; diagnosis; gene therapy; MRP1;
 KW multidrug resistance associated protein; chromosome 16q13.12; ss.
 XX Homo sapiens.
 OS
 XX WO200018912-A2.
 PN
 XX 06-APR-2000.
 PD
 XX 21-SEP-1999; 99WO-EP06991.
 PF
 XX 25-SEP-1998; 98US-0101706.
 PR
 XX (FARB) BAYER AG.
 PA
 XX Schmitz G, Klucken J;
 PI WPI; 2000-293151/25.
 DR
 XX Adenosine triphosphate binding proteins useful for identifying agents
 PT for treating atherosclerosis and other inflammatory disorders -
 XX
 XX Claim 9; Page 115-117; 154pp; English.
 XX The present sequence is that of human ATP binding cassette
 CC subfamily C protein ABC1 cDNA. The cDNA was identified using a
 CC differential display method in which monocytes from peripheral
 CC blood were subjected to macrophage differentiation and cholesterol
 CC loading with acetylated low density lipoproteins and subsequent
 CC deloading with high density lipoprotein (HDL3) to identify
 CC cholesterol sensitive genes. The gene maps to chromosome 16q13.12
 CC and is also termed MRP1 (multidrug resistance associated protein).
 CC The invention provides cholesterol-sensitive ABC genes (see
 CC AAZ94734-63). These genes, and polypeptides encoded by them,
 CC can be used for diagnostic and therapeutic applications, and for
 CC biochemical or cell-based assays to screen for pharmacologically
 CC active modulator compounds useful for the treatment of lipid
 CC disorders, atherosclerosis or other inflammatory diseases such as
 CC psoriasis and lupus erythematosus.
 XX
 SQ Sequence 5011 BP; 1063 A; 1499 C; 1394 G; 1055 T; 0 other;

Query Match 27.3%; Score 1229.2; DB 21; Length 5011;
 Best Local Similarity 55.8%; Pred. No. 1.7e-263;
 Matches 2539; Conservative 0; Mismatches 1933; Indels 80; Gaps 7;

QY 36 GTCTGGAACACAGACAGCTGAACTGCGCGCCAGCAGCTGCTGAGCTGTGCTTCT 95
 Db 238 GCTCTGGACTGGAATGTCAGTGGAAATACCAACCCAGCTTCAACGCTTCA 297
 QY 96 GAGAACAGCAGGGGTCTGGGTACCCCATGTACCTCTGGGTCTCTGGTCCCATCTACCT 155

Db 298 GAACACGGTCTCTGTTGGGCTGTTTACCTCGGCCGTGTTCCCTTCTACTT 357
QY 156 CCTCTTCATCCACACCATGGCGGGGCTACCTCCGGATGTCGCCACTTTCACAAAGCAA 215
Db 358 CCTCTATCTCTCCGACATACCGAGGCTACATTCAGATACACCTCTCAACAAACCAA 417
QY 216 GATGGTCTTTGGATTCCGCCCTCATAGTCCCTGTGTACCTCCAGCGTGTCTGCTCTTTG 275
Db 418 AACTGCCCTTGGGATTTTGTGTGGATCTGCTGTGGCAGACCTCTTACTCTTTCTG 477
QY 276 GAAATCCAAACAGGAACGCTCAGGCCCCAGAAATTCCTATTTCATCCTACTGTGTGGCT 335
Db 478 GGAAGAAGTGGGCAATATCTCGGCCCGAGTGTCTGTGTGTCAGCCCACTCTCTTGGG 537
QY 336 CACACAGATGAGCTTCGAGTGTCTTCATGATTCACACCGAGGAGAAAGGAGTCCAGTC 395
Db 538 CATCACACGCTGCTTGTCTACCTTTTAAATTCAGCTGGAGAGGAGGAGTTCAGTC 597
QY 396 ATCTGGAGTCTGTTGGTGTGCTCTCTGCTTGTCTTGTCTTGTCCAGCTACCAACGCTGC 455
Db 598 TTCAGGATCATGCTTCTTCTGCTGTGTGTAGCCCTAGTGTGTGCCCTAGCCATCTCTGAG 657
QY 456 CCAGCAG-----GCCCTCCGAGCGGGCTTCCAGAGCGACCTCTGCGCCACCTGTC 506
Db 658 ATCCAAATATTGACAGCCTTAAAGAGGATGCCAGTGGACCTGTTCTGTGACATCAC 717
QY 507 CACTACCTATGCTCTCTGTGTGTGGACAGTGTGTGCTGTCTGCTGCTGCGGATCA 566
Db 718 TTTCTAGCTACTTTTCCCTCTTACTCATTCAGCTGCTGCTGTCTGCTTCTCAGATCG 777
QY 567 ACCCCCTTCTCCCTGAGACACCCAGAGTCTTAACCCCTGTCCAGAGACTGGGGCAGC 626
Db 778 CTCACCCCTGTTCTCGGAACACCTTCCAGCACCCCTTAATCCCTGCCCAGAGTCCAGCGCTC 837
QY 627 CTTCCTCCCTCAAAAGCAGTCTGTGTGGTCTTCTGGCTGTGTGGAGGGATACAGGAG 686
Db 838 CTTCCTGTGAGGATCACTCTGTGTGGATCAGAGGTGATGTCTCGGGGCTACCGCCA 897
QY 687 GCACGTGAGACCAAGACCTCTGTGTGGTGGAGAGAAACTCTCTCAGAGAACTTGT 746
Db 898 GCCCTTGGAGGCGAGTGACCTCTGTGTCTTAAACAAAGGAGGACACGTCGGAACAGTCGT 957
QY 747 TTCCTGGCTTGAAGAGAGTGGATAGGACGCG-----AGTGACGCCGAGGACACAA 802
Db 958 GCCTGTTTGTGAAGACTTGAAGAGGAATCGCCCAAGACTAGGAAGCAGCCGGTGA 1017
QY 803 AGGCAATAGCATTTAAAGGAAGGCGGAGTGGCATGAAGGCTCCA----- 849
Db 1018 GGTGTGTACTCTCTCAAGGATCTCTCCAGCGCGGAAGAGAGTTCCAAGGTGGATCGAA 1077
QY 850 -----GAGACGAGCCCTCTCTAGCGCAAGAGGAGCGGAGTGGCGCCCACTGCT 899
Db 1078 TGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCAAGTCCCAAGAGGAGTGGAAACCCCTCTGTT 1137
QY 900 GAAGGCCATCTGCAGGTGTTCCATTCTACCTTCTCTTGGGACCCCTCAGCCCTCATCAT 959
Db 1138 TAGGTGTTATACAGACCTTTGGGCGCTTCTTCTCATGAGTCTTCTTCAAGGCCAT 1197
QY 960 CAGTGATGTCTTCAGGTCTCACTGTCTCCCAAGGTGTCTCAGCCTTTTCTTGAGTTTATGG 1019
Db 1198 CCAGGACCTGATGATGTTTTCGGGGCCGAGATCTTAAAGTGTCTCATCAAGTTCGTGAA 1257
QY 1020 TGATCCCAAGCCTCCAGCCTGGAAGGCTTACCTCTCTCGCGCTGTGATGTCTCTCAGC 1079
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QY 1080 CTGCTGCAAAAGCTGTTTGACGACGACACATGTACAGGCTCAAGGTCGCCGAGATGAG 1139
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QY 1140 GTTGGCTCGGCCATCACTTGGCTGTGTACAGAAAGGTCTTGGCTGTCTTCCAGCGGCTC 1199

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QY 1200 CAGAAAGCCAGTGGGCTGGTGTGATGTGTTCAATCTGGTGTCCGTGGAGCTGACGCGGT 1259
Db 1438 CAGAAATCCTCCAGGTCGGGGAGATTCTCAACCTCATGTCTGTGGAGCTCAGAGTT 1497
QY 1260 GACCGAGAGCTCTCTACCTCAACGGGTGTGGCTGCTCTGCTGTGATGCTGTGCTG 1319
Db 1498 CATGGACTTGGCCACGTATCAATGATCTGCTGAGCCCCCTGCAAGTATCATCTTGC 1557
QY 1320 CTTCGTCTATCTCTGGCAGCTCTCGGGCCCTCCGCCCTCACTGCATCGCTCTCTTCT 1379
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Db 1978 TCCCTGAACATTTCTCCCATGGTCTATCAGCAGCATCTGTCAGGCGAGTGTCTCCCTCAA 2037
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DB 2937 TCAGCAGCTCTCTCTCTATAGTGGGACATCAGCAGGACCAACACAGCAGCCAGAAC 2996
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DB 3117 TCTCTCTCAGCATCT 3176
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DB 3177 ATTGGCTCAGCCTCTGAGCTGATGACCCCATCTGTCAGCGGACTCAGGAGCAGCAAG 3236
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DB 3417 ACCGCTTCCAGAGGAGTGGACAGTGGACTCCATCCCGAGGTCAATCAAGATGT 3476
QY 3197 TGCTGATGTAGCCTTTTGGACTCTGGAGGTTCAGCTGTGTGGTGGCTGAGTCCAC 3256
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QY 3317 TGGTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCAGCTACTGCTCTGTCTGTCTCC 3376
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QY 3377 ACATGGCTGAGACGTTTCCAGCGCAGCAGTGTCTCGGGCAATTCGAAACCCAGCCCT 3436
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DB 3957 TGGAAACCAACATCTGTGGCGTGGAGGCTCAAGGAGTATTCAGAGACTGAGAGAGG 4016
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DB 4017 CGCCCTGGCAATCCAGGAGACAGCTCCGCCAGCAGCTGGCCCCAGGTGGGCGGAGTGG 4076
QY 3797 AGTTCCGGACCTTGTGGCTTAAGATGCCAGCTGAGCTCCCGCTGGCTGTGACGGGCTGT 3856
DB 4077 AATTCGGAACCTACTCTCGCTCCGAGAGGACCTGGACTTCTGTTCTCAGGCACATCA 4136
QY 3857 CTTTCAAGATCCACGAGGAGGAGTGGGCTGCTTGGCAGGACCGGGGAGGGAAGT 3916
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QY 3917 CTTCCCTGCGCAGTGGGCTGCTCGGCTCCAGGAGCAGCTGAGGTGGGATCTGATCG 3976
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QY 4337 GCTGGTTTGCAGTGCATGTCTGCCCATTTGCCACCCCTGCGCTCGGTGATGACT 4396
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QY 4397 GTGCCCGGTTCTGGTCATGGACAAGGGGAGGTGGCAGAGAGCGGCCGCCGCCAGC 4456

Db 4677 ACAAGGGTATCTCTTGACAAAGGAGAAATCCAGGAGTACGGCGCCCACTGGACC 4736
 Qy 4457 TGCTGGCCCAAGGGCTGTTTACAGACTGGCCAGGACTAGGCTGT 4508
 Db 4737 TCCTGCACAGAGAGTCTTTTACAGCATGGCCAAAGACGGCGGCTTGGT 4788

RESULT 15
 ABK92125
 ID ABK92125 standard; DNA; 5011 BP.
 XX AC ABK92125;
 XX 15-AUG-2002 (first entry)
 DE Prostate cancer-associated DNA sequence #11.
 XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.
 XX Mammalia.
 XX W0200230268-A2.
 PN 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US32045.
 XX 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Glsh KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 PI WPI; 2002-471335/50.
 DR P-PSDB; ABG61810.
 DR
 XX Detecting a prostate cancer-associated transcript in a cell in a
 PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue
 XX Claim 22; Page 308-309; 436pp; English.
 XX The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridise to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences.
 XX Sequence 5011 BP; 1063 A; 1499 C; 1394 G; 1055 T; 0 other;
 SQ

Query Match 27.3%; Score 1229.2; DB 24; Length 5011;
 Best Local Similarity 55.8%; Pred. No. 1.7e-263;
 Matches 2539; Conservative 0; Mismatches 1933; Indels 80; Gaps 7;
 Qy 36 GGTCTGGAACACAGAGAGCTGAACCTCCGCCACACAGCTGCTGAGCTGTGCTTCT 95
 Db 238 GCTCTGGGACTGGAATGTCACGTGAATACAGCAACCCGACTTCACCAAGTGCATTCA 297
 Qy 96 GAGAACAGCAGGGGTCTGGGTATACCTTCTGGTCTTGGTCCCTACCTACCT 155
 Db 298 GAAACACGGTCCCTGCTGGTGCCTTGTGTTTACCTCTGGGCTGTTTCCCTTCTACTT 357
 Qy 156 CCTCTTATCCACACCATGCGGGGCTACCTCCGGATGTCCCTACTCTTCAAAGCCAA 215
 Db 358 CCTCTATCTCTCCGACATGACCGAGGTACATTCAGATGACACCTCTCAACAAACCAA 417
 Qy 216 GATGTGCTTGATTCGCCCTCATAGTCTGTGTACCTCCAGGTGGCTGCTGCTTTTG 275
 Db 418 AACTGCTTGGATTTTGTCTGTGATCGTCTGGGAGACCTCTTCTACTCTTTCTG 477
 Qy 276 GAAATCCAACAGGGAAGCCTTGAGGCCCAAGATTTCCTCATCTTCTACTGTGTGGCT 335
 Db 478 GGAAGAAAGTCGGGCAATATCTCTGCCCACTGTTTCTGGTCAGCCCACTCTTTGGG 537
 Qy 336 CACACAGATGAGCTTCGCAGATGTTCTGATCACACCGAGAGAAAGAGGATCCAGTC 395
 Db 538 CATCACACGCTGCTTGCTACCTTTTAAATTCAGCTGGAGAGAGGAGGAGTTCAGTC 597
 Qy 396 ATCTGGAGTGTGTTGGTTACTGCTTCTGCTTTGCTTCTTCCAGCTACCAACGCTGC 455
 Db 598 TTCAGGATCATGCTCACTTCTTGCTGTGAGCTGTGTGCTTACGCTTCTGAG 657
 Qy 456 CCAGCAG-----GCCTCCGGAGCGGCTTCCAGAGCACCTGTCCGCCACCTGTC 506
 Db 658 ATCCAAATATATGACAGCCTTAAAGAGAGATGCCACAGGTGAGACTGTTCTGTCATCAC 717
 Qy 507 CACCTACCTATGCTCTGCTGGTGGTGCACAGTTTGTGCTGCTGCTGGCGGATCA 566
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 Qy 567 ACCCCCTTCTTCCCTGAAGACCCCAAGCTTAACCCCTGTCAGAGACTGGGGCAGC 626
 Db 778 CTCACCCCTGTTCTCGGAACCACTCCAGACCTTAATCCCTGCCAGAGATCCAGCGCTTC 837
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 Db 838 CTTCTGTGAGGATCACTTCTGTGGATCACAGGTTGATTGTCCGGGGCTACCGCCA 897
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 Db 898 GCCCTTGAGGGCAGTGACCTCTGCTCTTAAACAAGGAGGACAGCTCGGAACAAGTCGT 957
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 Qy 803 AGGCAATAGACTTTAAAGAAAGCGGCGAGTGGCATGAAGGCTCCA-----849
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 Db 1078 TGAGGAGTGGAGGCTTTGATCGTCAAGTCCCAAGAGAGTGGAAACCCCTCTCTGTT 1137
 Qy 900 GAAGGCATCTGGCAGGTTTCCATTCCTTCTCTCTGGGACCCCTCAGCCTCATCAT 959
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 Qy 960 CAGTGTGTCTTTCAGGTTTACTGTCCCAAGCTGCTCAGCCCTTTTCTGAGGTTTATTGG 1019
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Db 3417 ACCGCTTCTCAAGAGAGCTGGACACAGTGGACTCCATATCCCGAGGTCATCAAGATGT 3476
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Db 3837 CTGCCCTGTTGGGTTGATCTCCAGGCACAGCCTCAGTGTGGCTTGGTGGGCTCTCAG 3896
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QY 4277 ACGAGGCTACTCTCTCCGCTGGAGCCCTGGCAACGAGCTGCAGATGCAGGCCATCTCGGGA 4336
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Job time : 584.826 secs

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:10 : Search time 7426.08 Seconds
(without alignments)
17670.781 Million cell updates/sec

Title: US-09-647-140A-7
Perfect score: 4509
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba:*
- 2: gb_htg:*
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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	4499.4	99.8	4535	9	AF076622	AF076622 Homo sapi
4	3030	67.2	5728	6	AX400803	AX400803 Sequence
5	3030	67.2	5728	10	AB010466	AB010466 Rattus norv
6	3030	67.2	5775	10	RN073038	U73038 Rattus norv
7	3007.2	66.7	4980	6	AX282516	AX282516 Sequence
8	3007.2	66.7	4980	10	AB028737	AB028737 Mus muscu
9	1229.2	27.3	5011	9	HUMMRPX	L05628 Human multi
10	1227.6	27.2	5011	6	AR070199	AR070199 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AF168791
DEFINITION Homo sapiens multi-specific organic anion transporter-E mRNA,
partial cds.
ACCESSION AF168791
VERSION AF168791.1
KEYWORDS GI:5764414
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4509)
AUTHORS Belinsky,M.G. and Kruh,G.D.
TITLE MOAT-E (ARA) is a full length MRP/cMOAT subfamily transporter

JOURNAL expressed in kidney and liver
 Br. J. Cancer (1999). In press
 REFERENCE 2 (bases 1 to 4509)
 AUTHORS Belinsky, M.G. and Kruh, G.D.
 TITLE Direct Submission
 JOURNAL Submitted (13-JUL-1999) Medical Oncology, Fox Chase Cancer Center,
 7701 Burholme Avenue, Philadelphia, PA 18974, USA
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			0;	Gaps
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DEFINITION Sequence 2 from Patent W00162977.
ACCESSION AX282510
VERSION AX282510.1 GI:16609640

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

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SOURCE	Homo sapiens	Db		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	144	CCATGTACCTCTGGGTCTTGGTCCCATCTACCTCTCTTCTATCCACCAACCAATGCGCGG	203
REFERENCE	1 (bases 1 to 4535)	Qy	181	GSCTACCTCGGATCTGCCACTCTTCAAGCAAGATGGTCTGGATTGCGCCCTCATATA
AUTHORS	Kool, M., van der Linden, M., de Haas, M., Baas, F. and Borst, P.	Db	204	GGCTACCTGTGGATGTCCCACTCTTCAAGCAAGATGGTCTGGATTGCGCCCTCATATA
TITLE	Expression of human MRP6, a homologue of the multidrug resistance protein gene MRP1, in tissues and cancer cells	Qy	241	GTCTGTGTACCTCCAGGCTGGCTCTTGGGAAATCCAAAGCAAGCAAGCAAGCAAGCAAG
JOURNAL	Cancer Res. 59 (1), 175-182 (1999)	Db	264	GTCTGTGTACCTCCAGGCTGGCTCTTGGGAAATCCAAAGCAAGCAAGCAAGCAAGCAAG
MEDLINE	99107222	Qy	301	GCCCAGAAATTCCTCATCTACTGTGTGGCTCAACCAAGCAAGCAAGCAAGCAAGCAAG
PUBMED	9892204	Db	324	GCCCAGAAATTCCTCATCTACTGTGTGGCTCAACCAAGCAAGCAAGCAAGCAAGCAAG
REFERENCE	2 (bases 1 to 4535)	Qy	361	CTGATTACACCGAGAGGAAAGGAGTCCAGTCTGAGTCTGTTGGTTACTGG
AUTHORS	Kool, M.	Db	384	CTGATTACACCGAGAGGAAAGGAGTCCAGTCTGAGTCTGTTGGTTACTGG
TITLE	Direct Submission	Qy	421	CTTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
JOURNAL	Submitted (05-JUL-1998) Molecular Biology, The Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands	Db	444	CTTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
FEATURES	Location/Qualifiers	Qy	481	CAGAGGACCTGTCCGCCACCTGTCTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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ORIGIN				
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Best Local Similarity	99.9%; Pred. No. 0;			
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RESULT 5
AB010466

LOCUS AB010466 5728 bp mRNA linear ROD 20-JUN-1998
DEFINITION Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1), complete cds.

ACCESSION AB010466
VERSION AB010466.1 GI:3242457

KEYWORDS multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1).

SOURCE Rattus norvegicus (strain:Sprague-Dawley) adult male liver cdna to mRNA.

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (sites)
Hirohashi,T., Suzuki,H., Ito,K., Ogawa,K., Kume,K., Shimizu,T. and Sugiyama,Y.
Hepatic expression of multidrug resistance-associated protein-like proteins maintained in eisa hyperbilirubinemic rats
Mol. Pharmacol. 53 (6), 1068-1075 (1998)
JOURNAL MEDLINE 98279126
REFERENCE 2 (bases 1 to 5728)
AUTHORS Hirohashi,T.

TITLE Direct Submission
JOURNAL Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceutical Sciences, Tokyo University, Department of Pharmaceutics; Hongo 7-3-1, Bunkyo-ku, Tokyo 113, Japan
(E-mail:hirohashi@sei.izai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045, Fax:81-3-5800-6949)

FEATURES

Location/Qualifiers

Source

1. 5728

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polyA_site

BASE COUNT 1092 a 1676 c 1297 t

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Best Local Similarity 80.3%; Pred. No. 0;

Matches 3629; Conservative 0; Mismatches 850; Indels 39; Gaps 5;

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DB 103 CTGTGGCCATACCTTGTCTCAACCTGTGCTTCCCTGCGAGCGCGGGAGCTGGGTGCC 162

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QY 181 GGTACCTCCGATGTCCCATCTTCAAGCAAGAGAGTGGTGGATTCGGCCCTCAT 240

DB 223 TGCTACCTCCGATGTCCCGCTCTTCAAAATCAAAATGAGTGGTCTGGCCCTCATC 282

QY 241 GTCTGTGTACCTCCAGCGTGGCTGTGCTCTTTGGAAAATCAACAGGGAACGCCCTGAG 300

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RESULT 6

RNU73038

LOCUS

LOCUS Rattus norvegicus liver multidrug resistance-associated protein 6
 NM03050 573 bp MIM# 116443
 DEFINITION Rattus norvegicus liver multidrug resistance-associated protein 6

CONFIDENTIAL

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

(mrp6) mRNA, complete cds.
U73038
U73038.1 GI:4225851

KEYWORDS
SOURCE
ORGANISM

. Rattus norvegicus.
Rattus norvegicus

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Query Match

Best Local Similarity:

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80.38; Pred. No. 0;

80.3%; Pred. No. 0;

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[illegible]

BASE COUNT	970 a	1471 c	1461 g	1078 t
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QY	1441	ATGAG	CGCAGAG	GA	ACTC	ACGGC	ACGGCT	CAC	AGCTCT	1500
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QY	1501	ATCAAG	TTCCAT	TGCT	TGGAG	GGAGCCT	TTCT	TGGAC	AGAGT	1560
DB	1506	ATCAAG	TCCAC	GGCT	TGGAG	GATGCCT	TCT	TGGAG	CGACT	1565
QY	1561	GAGCT	GGGCGCCT	TT	CGGAC	CTCCGGC	CTCT	TCT	TGTGT	1620
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DB	1626	TGTCT	ACATTT	CTG	TGCGCT	TGTGT	TGT	GTCTCC	ACCT	1685
QY	1678	AATGCT	ATGAAT	TCAG	AGAAAG	CCCTTT	TGT	GACTCT	CA	1737
DB	1686	AATGCC	ATGATG	CAG	AGAAAG	CCCTTT	TGT	GACGCT	CA	1745
QY	1738	GCC	AGGCTT	TCC	TCCCTT	CTCA	TCCACT	CCCT	CTG	1797
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DB	1866	TCC	AGCGC	---	TC	CTG	AAAG	ATCG	AA	1922
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DB	1923	CAG	GAAG	CCCC	ACCT	TG	CTG	CA	CGG	1982
QY	1978	GCT	GT	TG	CTG	CTC	AGT	GGG	CG	2037
DB	1983	GCT	GT	TG	GGT	CTC	AGT	GGG	CG	2042
QY	2038	CTG	T	CA	AGG	TG	AGG	GGT	T	2097
DB	2043	CTG	T	CA	AGG	TG	AGG	GGT	T	2102
QY	2098	GC	T	CGG	TG	CA	GA	AG	CT	2157
DB	2103	GC	T	CGG	TG	CA	GA	AG	CT	2162

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RESULT 8
AB028737
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DEFINITION Mus musculus MRP6 mRNA for multidrug resistance-associated protein-6, complete cds.
ACCESSION AB028737
VERSION AB028737.1 GI:5821429
KEYWORDS MRP6; multidrug resistance-associated protein-6.
SOURCE Mus musculus (strain:ddv), male liver cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4980)
AUTHORS Morikawa,A., Suzuki,H., Hirohashi,T. and Sugiyama,Y.
TITLE Mus musculus mRNA for multidrug resistance-associated protein 6 (MRP6), complete cds
JOURNAL Published Only in Databse (1999)
REFERENCE 2 (bases 1 to 4980)
AUTHORS Morikawa,A., Suzuki,H., Hirohashi,T. and Sugiyama,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1999) Akiko Morikawa, University of Tokyo, Graduate School of Pharmaceutical Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:morikawa@sei.zai.f.u.tokyo.ac.jp, Tel:81-3-5802-2045, Fax:81-3-5800-6949)

FEATURES
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ORIGIN

Query Match 27.2%; Score 1227.6; DB 6; Length 5011;
Best Local Similarity 55.8%; Pred. No. 2.9e-221;
Matches 2538; Conservative 0; Mismatches 1934; Indels 80; Gaps 7;

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QY	3137	ACCCTTCTCCAAGGAGACAGACGGTTGACGTGGACATTTCCAGACAAACTCCCGTCCC	3196

Db	3416	ACCGCTTCTCCAGGAGCTGGACACAGTGGACATCCATGATCCCGAGGTCATCAAGATGT	3475
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Db	3476	TCATGGGCTCCCTGTGTTCAACGTATTGGTGCCCTGSCATCTGTTATCTCTGCTGCCACGCCCA	3535
Qy	3257	TGGCCACTGTGGCCATCTCTGCCACTCTTTCTCTCTACGCTGGGTTTTCAGAGCCTGTATG	3316
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Qy	3737	CTCCCTGGAGGCTGCCACATGTGCAGCTCAGCCCCCTTGGCTCAGGGGGGGCAGATCG	3796
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Qy	3857	CTTCAAGATCACGACGAGAGAAGTGGGCATCTTTGGCAGGACCCGGGGCAGGAAAGT	3916
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Qy	4157	GCCTCCCGCCAGCTGCAGTACAAGTGTGCTGACCGGCGAGGACCTGAGCGTGGGCC	4216
Db	4436	CCCTTCTTGACAAGCTAGACCATGAATGTGCAGAAGCGGGGAGAACCTCAGTGTGCGGC	4495
Qy	4217	AGAAACAGCTCTGTGCTGCGCACGTCGCCCTTCTCTCGGAAGACCCAGATCTCATCTCTGG	4276

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QY 900 GAAGGCATCTGCGAGGTGTTCAATCTACCTTCCTCTGGGACCCCTCAGCCTCATCAT 959
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KEYWORDS	GI:7221086		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 5011)		
TITLE	Daeley, R.G. and Cole, S.P.C.		
JOURNAL	Methods for conferring multidrug resistance on a cell		
FEATURES	Patent: US 5891724-A 1 06-APR-1999;		
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AR093439 LOCUS 5011 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6001563.
ACCESSION AR093439
VERSION AR093439.1 GI:10020188

KEYWORDS

Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 5011)

AUTHORS Deeley R.G. and Cole, S.P.C.

TITLE Methods for identifying chemosensitizers

JOURNAL Patent: US 6001563-A 14-DEC-1999;

FEATURES Location/Qualifiers

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/organism="unknown"

BASE COUNT 1064 a 1497 c 1394 g 1056 t

ORIGIN

Query Match 27.1%; Score 1222.8; DB 6; Length 5011;
Best Local Similarity 55.7%; Pred. No. 2.3e-220;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;

QY 36 GGCTGGACACGAGAGCTGAACCTGCCGCCACGAGCGCTGCTGAGCGCTGCTTCT 95
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QY 96 GAGAACAGCAGGGGTCTGGGTACCCGCCATGTACCTCTGGTCTTGGTCCCATCTACCT 155
Db 297 GAACAGGCTCTGCTGGGTGCTTGTGTTTACCTCTGGGCTGTTTCCCTTCTACTT 356
QY 156 CCTCTTCATCCACCATGCGCGGGGTACCTCCGGATGTCGCCACTCTTCAAAAGCCAA 215
Db 357 CCTCTATCTCTCCGACATGACCGAGGTACATTCAGATGACACCTCTCAACAAACCAA 416
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QY 1140 GTTCGCTGCGCCCATCACTGGCTGTGTACAGAAAGGCTCTGGCTCTGTCCAGCGGCTC 1199
Db 1377 GATCAAGACCGCTGTCTATGGGGCTGTCTATCGGAAGCCCTGTGTATCAACCATTCAGC 1436
QY 1200 CAGAAAGCCAGTGGCTGGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGACGCGCT 1259
Db 1437 CAGAAAATCTCCACGGTGGGAGATTTGCAACCTCATGTCTGTGGACGCTCAGAGGTT 1496
QY 1260 GACCGAGAGGCTCTTACCTCAACGGGCTGTGGTGCCTCTCTGTGTGGATCTGTGCTG 1319
Db 1497 CATGGACTTGGCCACCGTACATTAACATGATCTGGTACGCCCCCTGCAAGTCACTCTGC 1556
QY 1320 CTTCGCTATCTCTGGCAGCTCTCTGGGCGCTCCGCGCTCACCTGCTGCTGTCTCTCT 1379
Db 1557 TCTCTACTCTCTGGCTGAATCTGGCCCTTCGGTCTGGCTGGAGTGGGGTGTGTT 1616
QY 1380 GAGCCTCTCTCTCTGAATTTCTCAATCTCCAAAGAAAGAACCAACCATCAGGAGGAGCA 1439
Db 1617 CCTATGTTGGCCGCTCAATCTGTGATGGGATGAAGACCAAGACGTATCAGGTGGGCCA 1676
QY 1440 AATGAGCAGAGGACTCAGGCGACGGCTCACGAGCTCTATCTCTCAGGAACCTCGAAGAC 1499
Db 1677 CATGAAGAGCAAGAGCAATCGGATCAAGCTGATGAACGAAATTTCTCAATGGGATCAAGT 1736
QY 1500 CATCAAGTTCATGGCTGGGAGGAGCTTTCTTGGACAGAGTCTCTGGCATTCGAGGCCA 1559
Db 1737 GCTAAAGCTTTATGCTGGGAGCTGGCATTCAGGACCAAGGCTGTGGCCATCAGGACGA 1796
QY 1560 GGAGCTGGGCGCTTGGGACCTCCGCGCTCTCTCTCTGTGTGCTGTGCTGTGCTTCCA 1619

Db 1797 GGAGCTGAAGTGTCTGAAGAACTCTCCCTACCTGTACAGCCGTGGGACACCTTCACCTGGGT 1856
Qy 1620 AGTGTCTACATTTCTGGTGGCACTGGTGGTGTGTCTGTCCACACTCTGTGTGGCCGGAGAA 1679
Db 1857 CTGCACGGCCCTTCTGTGTGGCCCTTGTGCACATTTGCCGTCTACGTGACCATTTGACGAGAA 1916
Qy 1680 TGCTA---TGATGACAGAGAAGCCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 1736
Db 1917 CAACATCTGTGATGCCACAGACGCTCTGTCTTTTGGCTTGTTCACATCTCCGGTT 1976
Qy 1737 GCGCCAGGCTTTCTTCCTCCATCCACTCCCTGTCACAGGCCCGGGTCTCCTTGA 1796
Db 1977 TCCCTGAACATTTCCCCATGGTCATCAGCAGCATGTCGAGGAGTGTCTCCCTCAA 2036
Qy 1797 CGGTCTGTCTACCTTCTCTGCTGGAAGAAGTGTGACCTGTGTCTGATCAAGTTC 1856
Db 2037 ACGCTGAGGATCTTCTCTCCATGAGAGCTGGAACCTGACAGCATCGAGCGACGGCC 2096
Qy 1857 CTCCTGGAAGCGCTCGCGGAGGATTTGATCACCATACACATGACAGTTCGGCTGTGTC 1916
Db 2097 TGTCAAAGACGGGGGACGAAACAGCATCACCGTGAGGAATGCCACATTCACCTGGCC 2156
Qy 1917 CCAGAAAGCCCTCCCTCCCTCCACAGAAATAAACCCTACGCTGCCCCAGGGGTCTGCT 1976
Db 2157 CAGGACGACCCCTCCACACTGAATGGCATCACTTCTCCATCCCCGAAGTGTCTTGGT 2216
Qy 1977 GGCTGTGTCTGGTCCAGTGGGGGAGGAAGTCTCTCCCTGTCTCGCCCTCTTGGGGA 2036
Db 2217 GGCGGTGTGGCCAGGTGGGTGCGGAAAGTTGTCTCCCTGCTCTCAGCCCTTGGCTGA 2276
Qy 2037 GCTGTCAAAGTGTGAGGGTTCGTGAGCATCGAGGTGCTGTGGCTACGTGCCCCAGGA 2096
Db 2277 GATGCAAAAGTGGAGGGGACGTGGTATCAAGGGTCTCCGTGGCTATGTGCCACAGCA 2336
Qy 2097 GGCCTGGTGTGAGAACACCTCTGTGTGTAGAGAAATGTGTCTCGGACGAGCTGGACCC 2156
Db 2337 GGCCTGGATTCAGAAATGATTTCTCCGAGAAACATCCTTTTGGATGTGAGCTGGAGGA 2396
Qy 2157 ACCCTGGCTGGAGAGTACTAGAAAGCTGTGCCCTGCGAGCAGATGTGACAGCTTCCC 2216
Db 2397 ACCATATTACAGTCCGTGTATACAGGCTGTGCCCTCTCCACAGACCTGGAAATCCTGCC 2456
Qy 2217 TGAGGAATCCACATTTCAATTTGGGAGCAGGCGATGATCTCTCCGGAGGCCAGAGCA 2276
Db 2457 CAGTGGGATGGGACAGAGATTTGGCGGAAAGGGCGTGAACCTGTCTGGGGACAGAGCA 2516
Qy 2277 GCGGCTGAGCTGCGCGGGCTGTATACAGAAAGGACGCTGTGTACCTGTGGATGACCC 2336
Db 2517 GCGGCTGAGCTGCGCGGGCGGTACTCCAGCGCTGACATTTACCTTCTCGATGATCC 2576
Qy 2337 CCTGGCGCCCTTGATGCCACGTTGGCCAGCATGTCTTCAACAGAGTCAATTTGGGCTGG 2396
Db 2577 CCTCTACAGATGATGCCATGTGGGAAACACATCTTTGAAATGTGATTTGGCCCAA 2636
Qy 2397 TGGCTACTCCAGGAACACACAGGATTCGTGTCGACGACGATCTCCACATCTCGGCCCA 2456
Db 2637 GGGGATCTGAAGAACAGACGGGATCTTGGTCAGACAGCATGAGTACTTGGCGCA 2696
Qy 2457 GGCTGATTTGATCATAGTGTGGCAATGGGCCATCGACAGATGGTTCCTACCAAGGA 2516
Db 2697 GTTGGAGCTCATCTGTCATGAGTGGCGGAAGATCTGTGATGGGTCTCTACCAAGGA 2756
Qy 2517 GCTTCTCAGAGGAAGGGGCCCTCTGTGTCTTCTGATCAAGCCAGACGACGAGGA 2576
Db 2757 GCTGCTGGCTCAGAGCGGCGCTTCG-CTGAGTTCTCTGCGTACCTATGTCACGACACAGC 2815
Qy 2577 TAGAGGAGAGGAGAAACAGACCTGGGACGACGACCAAGAACCCAGAGGACCTCTGC 2636
Db 2816 AGGAGAGGATGACAGGAGAAAGGGGTACAGGGCGTCCAGGGTCCAGGGAAGGAACAA 2875
Qy 2637 AGGAGAGGCGCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTCAGAGAG- 2691
Db 2876 AGCAATGGAGATGGCATCTGCTGTCACGACGACAGTGTGAGGGAAGCAACTGCAGAGACG 2935

Qy 2692 -----GACCGTACCACCTTCAGAGGCCAGCA-- 2716
Db 2936 TCAGCAGCTCCCTCCTCTATATATGGGAGCATCAGCAGGCAACCAACAGCACCGCAGAAC 2995
Qy 2717 CAGAGTTCCTCTGGATGACCTCTGACAGGCGAGGATGGCCAGCAGGAAAGGACGACATCC 2776
Db 2996 TGCAGAAAGCTGAGGCCAAGAAGGAGGACCTTGGAAAGCTGATGGAGGCTGACAAGGCGC 3055
Qy 2777 AATACGGCAGGTGAAGGCCACAGTCACCTGGCTTACCTGGTGGCCGTGGGACCCGCC 2836
Db 3056 AGACAGGCGAGGTCAAGCTTTCGGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCA 3115
Qy 2837 TCTGCTCTACGACACTTCTCTCTCTGCGCAGCAAGTGGCTCTCTTCTGCCGGGGT 2896
Db 3116 TCTCTCTCTCAGCATCTCTCTTTTCATGTGAACCATGTGTCGCGCTGGCTTCCAAT 3175
Qy 2897 ACTGCTGAGCCTGTGGCGGACGACCTTGCAGTAGGTGGGAGCAGACGACGACGCGC 2956
Db 3176 ATTGGCTCAGCCTCTGGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3235
Qy 2957 TCGTGGCGGATCTTCGGGCTCTCGGCTGTCTCCAAAGCCATTTGGGTGTGTGGCTCCA 3016
Db 3236 TCCGCTGAGCTCTTATGAGCCCTGGGCAATTTCAAGGGATCGCCGTGTGTGGCTACT 3295
Qy 3017 TGGCTGCGGTGCTCTAGTGGGGCGCGGCAATTCAGGTTGTCTTCTTCCAGAGGCTCCTGT 3076
Db 3296 CCATGCGCTGTCCATCGGGGGATCTTGGCTTCCGCTGTCTGACGTGGACCTCTCTG 3355
Qy 3077 GGGATGTGTGGATCTCCCATCAGCTTCTTTGAGCGGACACCATTTGCTACCTCTCTAA 3136
Db 3356 ACAGCATCTCGGCTCACCATGAGCTTCTTTGAGCGGACCCCGAGTGGGACCTGGTGA 3415
Qy 3137 ACCGTTCTCCAAAGAGACAGACAGGTTGAGTGGACATTCAGACAAATCTCCGTCOC 3196
Db 3416 ACCGTTCTCCAAAGAGTGGACAGAGTGGATCTTATCTGCTGGGCGACGCGCA 3475
Qy 3197 TGCTGATGTAGCCCTTGGACTCTCTGAGGTCAGCTTGGTGGGAGTGGGAGTGGGAGTGG 3256
Db 3476 TCATGGGCTCCTGTCAACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3535
Qy 3257 TGGCCACTGTGGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3316
Db 3536 TCGCGCCATCATCATCCGCCCTTGGCCCTACTCTACTTCTTCTGCTGCTGCTGCTGCTGCT 3595
Qy 3317 TGGTGTAGTCTCATCGAGTGTGAGCTTGGAGTGTGAGCTGAGCTGCTGCTGCTGCTGCTGCT 3376
Db 3596 TGGCTTCTCCCGCAGCTGAAGCGCTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGG 3655
Qy 3377 ACATGGCTGAGAGCTTCCAGGCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3436
Db 3656 ATTTCAAGGACCTTGTGGGGTACCGTCTATTCGAGCCTTCGAGGAGCAGGAGCGCT 3715
Qy 3437 TTGTGGCTCAGAAATGCTCCGCTAGATGAAGCAGAGGATCAGTTTCCCGGACTGG 3496
Db 3716 TCATCCACAGAGTGACCTGAAGTGGAGAGAGACAGAGGCTTATTAACCCAGCATCG 3775
Qy 3497 TGGCTGACAGTGTGGCGCCAAATGTGGAGTCTCTGGGAATGGCTGTGTGGTGGAG 3556
Db 3776 TGGCAACAGTGTGGCGCTGGCGCTGGAGTGTGTGGCAACTGCATCTGCTGTTG 3835
Qy 3557 CCGCAGCTGTGCTGTGAGCAAGCCACCTCAGTGTGGCTCTGCTGCTGCTGCTGCTGCTGCT 3616
Db 3836 CTGGCTTGTGGCTGATCTCCAGGACAGCTCAGTGTGGCTTGTGGGCTCTCTG 3895
Qy 3617 TCTGCTGCTCCTCAGGTGACACACATGCTGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 3676
Db 3896 TGCTTACTCATTCAGGTCAACAGTACTTGAAGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 3955
Qy 3677 TAGAGACAGATCTGTGATGTGGGAGTGTGAGGATATGCTTGGAGCCCGCAGGAGG 3736
Db 3956 TGGAAACCAACATCTGTGGCGCTGGAGGCTCAAGGAGTATTCAGAGACTGAGAGGAGG 4015

Db	1257	TGACAGGAAGGCCACAGATGCGAGGGTACTTCTACACGCTGCTGCTTTGTCTACATGC	1316
QY	1080	CTGCCTGCAAAAGCGCTGTTTGAGCAGCAAGAACATGTACAGAGCTCAAGGTGCGCGAGATGAG	1139
Db	1317	CTGCCTGCAGACCCCTGCTGCTGCACCACTACTTCCACATCTGCTTCGTCACTGGCATGAG	1376
QY	1140	GTTCGGTCCGGCATCATCTGGGCTTGGTGTACAGAAAGTCTCTGCTCTGTCCAGCGGCTC	1199
Db	1377	GATCAAGACCGCTCATTTGGGGCTGTCTATCGGAAGCCCTGGTGATCACCAATTCAGC	1436
QY	1200	CAGAAAGGCCAGTGGGTGGTGATCTGGTCAATCTGGTGTCCGTGAGACGTGCAGCGGCT	1259
Db	1437	CAGAAATCCTCCACGGTGGGAGATTGTCAAOCTCATGTCTGTGACGCTCAGAGGTT	1496
QY	1260	GACGAGAGCGTCTCTACTCTCAACGGCTGTGGCTGCTCTCTCTGGATCTGGTGTGCTG	1319
Db	1497	CATGGACTGGCCACGTACATTTAAATGATGTGGTCAACCCCTGCAAGTCATCTCTTGC	1556
QY	1320	CTTTCGTCTATCTTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCCT	1379
Db	1557	TCCTACCTCCCTGTGSCCTGAATCTGGGCCCTTCCGTCTGCTGAGTGGCGGTGATGGT	1616
QY	1380	GAGCCTCTCCCTCTGAAATTTCTTCAATCCAGAAAGAACCAACCATCAGGAGGAGCA	1439
Db	1617	CCTCATGGTGGCCGTCAATGTCTGTATGGCATGAAGACCAAGACGTATCAGGTGGGCCA	1676
QY	1440	AATGAGGCAGAGGACTCACGGGCACGGCTCACAGCTCTATCTCTCAGGAACCTCGAAGC	1499
Db	1677	CATGNAGACCAAGACAAATCGGATCAAGCTGATGAACGAAATTTCTTAATGGGATCAAAGT	1736
QY	1500	CATCAAGTTCCATGGCTGGGAGGGAGCCCTTCTTGACAGAGTCTCTGGGCATCCGAGGCCA	1559
Db	1737	GCTAAGCTTTATGCTGGGACCTGGCATTTCAAGGACAAGTGTCTGCCCATCAGCGAGGA	1796
QY	1560	GGAGCTGGCGGCTTTCGGGACCTCCGGGCTCCTCTTCTCTGTGTGCTGTGCTTCTTCCA	1619
Db	1797	GGAGCTGAAGGTGCTGAAGAAAGTCTGGCCTACTGCTGACGCCGTGGGCACCTTCACCTGGGT	1856
QY	1620	AGTGTCTACATTTCTGGTGGCACTGGTGGTGTGCTGTGCACACTCTGGTGGCCGAGAA	1679
Db	1857	CTGCAGCCCTTTCTGGTGGCCCTTGTGCACATTTTGGCCTCTACGTGACCATTTGACGAGAA	1916
QY	1680	TGCTA---TGAATGACAGAAAGCCCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAA	1736
Db	1917	CAACATCCTGGATGCCACAGACGCTTCTGTGCTTTGGSCCTTGTTCACATCCTCCGCTT	1976
QY	1737	GGCCAGGCTTTCCTGCCCTTCTCATCACTCCCTCTGTCCAGGCCGGGTGCTTCTTGA	1796
Db	1977	TCGCCCTCAACATCTCCCATGGTCAATCAGCAGCATCGTGCAGGCGAGTGTCTCCCTCAA	2036
QY	1797	CCGCTGGTCACTTCTCTGCTCGAGAAAGTTGACCCCTGGTGTGTGAGACTCAAGTTC	1856
Db	2037	ACGCTTGAGATCTTTTCTCTCCATGAGAGCTGGAACCTCAGACATCTCAGGACGCGCC	2096
QY	1857	CTCTGGAAGCGCTGCGGGAAGGATTTGATCACCATACACAGTGCACACTTCGCTCTGGTC	1916
Db	2097	TGTCAAAGACGGCGGGGACCAACAGCATCACCGTGAGGAATGCCATTCACCTGSGC	2156
QY	1917	CCAGGAAAGCCCTTCCCTTGCCCTCCACAGAAATAACCTCACGGTGGCCCGCAGGGCTGTCTGCT	1976
Db	2157	CAGGAGCGACCTCCCCACACTCAATGGGATCACCTTCTTCCATCCCGAAGGTGCTTTGGT	2216
QY	1977	GGCTGTGTGCGGTCCAGTGGGGCAGGAGTCTCCTCCTGCTGTGCTCCGCCCTCTTGGGGA	2036
Db	2217	GGCGGTGTGGGCAGGTGGGGCTGCGGAAAGTTGTCCCTGCTCTCAGCCCTCTTTGGCTGA	2276
QY	2037	GCTGTCAAAAGGTGGAGGGTTCTGTGAGCATCAGGSGGTGCTGTGCTGTACGTGCCACAGGA	2096
Db	2277	GATGGACAAGTGGAGGGCAGCTGGCTATCAAGGGCTCCGTGGCTTATGTGCCACAGCA	2336
QY	2097	GGCCTGGGTGCAGAACCCCTCTGTGGTAGAAATGTGTGCTTTCGGGACGAGAGCTGGACC	2156

